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(54) Title: METHODS OF DIAGNOSIS OF ANGIOGENESIS, COMPOSITIONS AND METHODS OF SCREENING FOR AN-GIOGENESIS MODULATORS

(57) Abstract: Described herein are methods and compositions that can be used for diagnosis and treatment of angiogenic phenotypes and angiogenesis-associated diseases. Also described herein are methods that can be used to identify modulators of angiogenstype.

METHODS OF DIAGNOSIS OF ANGIOGENESIS, COMPOSITIONS AND METHODS OF SCREENING FOR ANGIOGENESIS MODULATORS

CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims priority to USSN 09/784,356, filed February 14 2001;

USSN 09/791,390, filed February 22, 2001; USSN 60/285,475, filed April 19, 2001, USSN 60/310,025, filed August 3, 2001, and USSN 60/334,244, filed November 29, 2001, each of which is herein incorporated by reference in its entirety.

FIELD OF THE INVENTION

The invention relates to the identification of nucleic acid and protein expression profiles and nucleic acids, products, and antibodies thereto that are involved in angiogenesis; and to the use of such expression profiles and compositions in diagnosis and therapy of angiogenesis. The invention further relates to methods for identifying and using agents and/or targets that modulate angiogenesis.

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BACKGROUND OF THE INVENTION

Both vasculogenesis, the development of an interactive vascular system comprising arteries and veins, and angiogenesis, the generation of new blood vessels, play a role in embryonic development. In contrast, angiogenesis is limited in a normal adult to the placenta, ovary, endometrium and sites of wound healing. However, angiogenesis, or its absence, plays an important role in the maintenance of a variety of pathological states. Some of these states are characterized by neovascularization, e.g., cancer, diabetic retinopathy, glaucoma, and age related macular degeneration. Others, e.g., stoke, infertility, heart disease, ulcers, and seleroderma, are diseases of angiogenic insufficiency.

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Angiogenesis has a number of stages (see, e.g., Folkman, J.Natl Cancer Inst. 82:4-6, 1990; Firestein, J Clin Invest. 103:3-4, 1999; Koch, Arthritis Rheum. 41:951-62, 1998; Carter, Oncologist 5(Suppl 1):51-4, 2000; Browder et al., Cancer Res. 60:1878-86, 2000; and Zhu and Witte, Invest New Drugs 17:195-212, 1999). The early stages of angiogenesis

include endothelial cell protease production, migration of cells, and proliferation. The early stages also appear to require some growth factors, with VEGF, TGF- α , angiostatin, and selected chemokines all putatively playing a role. Later stages of angiogenesis include population of the vessels with mural cells (pericytes or smooth muscle cells), basement membrane production, and the induction of vessel bed specializations. The final stages of vessel formation include what is known as "remodeling", wherein a forming vasculature becomes a stable, mature vessel bed. Thus, the process is highly dynamic, often requiring coordinated spatial and temporal waves of gene expression.

Conversely, the complex process may be subject to disruption by interfering with one or more critical steps. Thus, the lack of understanding of the dynamics of angiogenesis prevents therapeutic intervention in serious diseases such as those indicated. It is an object of the invention to provide methods that can be used to screen compounds for the ability to modulate angiogenesis. Additionally, it is an object to provide molecular targets for therapeutic intervention in disease states which either have an undesirable excess or a deficit in angiogenesis. The present invention provides solutions to both.

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SUMMARY OF THE INVENTION

The present invention provides compositions and methods for detecting or modulating angiogenesis associated sequences.

In one aspect, the invention provides a method of detecting an angiogenesisassociated transcript in a cell in a patient, the method comprising contacting a biological sample from the patient with a polynucleotide that selectively hybridized to a sequence at least 80% identical to a sequence as shown in Tables 1-8. In one embodiment, the biological sample is a tissue sample. In another embodiment, the biological sample comprises isolated nucleic acids, which are often mRNA.

In another embodiment, the method further comprises the step of amplifying nucleic acids before the step of contacting the biological sample with the polynucleotide. Often, the polynucleotide comprises a sequence as shown in Tables 1-8. The polynucleotide can be labeled, for example, with a fluorescent label and can be immobilized on a solid surface.

In other embodiments the patient is undergoing a therapeutic regimen to treat a disease associated with angiogenesis or the patient is suspected of having an angiogenesisassociated disorder.

In another aspect, the invention comprises an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-8. The nucleic acid molecule can be labeled, for example, with a fluorescent label.

In other aspects, the invention provides an expression vector comprising an isolated nucleic acid molecule consisting of a polynucleotide sequence as shown in Tables 1-8 or a host cell comprising the expression vector.

In another embodiment, the isolated nucleic acid molecule encodes a polypeptide having an amino acid sequence as shown in Table 8.

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In another aspect, the invention provides an isolated polypeptide which is encoded by a nucleic acid molecule having polynucleotide sequence as shown in Tables 1-8. In one embodiment, the isolated polypeptide has an amino acid sequence as shown in Table 8.

In another embodiment, the invention provides an antibody that specifically binds a polypeptide that has an amino acid sequence as shown in Table 8 or which is encoded by a nucleotide sequence of Tables 1-8. The antibody can be conjugated or fused to an effector component such as a fluorescent label, a toxin, or a radioisotope. In some embodiments, the antibody is an antibody fragment or a humanized antibody.

In another aspect, the invention provides a method of detecting a cell undergoing angiogenesis in a biological sample from a patient, the method comprising contacting the biological sample with an antibody that specifically binds to a polypeptide that has an amino acid sequence as shown in Table 8 or which is encoded by a nucleotide sequence of Tables 1-8. In some embodiments, the antibody is further conjugated or fused to an effector component, for example, a fluorescent label.

In another embodiment, the invention provides a method of detecting antibodies specific to angiogenesis in a patient, the method comprising contacting a biological sample from the patient with a polypeptide which is encoded by a nucleotide sequence of Tables 1-8.

The invention also provides a method of identifying a compound that modulates the activity of an angiogenesis-associated polypeptide, the method comprising the steps of: (i) contacting the compound with a polypeptide that comprises at least 80% identity to an amino acid sequence as shown in Table 8 or which is encoded by a nucleotide sequence of Tables 1-8; and (ii) detecting an increase or a decrease in the activity of the polypeptide. In one embodiment, the polypeptide has an amino acid sequence as shown in Table 8 or is a

polypeptide encoded by a nucleotide sequence of Tables 1-8. In another embodiment, the polypeptide is expressed in a cell.

The invention also provides a method of identifying a compound that modulates angiogenesis, the method comprising steps of: (i) contacting the compound with a cell undergoing angiogenesis; and (ii) detecting an increase or a decrease in the expression of a polypeptide sequence as shown in Table 8 or a polypeptide which is encoded by a nucleotide sequence of Tables 1-8. In one embodiment, the detecting step comprises hybridizing a nucleic acid sample from the cell with a polynucleotide that selectively hybridizes to a sequence at least 80% identical to a sequence as shown in Tables 1-8. In another embodiment, the method further comprises detecting an increase or decrease in the expression of a second sequence as shown in Table 8 or a polypeptide which is encoded by a nucleotide sequence of Tables 1-8.

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In another embodiment, the invention provides a method of inhibiting angiogenesis in a cell that expresses a polypeptide at least 80% identical to a sequence as shown in Table 8 or which is 80% identical to a polypeptide encoded by a nucleotide sequence of Tables 1-8, the method comprising the step of contacting the cell with a therapeutically effective amount of an inhibitor of the polypeptide. In one embodiment, the polypeptide has an amino acid sequence shown in Table 8 or is a polypeptide which is encoded by a nucleotide sequence of Tables 1-8. In another embodiment, the inhibitor is an antibody.

In other embodiments, the invention provides a method of activating angiogenesis in a cell that expresses a polypeptide at least 80% identical to a sequence as shown in Table 8 or at least 80% identical to a polypeptide which is encoded by a nucleotide sequence of Tables 1-8, the method comprising the step of contacting the cell with a therapeutically effective amount of an activator of the polypeptide. In one embodiment, the polypeptide has an amino acid sequence shown in Table 8 or is a polypeptide which is encoded by a nucleotide sequence of Tables 1-8.

Other aspects of the invention will become apparent to the skilled artisan by the following description of the invention.

Tables 1-8 provide nucleotide sequence of genes that exhibit changes in expression levels as a function of time in tissue undergoing angiogenesis compared to tissue that is not

DESCRIPTION OF THE SPECIFIC EMBODIMENTS

In accordance with the objects outlined above, the present invention provides novel methods for diagnosis and treatment of disorders associated with angiogenesis (sometimes referred to herein as angiogenesis disorders or AD), as well as methods for screening for compositions which modulate angiogenesis. By "disorder associated with angiogenesis" or "disease associated with angiogenesis" herein is meant a disease state which is marked by either an excess or a deficit of blood vessel development. Angiogenesis disorders asociated with increased angiogenesis include, but are not limited to, cancer and proliferative diabetic retinopathy. Pathological states for which it may be desirable to increase angiogenesis include stroke, heart disease, infertility, ulcers, wound healing, ischemia, and scleradoma. Solid tumors typically require angiogenesis to support or sustain growth, e.g., breast, colon, lung, brain, bladder, and prostate tumors. Other AD include, e.g., arthritis, inflammatory bowel disease, diabetis retinopathy, macular degeneration, atherosclerosis, and psoriasis. Also provided are methods for treating AD.

15 Definitions

The term "angiogenesis protein" or "angiogenesis polynucleotide" refers to nucleic acid and polypeptide polymorphic variants, alleles, mutants, and interspecies homologs that: (1) have an amino acid sequence that has greater than about 60% amino acid sequence identity, 65%, 70%, 75%, 80%, 85%, 90%, preferably 91%, 92%, 93%, 94%, 95%, 20 96%, 97%, 98% or 99% or greater amino acid sequence identity, preferably over a region of over a region of at least about 25, 50, 100, 200, 500, 1000, or more amino acids, to an angiogenesis protein sequence of Table 8: (2) bind to antibodies, e.g., polyclonal antibodies. raised against an immunogen comprising an amino acid sequence of Table 8, and conservatively modified variants thereof; (3) specifically hybridize under stringent 25 hybridization conditions to an anti-sense strand corresponding to a nucleic acid sequence of Tables 1-8 and conservatively modified variants thereof: (4) have a nucleic acid sequence that has greater than about 95%, preferably greater than about 96%, 97%, 98%, 99%, or higher nucleotide sequence identity, preferably over a region of at least about 25, 50, 100, 200, 500, 1000, or more nucleotides, to a sense sequence corresponding to one set out in 30 Tables 1-8. A polynucleotide or polypeptide sequence is typically from a mammal including, but not limited to, primate, e.g., human; rodent, e.g., rat, mouse, hamster; cow, pig. horse, sheep, or any mammal. An "angiogenesis polypeptide" and an "angiogenesis polynucleotide," include both naturally occurring or recombinant.

A "full length" angiogenesis protein or nucleic acid refers to an agiogenesis polypeptide or polynucleotide sequence, or a variant thereof, that contains all of the elements normally contained in one or more naturally occurring, wild type angiogenesis polynucleotide or polypeptide sequences. The "full length" may be prior to, or after, various stages of post-translation processing.

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"Biological sample" as used herein is a sample of biological tissue or fluid that contains nucleic acids or polypeptides, e.g., of an angiogenic protein. Such samples include, but are not limited to, tissue isolated from primates, e.g., humans, or rodents, e.g., mice, and rats. Biological samples may also include sections of tissues such as biopsy and autopsy samples, and frozen sections taken for histologic purposes. A biological sample is typically obtained from a eukaryotic organism, most preferably a mammal such as a primate e.g., chimpanzee or human; cow; dog; cat; a rodent, e.g., guinea pig, rat, mouse; rabbit; or a bird; reptile; or fish.

"Providing a biological sample" means to obtain a biological sample for use in methods described in this invention. Most often, this will be done by removing a sample of cells from an animal, but can also be accomplished by using previously isolated cells (e.g., isolated by another person, at another time, and/or for another purpose), or by performing the methods of the invention in vivo. Archival tissues, having treatment or outcome histroy, will be particularly useful.

The terms "identical" or percent "identity," in the context of two or more nucleic acids or polypeptide sequences, refer to two or more sequences or subsequences that are the same or have a specified percentage of amino acid residues or nucleotides that are the same (i.e., about 70% identity, preferably 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or higher identity over a specified region (e.g., SEQ ID NOS:1-229), when compared and aligned for maximum correspondence over a comparison window or designated region) as measured using a BLAST or BLAST 2.0 sequence comparison algorithms with default parameters described below, or by manual alignment and visual inspection (see, e.g., NCBI web site http://www.ncbi.nlm.nih.gov/BLAST/ or the like). Such sequences are then said to be "substantially identical." This definition also refers to, or may be applied to, the compliment of a test sequence. The definition also includes sequences that have deletions and/or additions, as well as those that have substitutions. As described below, the preferred algorithms can account for gaps and the like. Preferably, identity exists over a region that is at least about 25 amino acids or nucleotides in length, or more preferably over a region that is 50-100 amino acids or nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algorithm program parameters are designated. Preferably, default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, Adv. Appl. Math. 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, J. Mol. Biol. 48:443 (1970), by the search for similarity method of Pearson & Lipman, Proc. Nat'l. Acad. Sci. USA 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, WI), or by manual alignment and visual inspection (see, e.g., Current Protocols in Molecular Biology (Ausubel et al., eds. 1995 supplement)).

A preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., Nuc. Acids Res. 25:3389-3402 (1977) and Altschul et al., J. Mol. Biol. 215:403-410 (1990), respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gow/). This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as

far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always > 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the 5 word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) of 10, M=5, N=-4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, Proc. Natl. Acad. Sci. USA 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.

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The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, Proc. Nat'l. Acad. Sci. USA 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001.

An indication that two nucleic acid sequences or polypeptides are substantially identical is that the polypeptide encoded by the first nucleic acid is immunologically cross reactive with the antibodies raised against the polypeptide encoded by the second nucleic acid, as described below. Thus, a polypeptide is typically substantially identical to a second polypeptide, for example, where the two peptides differ only by conservative substitutions. Another indication that two nucleic acid sequences are substantially identical is that the two molecules or their complements hybridize to each other under stringent conditions, as described below. Yet another indication that two nucleic acid sequences are substantially identical is that the same primers can be used to amplify the sequences.

A "host cell" is a naturally occurring cell or a transformed cell that contains an expression vector and supports the replication or expression of the expression vector. Host cells may be cultured cells, explants, cells in vivo, and the like. Host cells may be

prokaryotic cells such as *E. coli*, or eukaryotic cells such as yeast, insect, amphibian, or mammalian cells such as CHO, HeLa, and the like (see, *e.g.*, the American Type Culture Collection catalog or web site, www.atcc.org).

The terms "polypeptide," "peptide" and "protein" are used interchangeably herein to refer to a polymer of amino acid residues. The terms apply to amino acid polymers in which one or more amino acid residue is an artificial chemical mimetic of a corresponding naturally occurring amino acid, as well as to naturally occurring amino acid polymers and non-naturally occurring amino acid polymer.

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The term "amino acid" refers to naturally occurring and synthetic amino acids, as well as amino acid analogs and amino acid mimetics that function in a mamer similar to the naturally occurring amino acids. Naturally occurring amino acids are those encoded by the genetic code, as well as those amino acids that are later modified, e.g., hydroxyproline, γ-carboxyglutamate, and O-phosphoserine. Amino acid analogs refers to compounds that have the same basic chemical structure as a naturally occurring amino acid, i.e., an a carbon that is bound to a hydrogen, a carboxyl group, an amino group, and an R group, e.g., homoserine, norleucine, methionine sulfoxide, methionine methyl sulfonium. Such analogs have modified R groups (e.g., norleucine) or modified peptide backbones, but retain the same basic chemical structure as a naturally occurring amino acid. Amino acid mimetics refers to chemical compounds that have a structure that is different from the general chemical structure of an amino acid, but that functions in a manner similar to a naturally occurring amino acid.

Amino acids may be referred to herein by either their commonly known three letter symbols or by the one-letter symbols recommended by the IUPAC-IUB Biochemical Nomenclature Commission. Nucleotides, likewise, may be referred to by their commonly accepted single-letter codes.

"Conservatively modified variants" applies to both amino acid and nucleic acid sequences. With respect to particular nucleic acid sequences, conservatively modified variants refers to those nucleic acids which encode identical or essentially identical amino acid sequences, or where the nucleic acid does not encode an amino acid sequence, to essentially identical sequences. Because of the degeneracy of the genetic code, a large number of functionally identical nucleic acids encode any given protein. For instance, the codons GCA, GCC, GCG and GCU all encode the amino acid alanine. Thus, at every position where an alanine is specified by a codon, the codon can be altered to any of the corresponding codons described without altering the encoded polypeptide. Such nucleic acid variations are "silent variations." which are one species of conservatively modified

variations. Every nucleic acid sequence herein which encodes a polypeptide also describes every possible silent variation of the nucleic acid. One of skill will recognize that each codon in a nucleic acid (except AUG, which is ordinarily the only codon for methionine, and TGG, which is ordinarily the only codon for tryptophan) can be modified to yield a functionally identical molecule. Accordingly, each silent variation of a nucleic acid which encodes a polypeptide is implicit in each described sequence with respect to the expression product, but not with respect to actual probe sequences.

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As to amino acid sequences, one of skill will recognize that individual substitutions, deletions or additions to a nucleic acid, peptide, polypeptide, or protein sequence which alters, adds or deletes a single amino acid or a small percentage of amino acids in the encoded sequence is a "conservatively modified variant" where the alteration results in the substitution of an amino acid with a chemically similar amino acid.

Conservative substitution tables providing functionally similar amino acids are well known in the art. Such conservatively modified variants are in addition to and do not exclude polymorphic variants, interspecies homologs, and alleles of the invention.

The following eight groups each contain amino acids that are conservative substitutions for one another:1) Alanine (A), Glycine (G); 2) Aspartic acid (D), Glutamic acid (E); 3) Asparagine (N), Glutamine (Q); 4) Arginine (R), Lysine (K); 5) Isoleucine (I), Leucine (L), Methionine (M), Valine (V); 6) Phenylalanine (F), Tyrosine (Y), Tryptophan (W); 7) Serine (S), Threonine (T); and 8) Cysteine (C), Methionine (M) (see, e.g., Creighton, Proteins (1984)).

Macromolecular structures such as polypeptide structures can be described in terms of various levels of organization. For a general discussion of this organization, see, e.g., Alberts et al., Molecular Biology of the Cell (3^{rd} ed., 1994) and Cantor and Schimmel, Biophysical Chemistry Part I: The Conformation of Biological Macromolecules (1980). "Primary structure" refers to the amino acid sequence of a particular peptide. "Secondary structure" refers to locally ordered, three dimensional structures within a polypeptide. These structures are commonly known as domains. Domains are portions of a polypeptide that form a compact unit of the polypeptide and are typically 25 to approximately 500 amino acids long. Typical domains are made up of sections of lesser organization such as stretches of β -sheet and α -helices. "Tertiary structure" refers to the complete three dimensional structure of a polypeptide monomer. "Quaternary structure" refers to the three dimensional

structure formed, usually by the noncovalent association of independent tertiary units.

Anisotropic terms are also known as energy terms.

A "label" or a "detectable moiety" is a composition detectable by spectroscopic, photochemical, biochemical, immunochemical, chemical, or other physical means. For example, useful labels include ³²P, fluorescent dyes, electron-dense reagents, enzymes (e.g., as commonly used in an ELISA), biotin, digoxigenin, or haptens and proteins which can be made detectable, e.g., by incorporating a radiolabel into the peptide or used to detect antibodies specifically reactive with the pentide.

An "effector" or "effector moiety" or "effector component" is a molecule that is bound (or linked, or conjugated), either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds, to an antibody. The "effector" can be a variety of molecules including, for example, detection moieties including radioactive compounds, fluroescent compounds, an enzyme or substrate, tags such as epitope tags, a toxin; a chemotherapeutic agent; a lipase; an antibiotic; or a radioisotope emitting "hard" e.g., beta radiation.

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A "labeled nucleic acid probe or oligonucleotide" is one that is bound, either covalently, through a linker or a chemical bond, or noncovalently, through ionic, van der Waals, electrostatic, or hydrogen bonds to a label such that the presence of the probe may be detected by detecting the presence of the label bound to the probe. Alternatively, method using high affinity interactions may achieve the same results where one of a pair of binding partners binds to the other, e.g., biotin, streptavidin.

As used herein a "nucleic acid probe or oligonucleotide" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e., A, G, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in a probe may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, for example, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages. It will be understood by one of skill in the art that probes may bind target sequences lacking complete complementarity with the probe sequence depending upon the stringency of the hybridization conditions. The probes are preferably directly labeled as with biotin to which a streptavidin

complex may later bind. By assaying for the presence or absence of the probe, one can detect the presence or absence of the select sequence or subsequence.

The term "recombinant" when used with reference, e.g., to a cell, or nucleic acid, protein, or vector, indicates that the cell, nucleic acid, protein or vector, has been modified by the introduction of a heterologous nucleic acid or protein or the alteration of a native nucleic acid or protein, or that the cell is derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all.

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The term "heterologous" when used with reference to portions of a nucleic acid indicates that the nucleic acid comprises two or more subsequences that are not found in the same relationship to each other in nature. For instance, the nucleic acid is typically recombinantly produced, having two or more sequences from unrelated genes arranged to make a new functional nucleic acid, e.g., a promoter from one source and a coding region from another source. Similarly, a heterologous protein indicates that the protein comprises two or more subsequences that are not found in the same relationship to each other in nature (e.g., a fusion protein).

A "promoter" is defined as an array of nucleic acid control sequences that direct transcription of a nucleic acid. As used herein, a promoter includes necessary nucleic acid sequences near the start site of transcription, such as, in the case of a polymerase II type promoter, a TATA element. A promoter also optionally includes distal enhancer or repressor elements, which can be located as much as several thousand base pairs from the start site of transcription. A "constitutive" promoter is a promoter that is active under most environmental and developmental conditions. An "inducible" promoter is a promoter that is active under environmental or developmental regulation. The term "operably linked" refers to a functional linkage between a nucleic acid expression control sequence (such as a promoter, or array of transcription factor binding sites) and a second nucleic acid sequence, wherein the expression control sequence directs transcription of the nucleic acid corresponding to the second sequence.

An "expression vector" is a nucleic acid construct, generated recombinantly or synthetically, with a series of specified nucleic acid elements that permit transcription of a particular nucleic acid in a host cell. The expression vector can be part of a plasmid, virus, or nucleic acid fragment. Typically, the expression vector includes a nucleic acid to be transcribed operably linked to a promoter.

The phrase "selectively (or specifically) hybridizes to" refers to the binding, duplexing, or hybridizing of a molecule only to a particular nucleotide sequence under stringent hybridization conditions when that sequence is present in a complex mixture (e.g., total cellular or library DNA or RNA).

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The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, Techniques in Biochemistry and Molecular Biology--Hybridization with Nucleic Probes, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at Tm, 50% of the probes are occupied at equilibrium). Stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion concentration (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes (e.g., 10 to 50 nucleotides) and at least about 60°C for long probes (e.g., greater than 50 nucleotides). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization. Exemplary stringent hybridization conditions can be as following: 50% formamide, 5x SSC, and 1% SDS, incubating at 42°C, or, 5x SSC, 1% SDS, incubating at 65°C, with wash in 0.2x SSC, and 0.1% SDS at 65°C. For PCR, a temperature of about 36°C is typical for low stringency amplification, although annealing temperatures may vary between about 32°C and 48°C depending on primer length. For high stringency PCR amplification, a temperature of about 62°C is typical, although high stringency annealing temperatures can range from about 50°C to about 65°C, depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90°C - 95°C for 30 sec - 2 min., an annealing phase lasting 30 sec. - 2 min., and an extension phase of about 72°C for 1 - 2 min. Protocols and guidelines for low and high stringency amplification

reactions are provided, e.g., in Innis et al. (1990) PCR Protocols, A Guide to Methods and Applications, Academic Press, Inc. N.Y.).

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, for example, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37°C, and a wash in 1X SSC at 45°C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and Current Protocols in Molecular Biology, ed. Ausubel, et al.

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The phrase "functional effects" in the context of assays for testing compounds that modulate activity of an angiogenesis protein includes the determination of a parameter that is indirectly or directly under the influence of the angiogenesis protein, e.g., a functional, physical, or chemical effect, such as the ability to increase or decrease angiogenesis. It includes binding activity, the ability of cells to proliferate, expression in cells undergoing angiogenesis, and other characteristics of angiogenic cells. "Functional effects" include in vitro, in vivo, and ex vivo activities.

By "determining the functional effect" is meant assaying for a compound that increases or decreases a parameter that is indirectly or directly under the influence of an angiogenesis protein sequence, e.g., functional, physical and chemical effects. Such functional effects can be measured by any means known to those skilled in the art, e.g., changes in spectroscopic characteristics (e.g., fluorescence, absorbance, refractive index), hydrodynamic (e.g., shape), chromatographic, or solubility properties for the protein, measuring inducible markers or transcriptional activation of the angiogenesis protein; measuring binding activity or binding assays, e.g. binding to antibodies, and measuring cellular proliferation, particularly endothelial cell proliferation, cell viability, cell division especially of endothelial cells, lumen formation and capillary or vessel growth or formation. Determination of the functional effect of a compound on angiogenesis can also be performed using angiogenesis assays known to those of skill in the art such as an in vitro assays, e.g., in vitro endothelial cell tube formation assays, and other assays such as the chick CAM assay, the mouse corneal assay, and assays that assess vascularization of an implanted tumor. The

functional effects can be evaluated by many means known to those skilled in the art, e.g., mieroscopy for quantitative or qualitative measures of alterations in morphological features, e.g., tube or blood vessel formation, measurement of changes in RNA or protein levels for angiogenesis-associated sequences, measurement of RNA stability, identification of downstream or reporter gene expression (CAT, luciferase, β -gal, GFP and the like), e.g., via chemiluminescence, fluorescence, colorimetric reactions, antibody binding, inducible markers, and ligand binding assays.

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"Inhibitors", "activators", and "modulators" of angiogenic polynucleotide and polypeptide sequences are used to refer to activating, inhibitory, or modulating molecules identified using in vitro and in vivo assays of angiogenic polynucleotide and polypeptide sequences. Inhibitors are compounds that, e.g., bind to, partially or totally block activity, decrease, prevent, delay activation, inactivate, desensitize, or down regulate the activity or expression of angiogenesis proteins, e.g., antagonists. "Activators" are compounds that increase, open, activate, facilitate, enhance activation, sensitize, agonize, or up regulate angiogenesis protein activity. Inhibitors, activators, or modulators also include genetically modified versions of angiogenesis proteins, e.g., versions with altered activity, as well as naturally occurring and synthetic ligands, antagonists, agonists, antibodies, small chemical molecules and the like. Such assays for inhibitors and activators include, e.g., expressing the angiogenic protein in vitro, in cells, or cell membranes, applying putative modulator compounds, and then determining the functional effects on activity, as described above. Activators and inhibitors of angiogenesis can also be identified by incubating angiogenic cells with the test compound and determining increases or decreases in the expression of 1 or more angiogenesis proteins, e.g., 1, 2, 3, 4, 5, 10, 15, 20, 25, 30, 40, 50 or more angiogenesis proteins, such as angiogenesis proteins comprising the sequences set out in Table 8.

Samples or assays comprising angiogenesis proteins that are treated with a potential activator, inhibitor, or modulator are compared to control samples without the inhibitor, activator, or modulator to examine the extent of inhibition. Control samples (untreated with inhibitors) are assigned a relative protein activity value of 100%. Inhibition of a polypeptide is achieved when the activity value relative to the control is about 80%, preferably 50%, more preferably 25-0%. Activation of an angiogenesis polypeptide is achieved when the activity value relative to the control (untreated with activators) is 110%, more preferably 150%, more preferably 200-500% (i.e., two to five fold higher relative to the control), more preferably 1000-3000% higher.

"Antibody" refers to a polypeptide comprising a framework region from an immunoglobulin gene or fragments thereof that specifically binds and recognizes an antigen. The recognized immunoglobulin genes include the kappa, lambda, alpha, gamma, delta, epsilon, and mu constant region genes, as well as the myriad immunoglobulin variable region genes. Light chains are classified as either kappa or lambda. Heavy chains are classified as gamma, mu, alpha, delta, or epsilon, which in turn define the immunoglobulin classes, IgG, IgM, IgA, IgD and IgE, respectively. Typically, the antigen-binding region of an antibody will be most critical in specificity and affinity of binding.

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An exemplary immunoglobulin (antibody) structural unit comprises a tetramer. Each tetramer is composed of two identical pairs of polypeptide chains, each pair having one "light" (about 25 kD) and one "heavy" chain (about 50-70 kD). The N-terminus of each chain defines a variable region of about 100 to 110 or more amino acids primarily responsible for antigen recognition. The terms variable light chain (V_L) and variable heavy chain (V_H) refer to these light and heavy chains respectively.

Antibodies exist, e.g., as intact immunoglobulins or as a number of well-characterized fragments produced by digestion with various peptidases. Thus, for example, pepsin digests an antibody below the disulfide linkages in the hinge region to produce F(ab)'2, a dimer of Fab which itself is a light chain joined to V_H-C_H1 by a disulfide bond. The F(ab)'2 may be reduced under mild conditions to break the disulfide linkage in the hinge region, thereby converting the F(ab)'2 dimer into an Fab' monomer. The Fab' monomer is essentially Fab with part of the hinge region (see Fundamental Immunology (Paul ed., 3d ed. 1993). While various antibody fragments are defined in terms of the digestion of an intact antibody, one of skill will appreciate that such fragments may be synthesized de novo either chemically or by using recombinant DNA methodology. Thus, the term antibody, as used herein, also includes antibody fragments either produced by the modification of whole antibodies, or those synthesized de novo using recombinant DNA methodologies (e.g., single chain Fv) or those identified using phage display libraries (see, e.g., McCafferty et al., Nature 348:552-554 (1990))

For preparation of antibodies, e.g., recombinant, monoclonal, or polyclonal antibodies, many technique known in the art can be used (see, e.g., Kohler & Milstein, Nature 256:495-497 (1975); Kozbor et al., Immunology Today 4: 72 (1983); Cole et al., pp. 77-96 in Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, Inc. (1985); Coligan, Current Protocols in Immunology (1991); Harlow & Lane, Antibodies, A Laboratory Manual (1988); and Goding, Monoclonal Antibodies: Principles and Practice (2d ed. 1986)).

Techniques for the production of single chain antibodies (U.S. Patent 4,946,778) can be adapted to produce antibodies to polypeptides of this invention. Also, transgenic mice, or other organisms such as other mammals, may be used to express humanized antibodies. Alternatively, phage display technology can be used to identify antibodies and heteromeric Fab fragments that specifically bind to selected antigens (see, e.g., McCafferty et al., Nature 348:552-554 (1990); Marks et al., Biotechnology 10:779-783 (1992)).

A "chimeric antibody" is an antibody molecule in which (a) the constant region, or a portion thereof, is altered, replaced or exchanged so that the antigen binding site (variable region) is linked to a constant region of a different or altered class, effector function and/or species, or an entirely different molecule which confers new properties to the chimeric antibody, e.g., an enzyme, toxin, hormone, growth factor, drug, etc.; or (b) the variable region, or a portion thereof, is altered, replaced or exchanged with a variable region having a different or altered antigen specificity.

The detailed description of the invention includes discussion of the following

15 aspects of the invention:

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Expression of angiogenesis-associated sequences

Informatics

Angiogenesis-associated sequences

Detection of angiogenesis sequence for diagnostic and

therapeutic applications

Modulators of angiogenesis

Methods of identifying variant angiogenesis-associated

Administration of pharmaceutical and vaccine compositions

Kits for use in diagnostic and/or prognostic applications.

25 Expression of angiogenesis-associated sequences

In one aspect, the expression levels of genes are determined in different patient samples for which diagnosis information is desired, to provide expression profiles. An expression profile of a particular sample is essentially a "fingerprint" of the state of the sample; while two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is unique to the state of the cell. That is, normal tissue may be distinguished from AD tissue. By comparing expression profiles of tissue in known different angiogenesis states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. The identification of sequences that are

differentially expressed in angiogenic versus non-angiogenic tissue allows the use of this information in a number of ways. For example, a particular treatment regime may be evaluated: does a chemotherapeutic drug act to down-regulate angiogenesis, and thus tumor growth or recurrence, in a particular patient. Similarly, diagnosis and treatment outcomes may be done or confirmed by comparing patient samples with the known expression profiles. Angiogenic tissue can also be analyzed to determine the stage of angiogenesis in the tissue. Furthermore, these gene expression profiles (or individual genes) allow screening of drug candidates with an eye to mimicking or altering a particular expression profile; for example, screening can be done for drugs that suppress the angiogenic expression profile. This may be done by making biochips comprising sets of the important angiogenesis genes, which can then be used in these screens. These methods can also be done on the protein basis; that is, protein expression levels of the angiogenic proteins can be evaluated for diagnostic purposes or to screen candidate agents. In addition, the angiogenic nucleic acid sequences can be administered for gene therapy purposes, including the administration of antisense nucleic acids, or the angiogenic proteins (including antibodies and other modulators thereof) administered as therapeutic drugs.

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Thus the present invention provides nucleic acid and protein sequences that are differentially expressed in angiogenesis, herein termed "angiogenesis sequences". As outlined below, angiogenesis sequences include those that are up-regulated (i.e. expressed at a higher level) in disorders associated with angiogenesis, as well as those that are down-regulated (i.e. expressed at a lower level). In a preferred embodiment, the angiogenesis sequences are from humans; however, as will be appreciated by those in the art, angiogenesis sequences from other organisms may be useful in animal models of disease and drug evaluation; thus, other angiogenesis sequences are provided, from vertebrates, including mammals, including rodents (rats, mice, hamsters, guinea pigs, etc.), primates, farm animals (including sheep, goats, pigs, cows, horses, etc). Angiogenesis sequences from other organisms may be obtained using the techniques outlined below.

Angiogenesis sequences can include both nucleic acid and amino acid sequences. In a preferred embodiment, the angiogenesis sequences are recombinant nucleic acids. By the term "recombinant nucleic acid" herein is meant nucleic acid, originally formed in vitro, in general, by the manipulation of nucleic acid e.g., using polymerases and endonucleases, in a form not normally found in nature. Thus an isolated nucleic acid, in a linear form, or an expression vector formed in vitro by ligating DNA molecules that are not normally joined, are both considered recombinant for the purposes of this invention. It is

understood that once a recombinant nucleic acid is made and reintroduced into a host cell or organism, it will replicate non-recombinantly, i.e. using the in vivo cellular machinery of the host cell rather than in vitro manipulations; however, such nucleic acids, once produced recombinantly, although subsequently replicated non-recombinantly, are still considered recombinant for the purposes of the invention.

Similarly, a "recombinant protein" is a protein made using recombinant techniques, i.e. through the expression of a recombinant nucleic acid as depicted above. A recombinant protein is distinguished from naturally occurring protein by at least one or more characteristics. For example, the protein may be isolated or purified away from some or all of the proteins and compounds with which it is normally associated in its wild type host, and thus may be substantially pure. For example, an isolated protein is unaccompanied by at least some of the material with which it is normally associated in its natural state, preferably constituting at least about 0.5%, more preferably at least about 5% by weight of the total protein in a given sample. A substantially pure protein comprises at least about 75% by weight of the total protein, with at least about 80% being preferred, and at least about 90% being particularly preferred. The definition includes the production of an angiogenesis protein from one organism in a different organism or host cell. Alternatively, the protein may be made at a significantly higher concentration than is normally seen, through the use of an inducible promoter or high expression promoter, such that the protein is made at increased concentration levels. Alternatively, the protein may be in a form not normally found in nature, as in the addition of an epitope tag or amino acid substitutions, insertions and deletions, as discussed below.

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In a preferred embodiment, the angiogenesis sequences are nucleic acids. As will be appreciated by those in the art and is more fully outlined below, angiogenesis sequences are useful in a variety of applications, including diagnostic applications, which will detect naturally occurring nucleic acids, as well as screening applications; for example, biochips comprising nucleic acid probes to the angiogenesis sequences can be generated. In the broadest sense, then, by "nucleic acid" or "oligonucleotide" or grammatical equivalents herein means at least two nucleotides covalently linked together. A nucleic acid of the present invention will generally contain phosphodiester bonds, although in some cases, nucleic acid analogs are included that may have alternate backbones, comprising, for example, phosphoramidate, phosphorothicate, phosphorodithicate, or Omethylphophoroamidite linkages (see Eckstein, Oligonucleotides and Analogues: A Practical Approach, Oxford University Press); and peptide nucleic acid backbones and linkages. Other

analog nucleic acids include those with positive backbones; non-ionic backbones, and non-ribose backbones, including those described in U.S. Patent Nos. 5,235,033 and 5,034,506, and Chapters 6 and 7, ASC Symposium Series 580, "Carbohydrate Modifications in Antisense Research", Ed. Y.S. Sanghui and P. Dan Cook. Nucleic acids containing one or more carbocyclic sugars are also included within one definition of nucleic acids.

Modifications of the ribose-phosphate backbone may be done for a variety of reasons, for example to increase the stability and half-life of such molecules in physiological environments or as probes on a biochip.

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As will be appreciated by those in the art, nucleic acid analogs may find use in the present invention. In addition, mixtures of naturally occurring nucleic acids and analogs can be made; alternatively, mixtures of different nucleic acid analogs, and mixtures of naturally occurring nucleic acids and analogs may be made.

Particularly preferred are peptide nucleic acids (PNA) which includes peptide nucleic acid analogs. These backbones are substantially non-ionic under neutral conditions, in contrast to the highly charged phosphodiester backbone of naturally occurring nucleic acids. This results in two advantages. First, the PNA backbone exhibits improved hybridization kinetics. PNAs have larger changes in the melting temperature (Tm) for mismatched versus perfectly matched basepairs. DNA and RNA typically exhibit a 2-4°C drop in Tm for an internal mismatch. With the non-ionic PNA backbone, the drop is closer to 7-9°C. Similarly, due to their non-ionic nature, hybridization of the bases attached to these backbones is relatively insensitive to salt concentration. In addition, PNAs are not degraded by cellular enzymes, and thus can be more stable.

The nucleic acids may be single stranded or double stranded, as specified, or contain portions of both double stranded or single stranded sequence. As will be appreciated by those in the art, the depiction of a single strand also defines the sequence of the complementary strand; thus the sequences described herein also provide the complement of the sequence. The nucleic acid may be DNA, both genomic and cDNA, RNA or a hybrid, where the nucleic acid may contain combinations of deoxyribo- and ribo-nucleotides, and combinations of bases, including uracil, adenine, thymine, cytosine, guanine, inosine, xanthine hypoxanthine, isocytosine, isoguanine, etc. As used herein, the term "nucleoside" includes nucleotides and nucleotide and nucleotide analogs, and modified nucleosides such as amino modified nucleosides. In addition, "nucleoside" includes non-naturally occurring analog structures. Thus for example the individual units of a peptide nucleic acid, each containing a base, are referred to herein as a nucleoside.

An angiogenesis sequence can be initially identified by substantial nucleic acid and/or amino acid sequence homology to the angiogenesis sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions.

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For identifying angiogenesis-associated sequences, the angiogenesis screen typically includes comparing genes identified in a modification of an *in vitro* model of angiogenesis as described in Hiraoka, Cell 95:365 (1998) with genes identified in controls. Samples of normal tissue and tissue undergoing angiogenesis are applied to biochips comprising nucleic acid probes. The samples are first microdissected, if applicable, and treated as is known in the art for the preparation of mRNA. Suitable biochips are commercially available, for example from Affymetrix. Gene expression profiles as described herein are generated and the data analyzed.

In a preferred embodiment, the genes showing changes in expression as

between normal and disease states are compared to genes expressed in other normal tissues, including, but not limited to lung, heart, brain, liver, breast, kidney, muscle, prostate, small intestine, large intestine, spleen, bone and placenta. In a preferred embodiment, those genes identified during the angiogenesis screen that are expressed in any significant amount in other tissues are removed from the profile, although in some embodiments, this is not necessary.

That is, when screening for drugs, it is usually preferable that the target be disease specific, to minimize possible side effects.

In a preferred embodiment, angiogenesis sequences are those that are upregulated in angiogenesis disorders; that is, the expression of these genes is higher in the
disease tissue as compared to normal tissue. "Up-regulation" as used herein means at least
about a two-fold change, preferably at least about a three fold change, with at least about
five-fold or higher being preferred. All accession numbers herein are for the GenBank
sequence database and the sequences of the accession numbers are hereby expressly
incorporated by reference. GenBank is known in the art, see, e.g., Benson, DA, et al.,
Nucleic Acids Research 26:1-7 (1998) and http://www.ncbi.nlm.nih.gov/. Sequences are also
avialable in other databases, e.g., European Molecular Biology Laboratory (EMBL) and
DNA Database of Japan (DDBJ). In addition, most preferred genes were found to be
expressed in a limited amount or not at all in heart, brain, lung, liver, breast, kidney, prostate,
small intestine and spleen.

In another preferred embodiment, angiogenesis sequences are those that are down-regulated in the angiogenesis disorder; that is, the expression of these genes is lower in angiogenic tissue as compared to normal tissue. "Down-regulation" as used herein means at least about a two-fold change, preferably at least about a three fold change, with at least about five-fold or higher being preferred.

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Angiogenesis sequences according to the invention may be classified into discrete clusters of sequences based on common expression profiles of the sequences. Expression levels of angiogenesis sequences may increase or decrease as a function of time in a manner that correlates with the induction of angiogenesis. Alternatively, expression levels of angiogenesis sequences may both increase and decrease as a function of time. For example, expression levels of some angiogenesis sequences are temporarily induced or diminished during the switch to the angiogenesis phenotype, followed by a return to baseline expression levels. Tables 1-8 provides genes, the mRNA expression of which varies as a function of time in angiogenesis tissue when compared to normal tissue.

In a particularly preferred embodiment, angiogenesis sequences are those that are induced for a period of time, typically by positive angiogenic factors, followed by a return to the baseline levels. Sequences that are temporarily induced provide a means to target angiogenesis tissue, for example neovascularized tumors, at a particular stage of angiogenesis, while avoiding rapidly growing tissue that require perpetual vascularization. Such positive angiogenic factors include α FGF, β FGF, VEGF, angiogenin and the like.

Induced angiogenesis sequences also are further categorized with respect to the timing of induction. For example, some angiogenesis genes may be induced at an early time period, such as within 10 minutes of the induction of angiogenesis. Others may be induced later, such as between 5 and 60 minutes, while yet others may be induced for a time period of about two hours or more followed by a return to baseline expression levels.

In another preferred embodiment are angiogenesis sequences that are inhibited or reduced as a function of time followed by a return to "normal" expression levels. Inhibitors of angiogenesis are examples of molecules that have this expression profile. These sequences also can be further divided into groups depending on the timing of diminished expression. For example, some molecules may display reduced expression within 10 minutes of the induction of angiogenesis. Others may be diminished later, such as between 5 and 60 minutes, while others may be diminished for a time period of about two hours or more

followed by a return to baseline. Examples of such negative angiogenic factors include thrombospondin and endostatin to name a few.

In yet another preferred embodiment are angiogenesis sequences that are induced for prolonged periods. These sequences are typically associated with induction of angiogenesis and may participate in induction and/or maintenance of the angiogenesis phenotype.

In another preferred embodiment are angiogenesis sequences, the expression of which is reduced or diminished for prolonged periods in angiogenic tissue. These sequences are typically angiogenesis inhibitors and their diminution is correlated with an increase in angiogenesis.

Informatics

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The ability to identify genes that undergo changes in expression with time during angiogenesis can additionally provide high-resolution, high-sensitivity datasets which can be used in the areas of diagnostics, therapeutics, drug development, biosensor 15 development, and other related areas. For example, the expression profiles can be used in diagnostic or prognostic evaluation of patients with angiogenesis-associated disease. Or as another example, subcellular toxicological information can be generated to better direct drug structure and activity correlation (see, Anderson, L., "Pharmaceutical Proteomics: Targets, Mechanism, and Function," paper presented at the IBC Proteomics conference, Coronado, CA (June 11-12, 1998)). Subcellular toxicological information can also be utilized in a biological sensor device to predict the likely toxicological effect of chemical exposures and likely tolerable exposure thresholds (see, U.S. Patent No. 5,811,231). Similar advantages accrue from datasets relevant to other biomolecules and bioactive agents (e.g., nucleic acids, saccharides, lipids, drugs, and the like). 25

Thus, in another embodiment, the present invention provides a database that includes at least one set of data assay data. The data contained in the database is acquired, e.g., using array analysis either singly or in a library format. The database can be in substantially any form in which data can be maintained and transmitted, but is preferably an electronic database. The electronic database of the invention can be maintained on any electronic device allowing for the storage of and access to the database, such as a personal computer, but is preferably distributed on a wide area network, such as the World Wide Web.

The focus of the present section on databases that include peptide sequence data is for clarity of illustration only. It will be apparent to those of skill in the art that similar databases can be assembled for any assay data acquired using an assay of the invention.

The compositions and methods for identifying and/or quantitating the relative and/or absolute abundance of a variety of molecular and macromolecular species from a biological sample undergoing angiogenesis, i.e., the identification of angiogenesis-associated sequences described herein, provide an abundance of information, which can be correlated with pathological conditions, predisposition to disease, drug testing, therapeutic monitoring, gene-disease causal linkages, identification of correlates of immunity and physiological status, among others. Although the data generated from the assays of the invention is suited for manual review and analysis, in a preferred embodiment, prior data processing using high-speed computers is utilized.

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An array of methods for indexing and retrieving biomolecular information is known in the art. For example, U.S. Patents 6,023,659 and 5,966,712 disclose a relational database system for storing biomolecular sequence information in a manner that allows sequences to be catalogued and searched according to one or more protein function hierarchies. U.S. Patent 5,953,727 discloses a relational database having sequence records containing information in a format that allows a collection of partial-length DNA sequences to be catalogued and searched according to association with one or more sequencing projects for obtaining full-length sequences from the collection of partial length sequences. U.S. Patent 5,706,498 discloses a gene database retrieval system for making a retrieval of a gene sequence similar to a sequence data item in a gene database based on the degree of similarity between a key sequence and a target sequence. U.S. Patent 5,538,897 discloses a method using mass spectroscopy fragmentation patterns of peptides to identify amino acid sequences in computer databases by comparison of predicted mass spectra with experimentally-derived mass spectra using a closeness-of-fit measure. U.S. Patent 5,926,818 discloses a multidimensional database comprising a functionality for multi-dimensional data analysis described as on-line analytical processing (OLAP), which entails the consolidation of projected and actual data according to more than one consolidation path or dimension. U.S. Patent 5,295,261 reports a hybrid database structure in which the fields of each database record are divided into two classes, navigational and informational data, with navigational fields stored in a hierarchical topological map which can be viewed as a tree structure or as the merger of two or more such tree structures.

The present invention provides a computer database comprising a computer and software for storing in computer-retrievable form assay data records cross-tabulated, e.g., with data specifying the source of the target-containing sample from which each sequence specificity record was obtained.

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In an exemplary embodiment, at least one of the sources of target-containing sample is from a control tissue sample known to be free of pathological disorders. In a variation, at least one of the sources is a known pathological tissue specimen, e.g., a neoplastic lesion or another tissue specimen to be analyzed for angiogenesis. In another variation, the assay records cross-tabulate one or more of the following parameters for each target species in a sample: (1) a unique identification code, which can include, e.g., a target molecular structure and/or characteristic separation coordinate (e.g., electrophoretic coordinates); (2) sample source; and (3) absolute and/or relative quantity of the target species present in the sample.

The invention also provides for the storage and retrieval of a collection of target data in a computer data storage apparatus, which can include magnetic disks, optical disks, magneto-optical disks, DRAM, SRAM, SGRAM, SDRAM, RDRAM, DDR RAM, magnetic bubble memory devices, and other data storage devices, including CPU registers and on-CPU data storage arrays. Typically, the target data records are stored as a bit pattern in an array of magnetic domains on a magnetizable medium or as an array of charge states or transistor gate states, such as an array of cells in a DRAM device (e.g., each cell comprised of a transistor and a charge storage area, which may be on the transistor). In one embodiment, the invention provides such storage devices, and computer systems built therewith, comprising a bit pattern encoding a protein expression fingerprint record comprising unique identifiers for at least 10 target data records cross-tabulated with target source.

When the target is a peptide or nucleic acid, the invention preferably provides a method for identifying related peptide or nucleic acid sequences, comprising performing a computerized comparison between a peptide or nucleic acid sequence assay record stored in or retrieved from a computer storage device or database and at least one other sequence. The comparison can include a sequence analysis or comparison algorithm or computer program embodiment thereof (e.g., FASTA, TFASTA, GAP, BESTFIT) and/or the comparison may be of the relative amount of a peptide or nucleic acid sequence in a pool of sequences determined from a polypeptide or nucleic acid sample of a specimen.

The invention also preferably provides a magnetic disk, such as an IBMcompatible (DOS, Windows, Windows95/98/2000, Windows NT, OS/2) or other format

(e.g., Linux, SunOS, Solaris, AIX, SCO Unix, VMS, MV, Macintosh, etc.) floppy diskette or hard (fixed, Winchester) disk drive, comprising a bit pattern encoding data from an assay of the invention in a file format suitable for retrieval and processing in a computerized sequence analysis, comparison, or relative quantitation method.

The invention also provides a network, comprising a plurality of computing devices linked via a data link, such as an Ethernet cable (coax or 10BaseT), telephone line, ISDN line, wireless network, optical fiber, or other suitable signal tranmission medium, whereby at least one network device (e.g., computer, disk array, etc.) comprises a pattern of magnetic domains (e.g., magnetic disk) and/or charge domains (e.g., an array of DRAM cells) composing a bit pattern encoding data acquired from an assay of the invention.

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The invention also provides a method for transmitting assay data that includes generating an electronic signal on an electronic communications device, such as a modern, ISDN terminal adapter, DSL, cable modern, ATM switch, or the like, wherein the signal includes (in native or encrypted format) a bit pattern encoding data from an assay or a database comprising a plurality of assay results obtained by the method of the invention.

In a preferred embodiment, the invention provides a computer system for comparing a query target to a database containing an array of data structures, such as an assay result obtained by the method of the invention, and ranking database targets based on the degree of identity and gap weight to the target data. A central processor is preferably initialized to load and execute the computer program for alignment and/or comparison of the assay results. Data for a query target is entered into the central processor via an I/O device. Execution of the computer program results in the central processor retrieving the assay data from the data file, which comprises a binary description of an assay result.

The target data or record and the computer program can be transferred to secondary memory, which is typically random access memory (e.g., DRAM, SRAM, SGRAM, or SDRAM). Targets are ranked according to the degree of correspondence between a selected assay characteristic (e.g., binding to a selected affinity moiety) and the same characteristic of the query target and results are output via an I/O device. For example, a central processor can be a conventional computer (e.g., Intel Pentium, PowerPC, Alpha, PA-8000, SPARC, MIPS 4400, MIPS 10000, VAX, etc.); a program can be a commercial or public domain molecular biology software package (e.g., UWGCG Sequence Analysis Software, Darwin); a data file can be an optical or magnetic disk, a data server, a memory device (e.g., DRAM, SRAM, SGRAM, SDRAM, EPROM, bubble memory, flash memory, etc.); an I/O device can be a terminal comprising a video display and a keyboard, a modem,

an ISDN terminal adapter, an Ethernet port, a punched card reader, a magnetic strip reader, or other suitable I/O device.

The invention also preferably provides the use of a computer system, such as that described above, which comprises: (1) a computer; (2) a stored bit pattern encoding a collection of peptide sequence specificity records obtained by the methods of the invention, which may be stored in the computer; (3) a comparison target, such as a query target; and (4) a program for alignment and comparison, typically with rank-ordering of comparison results on the basis of computed similarity values.

10 Angiogenesis-associated sequences

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Angiogenesis proteins of the present invention may be classified as secreted proteins, transmembrane proteins or intracellular proteins. In one embodiment, the angiogenesis protein is an intracellular protein. Intracellular proteins may be found in the cytoplasm and/or in the nucleus or associated with the intracellular side of the plasma membrane. Intracellular proteins are involved in all aspects of cellular function and replication (including, e.g., signaling pathways); aberrant expression of such proteins often results in unregulated or disregulated cellular processes (see, e.g., Molecular Biology of the Cell, 3rd Edition, Alberts, Ed., Garland Pub., 1994). For example, many intracellular proteins have enzymatic activity such as protein kinase activity, protein phosphatase activity, protease activity, nucleotide cyclase activity, polymerase activity and the like. Intracellular proteins also serve as docking proteins that are involved in organizing complexes of proteins, or targeting proteins to various subcellular localizations, and are involved in maintaining the structural integrity of organelles.

An increasingly appreciated concept in characterizing proteins is the presence in the proteins of one or more motifs for which defined functions have been attributed. In addition to the highly conserved sequences found in the enzymatic domain of proteins, highly conserved sequences have been identified in proteins that are involved in protein-protein interaction. For example, Src-homology-2 (SH2) domains bind tyrosine-phosphorylated targets in a sequence dependent manner. PTB domains, which are distinct from SH2 domains, also bind tyrosine phosphorylated targets. SH3 domains bind to proline-rich targets. In addition, PH domains, tetratricopeptide repeats and WD domains to name only a few, have been shown to mediate protein-protein interactions. Some of these may also be involved in binding to phospholipids or other second messengers. As will be appreciated by one of ordinary skill in the art, these motifs can be identified on the basis of primary

sequence; thus, an analysis of the sequence of proteins may provide insight into both the enzymatic potential of the molecule and/or molecules with which the protein may associate.

In another embodiment, the angiogenesis sequences are transmembrane proteins. Transmembrane proteins are molecules that span a phospholipid bilayer of a cell. 5 They may have an intracellular domain, an extracellular domain, or both. The intracellular domains of such proteins may have a number of functions including those already described for intracellular proteins. For example, the intracellular domain may have enzymatic activity and/or may serve as a binding site for additional proteins. Frequently the intracellular domain of transmembrane proteins serves both roles. For example certain receptor tyrosine kinases have both protein kinase activity and SH2 domains. In addition, autophosphorylation of tyrosines on the receptor molecule itself, creates binding sites for additional SH2 domain containing proteins.

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Transmembrane proteins may contain from one to many transmembrane domains. For example, receptor tyrosine kinases, certain cytokine receptors, receptor guanylyl cyclases and receptor serine/threonine protein kinases contain a single transmembrane domain. However, various other proteins including channels and adenylyl cyclases contain numerous transmembrane domains. Many important cell surface receptors such as G protein coupled receptors (GPCRs) are classified as "seven transmembrane domain" proteins, as they contain 7 membrane spanning regions. Characteristics of transmembrane domains include approximately 20 consecutive hydrophobic amino acids that may be followed or flanked by charged amino acids. Therefore, upon analysis of the amino acid sequence of a particular protein, the localization and number of transmembrane domains within the protein may be predicted (see, e.g. PSORT web site http://psort.nibb.ac.jp/).

The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. Many extracellular domains are involved in binding to other molecules. In one aspect, extracellular domains are found on receptors. Factors that bind the receptor domain include circulating ligands, which may be peptides, proteins, or small molecules such as adenosine and the like. For example, growth factors such as EGF, FGF and PDGF are circulating growth factors that bind to their cognate receptors to initiate a variety of cellular responses. Other factors include cytokines, mitogenic factors, neurotrophic factors and the like. Extracellular domains also bind to cell-associated molecules. In this respect, they mediate cell-cell interactions. Cellassociated ligands can be tethered to the cell for example via a glycosylphosphatidylinositol

(GPI) anchor, or may themselves be transmembrane proteins. Extracellular domains also associate with the extracellular matrix and contribute to the maintenance of the cell structure.

Angiogenesis proteins that are transmembrane are particularly preferred in the present invention as they are readily accessible targets for immunotherapeutics, as are described herein. In addition, as outlined below, transmembrane proteins can be also useful in imaging modalities. Antibodies may be used to label such readily accessible proteins in situ. Alternatively, antibodies can also label intracellular proteins, in which case samples are typically permeablized to provide access to intracellular proteins.

It will also be appreciated by those in the art that a transmembrane protein can be made soluble by removing transmembrane sequences, for example through recombinant methods. Furthermore, transmembrane proteins that have been made soluble can be made to be secreted through recombinant means by adding an appropriate signal sequence.

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In another embodiment, the angiogenesis proteins are secreted proteins; the secretion of which can be either constitutive or regulated. These proteins have a signal peptide or signal sequence that targets the molecule to the secretory pathway. Secreted proteins are involved in numerous physiological events; by virtue of their circulating nature, they serve to transmit signals to various other cell types. The secreted protein may function in an autocrine manner (acting on the cell that secreted the factor), a paracrine manner (acting on cells in close proximity to the cell that secreted the factor) or an endocrine manner (acting on cells at a distance). Thus secreted molecules find use in modulating or altering numerous aspects of physiology. Angiogenesis proteins that are secreted proteins are particularly preferred in the present invention as they serve as good targets for diagnostic markers, e.g., for blood or serum tests.

An angiogenesis sequence is typically initially identified by substantial nucleic acid and/or amino acid sequence homology or linkage to the angiogenesis sequences outlined herein. Such homology can be based upon the overall nucleic acid or amino acid sequence, and is generally determined as outlined below, using either homology programs or hybridization conditions. Typically, linked sequences on a mRNA are found on the same molecule.

As detailed in the definitions, percent identity can be determined using an algorithm such as BLAST. A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. The alignment may include the introduction of gaps in the sequences to be aligned. In addition, for sequences which contain either more or fewer nucleotides than

those of the nucleic acids of the figures, it is understood that the percentage of homology will be determined based on the number of homologous nucleosides in relation to the total number of nucleosides. Thus, for example, homology of sequences shorter than those of the sequences identified herein and as discussed below, will be determined using the number of nucleosides in the shorter sequence.

In one embodiment, the nucleic acid homology is determined through hybridization studies. Thus, e.g., nucleic acids which hybridize under high stringency to a nucleic acid of Tables 1-8, or its complement, or is also found on naturally occurring mRNAs is considered an angiogenesis sequence. In another embodiment, less stringent hybridization conditions are used; for example, moderate or low stringency conditions may be used, as are known in the art; see Ausubel, supra, and Tijssen, supra.

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In addition, the angiogenesis nucleic acid sequences of the invention, e.g., the sequence in Tables 1-8, are fragments of larger genes, i.e. they are nucleic acid segments. "Genee" in this context includes coding regions, non-coding regions, and mixtures of coding and non-coding regions. Accordingly, as will be appreciated by those in the art, using the sequences provided herein, extended sequences, in either direction, of the angiogenesis genes can be obtained, using techniques well known in the art for cloning either longer sequences or the full length sequences; see Ausubel, et al., supra. Much can be done by informatics and many sequences can be clustered to include multiple sequences, e.g., systems such as UniGene (see, http://www.ncbi.nlm.nih.gov/UniGene/).

Once the angiogenesis nucleic acid is identified, it can be cloned and, if necessary, its constituent parts recombined to form the entire angiogenesis nucleic acid coding regions or the entire mRNA sequence. Once isolated from its natural source, e.g., contained within a plasmid or other vector or excised therefrom as a linear nucleic acid segment, the recombinant angiogenesis nucleic acid can be further-used as a probe to identify and isolate other angiogenesis nucleic acids, for example extended coding regions. It can also be used as a "precursor" nucleic acid to make modified or variant angiogenesis nucleic acids and proteins.

The angiogenesis nucleic acids of the present invention are used in several ways. In a first embodiment, nucleic acid probes to the angiogenesis nucleic acids are made and attached to biochips to be used in screening and diagnostic methods, as outlined below, or for administration, for example for gene therapy, vaccine, and/or antisense applications. Alternatively, the angiogenesis nucleic acids that include coding regions of angiogenesis

proteins can be put into expression vectors for the expression of angiogenesis proteins, again for screening purposes or for administration to a patient.

In a preferred embodiment, nucleic acid probes to angiogenesis nucleic acids (both the nucleic acid sequences outlined in the figures and/or the complements thereof) are made. The nucleic acid probes attached to the biochip are designed to be substantially complementary to the angiogenesis nucleic acids, *i.e.* the target sequence (either the target sequence of the sample or to other probe sequences, for example in sandwich assays), such that hybridization of the target sequence and the probes of the present invention occurs. As outlined below, this complementarity need not be perfect; there may be any number of base pair mismatches which will interfere with hybridization between the target sequence and the single stranded nucleic acids of the present invention. However, if the number of mutations is so great that no hybridization can occur under even the least stringent of hybridization conditions, the sequence is not a complementary target sequence. Thus, by "substantially complementary" herein is meant that the probes are sufficiently complementary to the target sequences to hybridize under normal reaction conditions, particularly high stringency conditions, as outlined herein.

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A nucleic acid probe is generally single stranded but can be partially single and partially double stranded. The strandedness of the probe is dictated by the structure, composition, and properties of the target sequence. In general, the nucleic acid probes range from about 8 to about 100 bases long, with from about 10 to about 80 bases being preferred, and from about 30 to about 50 bases being particularly preferred. That is, generally whole genes are not used. In some embodiments, much longer nucleic acids can be used, up to hundreds of bases.

In a preferred embodiment, more than one probe per sequence is used, with either overlapping probes or probes to different sections of the target being used. That is, two, three, four or more probes, with three being preferred, are used to build in a redundancy for a particular target. The probes can be overlapping (i.e. have some sequence in common), or separate. In some cases, PCR primers may be used to amplify signal for higher sensitivity.

As will be appreciated by those in the art, nucleic acids can be attached or immobilized to a solid support in a wide variety of ways. By "immobilized" and grammatical equivalents herein is meant the association or binding between the nucleic acid probe and the solid support is sufficient to be stable under the conditions of binding, washing, analysis, and removal as outlined below. The binding can typically be covalent or non-covalent. By "non-covalent binding" and grammatical equivalents herein is meant one or more of electrostatic,

hydrophilic, and hydrophobic interactions. Included in non-covalent binding is the covalent attachment of a molecule, such as, streptavidin to the support and the non-covalent binding of the biotinylated probe to the streptavidin. By "covalent binding" and grammatical equivalents herein is meant that the two moieties, the solid support and the probe, are attached by at least one bond, including sigma bonds, pi bonds and coordination bonds. Covalent bonds can be formed directly between the probe and the solid support or can be formed by a cross linker or by inclusion of a specific reactive group on either the solid support or the probe or both molecules. Immobilization may also involve a combination of covalent and non-covalent interactions.

In general, the probes are attached to the biochip in a wide variety of ways, as will be appreciated by those in the art. As described herein, the nucleic acids can either be synthesized first, with subsequent attachment to the biochip, or can be directly synthesized on the biochip.

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The biochip comprises a suitable solid substrate. By "substrate" or "solid support" or other grammatical equivalents herein is meant a material that can be modified to contain discrete individual sites appropriate for the attachment or association of the nucleic acid probes and is amenable to at least one detection method. As will be appreciated by those in the art, the number of possible substrates are very large, and include, but are not limited to, glass and modified or functionalized glass, plastics (including acrylics, polystyrene and copolymers of styrene and other materials, polypropylene, polyethylene, polybutylene, polyurethanes, TeflonI, etc.), polysaccharides, nylon or nitrocellulose, resins, silica or silicabased materials including silicon and modified silicon, carbon, metals, inorganic glasses, plastics, etc. In general, the substrates allow optical detection and do not appreciably fluorescesee. A preferred substrate is described in copending application entitled Reusable Low Fluorescent Plastic Biochip, U.S. Application Serial No. 09/270,214, filed March 15, 1999, herein incomporated by reference in its entirety.

Generally the substrate is planar, although as will be appreciated by those in the art, other configurations of substrates may be used as well. For example, the probes may be placed on the inside surface of a tube, for flow-through sample analysis to minimize sample volume. Similarly, the substrate may be flexible, such as a flexible foam, including closed cell foams made of particular plastics.

In a preferred embodiment, the surface of the biochip and the probe may be derivatized with chemical functional groups for subsequent attachment of the two. Thus, for example, the biochip is derivatized with a chemical functional group including, but not

limited to, amino groups, carboxy groups, oxo groups and thiol groups, with amino groups being particularly preferred. Using these functional groups, the probes can be attached using functional groups on the probes. For example, nucleic acids containing amino groups can be attached to surfaces comprising amino groups, for example using linkers as are known in the art; for example, homo-or hetero-bifunctional linkers as are well known (see 1994 Pierce Chemical Company catalog, technical section on cross-linkers, pages 155-200, incorporated herein by reference). In addition, in some cases, additional linkers, such as alkyl groups (including substituted and heteroalkyl groups) may be used.

In this embodiment, oligonucleotides are synthesized as is known in the art, and then attached to the surface of the solid support. As will be appreciated by those skilled in the art, either the 5' or 3' terminus may be attached to the solid support, or attachment may be via an internal nucleoside.

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In another embodiment, the immobilization to the solid support may be very strong, yet non-covalent. For example, biotinylated oligonucleotides can be made, which bind to surfaces covalently coated with streptavidin, resulting in attachment.

Alternatively, the oligonucleotides may be synthesized on the surface, as is known in the art. For example, photoactivation techniques utilizing photopolymerization compounds and techniques are used. In a preferred embodiment, the nucleic acids can be synthesized in situ, using well known photolithographic techniques, such as those described in WO 95/25116; WO 95/35505; U.S. Patent Nos. 5,700,637 and 5,445,934; and references cited within, all of which are expressly incorporated by reference; these methods of attachment form the basis of the Affimetrix GeneChipTM technology.

Often, amplification-based assays are performed to measure the expression level of angiogenesis-associated sequences. These assays are typically performed in conjunction with reverse transcription. In such assays, an angiogenesis-associated nucleic acid sequence acts as a template in an amplification reaction (e.g., Polymerase Chain Reaction, or PCR). In a quantitative amplification, the amount of amplification product will be proportional to the amount of template in the original sample. Comparison to appropriate controls provides a measure of the amount of angiogenesis-associated RNA. Methods of quantitative amplification are well known to those of skill in the art. Detailed protocols for quantitative PCR are provided, e.g., in Innis et al. (1990) PCR Protocols, A Guide to Methods and Applications, Academic Press, Inc. N.Y.).

In some embodiments, a TaqMan based assay is used to measure expression.

TaqMan based assays use a fluorogenic oligonucleotide probe that contains a 5' fluorescent

dye and a 3' quenching agent. The probe hybridizes to a PCR product, but cannot itself be extended due to a blocking agent at the 3' end. When the PCR product is amplified in subsequent cycles, the 5' nuclease activity of the polymerase, e.g., AmpliTaq, results in the cleavage of the TaqMan probe. This cleavage separates the 5' fluorescent dye and the 3' quenching agent, thereby resulting in an increase in fluorescence as a function of amplification (see, for example, literature provided by Perkin-Elmer, e.g., www2.perkin-elmer.com).

Other suitable amplification methods include, but are not limited to, ligase chain reaction (LCR) (see, Wu and Wallace (1989) Genomics 4: 560, Landegren et al. (1988) Science 241: 1077, and Barringer et al. (1990) Gene 89: 117), transcription amplification (Kwoh et al. (1989) Proc. Natl. Acad. Sci. USA 86: 1173), self-sustained sequence replication (Guatelli et al. (1990) Proc. Nat. Acad. Sci. USA 87: 1874), dot PCR, and linker adapter PCR, etc.

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In a preferred embodiment, angiogenesis nucleic acids, e.g., encoding angiogenesis proteins are used to make a variety of expression vectors to express 15 angiogenesis proteins which can then be used in screening assays, as described below. Expression vectors and recombinant DNA technology are well known to those of skill in the art (see, e.g., Ausubel, supra, and Gene Expression Systems, Fernandez & Hoeffler, Eds, Academic Press, 1999) and are used to express proteins. The expression vectors may be either self-replicating extrachromosomal vectors or vectors which integrate into a host 20 genome. Generally, these expression vectors include transcriptional and translational regulatory nucleic acid operably linked to the nucleic acid encoding the angiogenesis protein. The term "control sequences" refers to DNA sequences used for the expression of an operably linked coding sequence in a particular host organism. Control sequences that are 25 suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation.

Generally, "operably linked" means that the DNA sequences being linked are contiguous,

and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is typically accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice. Transcriptional and translational regulatory nucleic acid will generally be appropriate to the host cell used to express the angiogenesis protein; for example, transcriptional and translational regulatory nucleic acid sequences from Bacillus are preferably used to express the angiogenesis protein in Bacillus. Numerous types of appropriate expression vectors, and suitable regulatory sequences are known in the art for a variety of host cells.

In general, transcriptional and translational regulatory sequences may include, but are not limited to, promoter sequences, ribosomal binding sites, transcriptional start and stop sequences, translational start and stop sequences, and enhancer or activator sequences. In a preferred embodiment, the regulatory sequences include a promoter and transcriptional start and stop sequences.

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Promoter sequences encode either constitutive or inducible promoters. The promoters may be either naturally occurring promoters or hybrid promoters. Hybrid promoters, which combine elements of more than one promoter, are also known in the art, and are useful in the present invention.

In addition, an expression vector may comprise additional elements. For example, the expression vector may have two replication systems, thus allowing it to be maintained in two organisms, for example in mammalian or insect cells for expression and in a procaryotic host for cloning and amplification. Furthermore, for integrating expression vectors, the expression vector contains at least one sequence homologous to the host cell genome, and preferably two homologous sequences which flank the expression construct. The integrating vector may be directed to a specific locus in the host cell by selecting the appropriate homologous sequence for inclusion in the vector. Constructs for integrating vectors are well known in the art (e.g., Fernandez & Hoeffler, supra). See also Kitamura, et al. (1995) PNAS 92:9146-9150.

In addition, in a preferred embodiment, the expression vector contains a selectable marker gene to allow the selection of transformed host cells. Selection genes are well known in the art and will vary with the host cell used.

The angiogenesis proteins of the present invention are produced by culturing a host cell transformed with an expression vector containing nucleic acid encoding an angiogenesis protein, under the appropriate conditions to induce or cause expression of the

angiogenesis protein. Conditions appropriate for angiogenesis protein expression will vary with the choice of the expression vector and the host cell, and will be easily ascertained by one skilled in the art through routine experimentation or optimization. For example, the use of constitutive promoters in the expression vector will require optimizing the growth and proliferation of the host cell, while the use of an inducible promoter requires the appropriate growth conditions for induction. In addition, in some embodiments, the timing of the harvest is important. For example, the baculoviral systems used in insect cell expression are lytic viruses, and thus harvest time selection can be crucial for product yield.

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Appropriate host cells include yeast, bacteria, archaebacteria, fungi, and insect and animal cells, including mammalian cells. Of particular interest are Saccharomyces cerevisiae and other yeasts, E. coli, Bacillus subtilis, Sf9 cells, C129 cells, 293 cells, Neurospora, BHK, CHO, COS, HeLa cells, HUVEC (human umbilical vein endothelial cells), THP1 cells (a macrophage cell line) and various other human cells and cell lines.

In a preferred embodiment, the angiogenesis proteins are expressed in mammalian cells. Mammalian expression systems are also known in the art, and include retroviral and adenoviral systems. Of particular use as mammalian promoters are the promoters from mammalian viral genes, since the viral genes are often highly expressed and have a broad host range. Examples include the SV40 early promoter, mouse mammary tumor virus LTR promoter, adenovirus major late promoter, herpes simplex virus promoter, and the CMV promoter (see, e.g., Fernandez & Hoeffler, supra). Typically, transcription termination and polyadenylation sequences recognized by mammalian cells are regulatory regions located 3' to the translation stop codon and thus, together with the promoter elements, flank the coding sequence. Examples of transcription terminator and polyadenlytion signals include those derived form SV40

The methods of introducing exogenous nucleic acid into mammalian hosts, as well as other hosts, is well known in the art, and will vary with the host cell used. Techniques include dextran-mediated transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, viral infection, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei.

In a preferred embodiment, angiogenesis proteins are expressed in bacterial systems. Bacterial expression systems are well known in the art. Promoters from bacteriophage may also be used and are known in the art. In addition, synthetic promoters

and hybrid promoters are also useful; for example, the tac promoter is a hybrid of the trp and lac promoter sequences. Furthermore, a bacterial promoter can include naturally occurring promoters of non-bacterial origin that have the ability to bind bacterial RNA polymerase and initiate transcription. In addition to a functioning promoter sequence, an efficient ribosome binding site is desirable. The expression vector may also include a signal peptide sequence that provides for secretion of the angiogenesis protein in bacteria. The protein is either secreted into the growth media (gram-positive bacteria) or into the periplasmic space, located between the inner and outer membrane of the cell (gram-negative bacteria). The bacterial expression vector may also include a selectable marker gene to allow for the selection of bacterial strains that have been transformed. Suitable selection genes include genes which render the bacteria resistant to drugs such as ampicillin, chloramphenicol, erythromycin. kanamycin, neomycin and tetracycline. Selectable markers also include biosynthetic genes, such as those in the histidine, tryptophan and leucine biosynthetic pathways. These components are assembled into expression vectors. Expression vectors for bacteria are well known in the art, and include vectors for Bacillus subtilis, E. coli, Streptococcus cremoris, and Streptococcus lividans, among others (e.g., Fernandez & Hoeffler, supra). The bacterial expression vectors are transformed into bacterial host cells using techniques well known in the art, such as calcium chloride treatment, electroporation, and others.

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In one embodiment, angiogenesis proteins are produced in insect cells.

Expression vectors for the transformation of insect cells, and in particular, baculovirus-based expression vectors, are well known in the art.

In a preferred embodiment, angiogenesis protein is produced in yeast cells. Yeast expression systems are well known in the art, and include expression vectors for Saccharomyces cerevisiae, Candida albicans and C. maltosa, Hansenula polymorpha, Kluyveromyces fragilis and K. lactis, Pichia guillerimondii and P. pastoris, Schizosaccharomyces pombe, and Yarrowia lipolytica.

The angiogenesis protein may also be made as a fusion protein, using techniques well known in the art. Thus, for example, for the creation of monoclonal antibodies, if the desired epitope is small, the angiogenesis protein may be fused to a carrier protein to form an immunogen. Alternatively, the angiogenesis protein may be made as a fusion protein to increase expression, or for other reasons. For example, when the angiogenesis protein is an angiogenesis peptide, the nucleic acid encoding the peptide may be linked to another nucleic acid for expression purposes. Fusion with detection epitope tags can be made, e.g., with FLAG, His 6, myc, HA, etc.

In one embodiment, the angiogenesis nucleic acids, proteins and antibodies of the invention are labeled. By "labeled" herein is meant that a compound has at least one element, isotope or chemical compound attached to enable the detection of the compound. In general, labels fall into three classes: a) isotopic labels, which may be radioactive or heavy isotopes; b) immune labels, which may be antibodies, antigens, or epitope tags and c) colored or fluorescent dyes. The labels may be incorporated into the angiogenesis nucleic acids, proteins and antibodies at any position. For example, the label should be capable of producing, either directly or indirectly, a detectable signal. The detectable moiety may be a radioisotope, such as ³H, ¹⁴C, ³²P, ³⁵S, or ¹²⁵I, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the label may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

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Accordingly, the present invention also provides angiogenesis protein sequences. An angiogenesis protein of the present invention may be identified in several ways. "Protein" in this sense includes proteins, polypeptides, and peptides. As will be appreciated by those in the art, the nucleic acid sequences of the invention can be used to generate protein sequences. There are a variety of ways to do this, including cloning the entire gene and verifying its frame and amino acid sequence, or by comparing it to known sequences to search for homology to provide a frame, assuming the angiogenesis protein has an identifiable motif or homology to some protein in the database being used. Generally, the nucleic acid sequences are input into a program that will search all three frames for homology. This is done in a preferred embodiment using the following NCBI Advanced BLAST parameters. The program is blastx or blastn. The database is nr. The input data is as "Sequence in FASTA format". The organism list is "none". The "expect" is 10; the filter is default. The "descriptions" is 500, the "alignments" is 500, and the "alignment view" is pairwise. The "Query Genetic Codes" is standard (1). The matrix is BLOSUM62; gap existence cost is 11, per residue gap cost is 1; and the lambda ratio is .85 default. This results in the generation of a putative protein sequence.

Also included within one embodiment of angiogenesis proteins are amino acid variants of the naturally occurring sequences, as determined herein. Preferably, the variants are preferably greater than about 75% homologous to the wild-type sequence, more

preferably greater than about 80%, even more preferably greater than about 85% and most preferably greater than 90%. In some embodiments the homology will be as high as about 93 to 95 or 98%. As for nucleic acids, homology in this context means sequence similarity or identity, with identity being preferred. This homology will be determined using standard techniques well known in the art as are outlined above for the nucleic acid homologies.

Angiogenesis proteins of the present invention may be shorter or longer than the wild type amino acid sequences. Thus, in a preferred embodiment, included within the definition of angiogenesis proteins are portions or fragments of the wild type sequences. herein. In addition, as outlined above, the angiogenesis nucleic acids of the invention may be used to obtain additional coding regions, and thus additional protein sequence, using techniques known in the art.

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In a preferred embodiment, the angiogenesis proteins are derivative or variant angiogenesis proteins as compared to the wild-type sequence. That is, as outlined more fully below, the derivative angiogenesis peptide will often contain at least one amino acid substitution, deletion or insertion, with amino acid substitutions being particularly preferred. The amino acid substitution, insertion or deletion may occur at any residue within the angiogenesis peptide.

Also included within one embodiment of angiogenesis proteins of the present invention are amino acid sequence variants. These variants typically fall into one or more of three classes: substitutional, insertional or deletional variants. These variants ordinarily are prepared by site specific mutagenesis of nucleotides in the DNA encoding the angiogenesis protein, using cassette or PCR mutagenesis or other techniques well known in the art, to produce DNA encoding the variant, and thereafter expressing the DNA in recombinant cell culture as outlined above. However, variant angiogenesis protein fragments having up to about 100-150 residues may be prepared by in vitro synthesis using established techniques. Amino acid sequence variants are characterized by the predetermined nature of the variation, a feature that sets them apart from naturally occurring allelic or interspecies variation of the angiogenesis protein amino acid sequence. The variants typically exhibit the same qualitative biological activity as the naturally occurring analogue, although variants can also be selected which have modified characteristics as will be more fully outlined below.

While the site or region for introducing an amino acid sequence variation is predetermined, the mutation per se need not be predetermined. For example, in order to optimize the performance of a mutation at a given site, random mutagenesis may be conducted at the target codon or region and the expressed angiogenesis variants screened for

the optimal combination of desired activity. Techniques for making substitution mutations at predetermined sites in DNA having a known sequence are well known, for example, M13 primer mutagenesis and PCR mutagenesis. Screening of the mutants is done using assays of angiogenesis protein activities.

Amino acid substitutions are typically of single residues; insertions usually will be on the order of from about 1 to 20 amino acids, although considerably larger insertions may be tolerated. Deletions range from about 1 to about 20 residues, although in some cases deletions may be much larger.

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Substitutions, deletions, insertions or any combination thereof may be used to arrive at a final derivative. Generally these changes are done on a few amino acids to minimize the alteration of the molecule. However, larger changes may be tolerated in certain circumstances. When small alterations in the characteristics of the angiogenesis protein are desired, substitutions are generally made in accordance with the amino acid substitution chart provided in the definition section.

Substantial changes in function or immunological identity are made by selecting substitutions that are less conservative than those provided in the definition of "conservative substitution". For example, substitutions may be made which more significantly affect: the structure of the polypeptide backbone in the area of the alteration, for example the alpha-helical or beta-sheet structure; the charge or hydrophobicity of the molecule at the target site; or the bulk of the side chain. The substitutions which in general are expected to produce the greatest changes in the polypeptide's properties are those in which (a) a hydrophibic residue, e.g. seryl or threonyl, is substituted for (or by) a hydrophobic residue, e.g. leucyl, isoleucyl, phenylalanyl, valyl or alanyl; (b) a cysteine or proline is substituted for (or by) any other residue; (c) a residue having an electropositive side chain, e.g. lysyl, arginyl, or histidyl, is substituted for (or by) an electronegative residue, e.g. glutamyl or aspartyl; or (d) a residue having a bulky side chain, e.g. phenylalanine, is substituted for (or by) one not having a side chain, e.g. glycine.

The variants typically exhibit the same qualitative biological activity and will elicit the same immune response as the naturally-occurring analog, although variants also are selected to modify the characteristics of the angiogenesis proteins as needed. Alternatively, the variant may be designed such that the biological activity of the angiogenesis protein is altered. For example, glycosylation sites may be altered or removed.

Covalent modifications of angiogenesis polypeptides are included within the scope of this invention. One type of covalent modification includes reacting targeted amino

acid residues of an angiogenesis polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N-or C-terminal residues of an angiogenesis polypeptide. Derivatization with bifunctional agents is useful, for instance, for crosslinking angiogenesis polypeptides to a water-insoluble support matrix or surface for use in the method for purifying anti-angiogenesis polypeptide antibodies or screening assays, as is more fully described below. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl, threonyl or tyrosyl residues, methylation of the γ -amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-

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terminal carboxyl group.

Another type of covalent modification of the angiogenesis polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence angiogenesis polypeptide, and/or adding one or more glycosylation sites that are not present in the native sequence angiogenesis polypeptide. Glycosylation patterns can be altered in many ways. For example the use of different cell types to express angiogenesis-associated sequences can result in different glycosylation patterns.

Addition of glycosylation sites to angiogenesis polypeptides may also be accomplished by altering the amino acid sequence thereof. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence angiogenesis polypeptide (for O-linked glycosylation sites). The angiogenesis amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the angiogenesis polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the angiogenesis polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

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Removal of carbohydrate moieties present on the angiogenesis polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo-and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of angiogenesis comprises linking the angiogenesis polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol, polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

Angiogenesis polypeptides of the present invention may also be modified in a way to form chimeric molecules comprising an angiogenesis polypeptide fused to another, heterologous polypeptide or amino acid sequence. In one embodiment, such a chimeric molecule comprises a fusion of an angiogenesis polypeptide with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino-or carboxyl-terminus of the angiogenesis polypeptide. The presence of such epitope-tagged forms of an angiogenesis polypeptide can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the angiogenesis polypeptide to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. In an alternative embodiment, the chimeric molecule may comprise a fusion of an angiogenesis polypeptide with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule, such a fusion could be to the Fc region of an IgG molecule.

Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)];

and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc., Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

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Also included with an embodiment of angiogenesis protein are other angiogenesis proteins of the angiogenesis family, and angiogenesis proteins from other organisms, which are cloned and expressed as outlined below. Thus, probe or degenerate polymerase chain reaction (PCR) primer sequences may be used to find other related angiogenesis proteins from humans or other organisms. As will be appreciated by those in the art, particularly useful probe and/or PCR primer sequences include the unique areas of the angiogenesis nucleic acid sequence. As is generally known in the art, preferred PCR primers are from about 15 to about 35 nucleotides in length, with from about 20 to about 30 being preferred, and may contain inosine as needed. The conditions for the PCR reaction are well known in the art (e.g., Innis, PCR Protocols, supra).

In addition, as is outlined herein, angiogenesis proteins can be made that are longer than those encoded by the nucleic acids of the figures, e.g., by the elucidation of extended sequences, the addition of epitope or purification tags, the addition of other fusion sequences, etc.

Angiogenesis proteins may also be identified as being encoded by angiogenesis nucleic acids. Thus, angiogenesis proteins are encoded by nucleic acids that will hybridize to the sequences of the sequence listings, or their complements, as outlined herein.

In a preferred embodiment, when the angiogenesis protein is to be used to generate antibodies, e.g., for immunotherapy or immunodiagnosis, the angiogenesis protein should share at least one epitope or determinant with the full length protein. By "epitope" or "determinant" herein is typically meant a portion of a protein which will generate and/or bind an antibody or T-cell receptor in the context of MHC. Thus, in most instances, antibodies made to a smaller angiogenesis protein will be able to bind to the full-length protein, particularly linear epitopes. In a preferred embodiment, the epitope is unique; that is, antibodies generated to a unique epitope show little or no cross-reactivity. In a preferred embodiment, the epitope is selected from a protein sequence set out in Table 8.

Methods of preparing polyclonal antibodies are known to the skilled artisan (e.g., Coligan, supra; and Harlow & Lane, supra). Polyclonal antibodies can be raised in a mammal, e.g., by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include a protein encoded by a nucleic acid of the figures or fragment thereof or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

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The antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized in vitro. The immunizing agent will typically include a polypeptide encoded by a nucleic acid of Tables 1-8, or fragment thereof, or a fusion protein thereof. Generally, either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

In one embodiment, the antibodies are bispecific antibodies. Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens or that have binding specificities for two epitopes on the same antigen. In one embodiment, one of the binding specificities is for a protein encoded by a nucleic acid Tables 1-8 or a fragment thereof, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit, preferably one that is tumor specific. Alternatively, tetramer-type technology may create multivalent reagents.

In a preferred embodiment, the antibodies to angiogenesis protein are capable of reducing or eliminating a biological function of an angiogenesis protein, as is described below. That is, the addition of anti-angiogenesis protein antibodies (either polyclonal or preferably monoclonal) to angiogenic tissue (or cells containing angiogenesis) may reduce or eliminate the angiogenesis activity. Generally, at least a 25% decrease in activity is preferred, with at least about 50% being particularly preferred and about a 95-100% decrease being especially preferred.

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In a preferred embodiment the antibodies to the angiogenesis proteins are humanized antibodies (e.g., Xenerex Biosciences, Mederex, Inc., Abgenix, Inc., Protein Design Labs, Inc.) Humanized forms of non-human (e.g., murine) antibodies are chimeric molecules of immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', F(ab')2 or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues form a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a nonhuman species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, a humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the framework (FR) regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human

immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta. Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as import residues, which are typically taken from an import variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such humanized antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

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Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et 20 al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in 25 humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks et al., Bio/Technology 10, 779-783 (1992); Lonberg et al., Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild et al., Nature Biotechnology 14, 845-51 (1996): Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. 30 Immunol. 13 65-93 (1995).

By immunotherapy is meant treatment of angiogenesis with an antibody raised against angiogenesis proteins. As used herein, immunotherapy can be passive or active.

Passive immunotherapy as defined herein is the passive transfer of antibody to a recipient

(patient). Active immunization is the induction of antibody and/or T-cell responses in a recipient (patient). Induction of an immune response is the result of providing the recipient with an antigen to which antibodies are raised. As appreciated by one of ordinary skill in the art, the antigen may be provided by injecting a polypeptide against which antibodies are desired to be raised into a recipient, or contacting the recipient with a nucleic acid capable of expressing the antigen and under conditions for expression of the antigen, leading to an immune response.

In a preferred embodiment the angiogenesis proteins against which antibodies are raised are secreted proteins as described above. Without being bound by theory, antibodies used for treatment, bind and prevent the secreted protein from binding to its receptor, thereby inactivating the secreted angiogenesis protein.

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In another preferred embodiment, the angiogenesis protein to which antibodies are raised is a transmembrane protein. Without being bound by theory, antibodies used for treatment, bind the extracellular domain of the angiogenesis protein and prevent it from binding to other proteins, such as circulating ligands or cell-associated molecules. The 15 antibody may cause down-regulation of the transmembrane angiogenesis protein. As will be appreciated by one of ordinary skill in the art, the antibody may be a competitive, noncompetitive or uncompetitive inhibitor of protein binding to the extracellular domain of the angiogenesis protein. The antibody is also an antagonist of the angiogenesis protein. 20 Further, the antibody prevents activation of the transmembrane angiogenesis protein. In one aspect, when the antibody prevents the binding of other molecules to the angiogenesis protein, the antibody prevents growth of the cell. The antibody may also be used to target or sensitize the cell to cytotoxic agents, including, but not limited to TNF-0, TNF-B, IL-1, INF-y and IL-2, or chemotherapeutic agents including 5FU, vinblastine, actinomycin D, cisplatin, methotrexate, and the like. In some instances the antibody belongs to a sub-type that 25 activates serum complement when complexed with the transmembrane protein thereby mediating cytotoxicity or antigen-dependent cytotoxicity (ADCC). Thus, angiogenesis is treated by administering to a patient antibodies directed against the transmembrane angiogenesis protein. Antibody-labeling may activate a co-toxin, localize a toxin payload, or 30 otherwise provide means to locally ablate cells.

In another preferred embodiment, the antibody is conjugated or fused to an effector moiety. The effector moiety can be any number of molecules, including labelling mojeties such as radioactive labels or fluorescent labels, or can be a therapeutic moiety. In

one aspect the therapeutic moiety is a small molecule that modulates the activity of the angiogenesis protein. In another aspect the therapeutic moiety modulates the activity of molecules associated with or in close proximity to the angiogenesis protein. The therapeutic moiety may inhibit enzymatic activity such as protease or collagenase activity associated with angiogenesis, or be an attractant of other cells, such as NK cells.

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In a preferred embodiment, the therapeutic moiety can also be a cytotoxic agent. In this method, targeting the cytotoxic agent to angiogenesis tissue or cells, results in a reduction in the number of afflicted cells, thereby reducing symptoms associated with angiogenesis. Cytotoxic agents are numerous and varied and include, but are not limited to, cytotoxic drugs or toxins or active fragments of such toxins. Suitable toxins and their corresponding fragments include diphtheria A chain, exotoxin A chain, ricin A chain, abrin A chain, curcin, crotin, phenomycin, enomycin and the like. Cytotoxic agents also include radiochemicals made by conjugating radioisotopes to antibodies raised against angiogenesis proteins, or binding of a radionuclide to a chelating agent that has been covalently attached to the antibody. Targeting the therapeutic moiety to transmembrane angiogenesis proteins not only serves to increase the local concentration of therapeutic moiety in the angiogenesis afflicted area, but also serves to reduce deleterious side effects that may be associated with the therapeutic moiety.

In another preferred embodiment, the angiogenesis protein against which the antibodies are raised is an intracellular protein. In this case, the antibody may be conjugated or fused to a protein which facilitates entry into the cell. In one case, the antibody enters the cell by endocytosis. In another embodiment, a nucleic acid encoding the antibody is administered to the individual or cell. Moreover, wherein the angiogenesis protein can be targeted within a cell, i.e., the nucleus, an antibody thereto contains a signal for that target localization, i.e., a nuclear localization signal.

The angiogenesis antibodies of the invention specifically bind to angiogenesis proteins. By "specifically bind" herein is meant that the antibodies bind to the protein with a K_d of at least about 0.1 mM, more usually at least about 1 μM , preferably at least about 0.1 μM or better, and most preferably, 0.01 μM or better. Selectivity of binding is also important.

In a preferred embodiment, the angiogenesis protein is purified or isolated after expression. Angiogenesis proteins may be isolated or purified in a variety of ways known to those skilled in the art depending on what other components are present in the sample. Standard purification methods include electrophoretic, molecular, immunological

and chromatographic techniques, including ion exchange, hydrophobic, affinity, and reversephase HPLC chromatography, and chromatofocusing. For example, the angiogenesis protein
may be purified using a standard anti-angiogenesis protein antibody column. Ultrafiltration
and diafiltration techniques, in conjunction with protein concentration, are also useful. For
general guidance in suitable purification techniques, see Scopes, R., Protein Purification,
Springer-Verlag, NY (1982). The degree of purification necessary will vary depending on
the use of the angiogenesis protein. In some instances no purification will be necessary.

Once expressed and purified if necessary, the angiogenesis proteins and nucleic acids are useful in a number of applications. They may be used as immunoselection reagents, as vaccine reagents, as screening agents, etc.

Detection of angiogenesis sequence for diagnostic and therapeutic applications

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In one aspect, the RNAexpression levels of genes are determined for different cellular states in the angiogenesis phenotype. Expression levels of genes in normal tissue (i.e., not undergoing angiogenesis) and in angiogenesis tissue (and in some cases, for varying severities of angiogenesis that relate to prognosis, as outlined below) are evaluated to provide expression profiles. An expression profile of a particular cell state or point of development is essentially a "fingerprint" of the state. While two states may have any particular gene similarly expressed, the evaluation of a number of genes simultaneously allows the generation of a gene expression profile that is reflective of the state of the cell. By comparing expression profiles of cells in different states, information regarding which genes are important (including both up- and down-regulation of genes) in each of these states is obtained. Then, diagnosis may be performed or confirmed to determine whether a tissue sample has the gene expression profile of normal or angiogenesic tissue. This will provide for molecular diagnosis of related conditions.

"Differential expression," or grammatical equivalents as used herein, refers to qualitative or quantitative differences in the temporal and/or cellular gene expression patterns within and among cells and tissue. Thus, a differentially expressed gene can qualitatively have its expression altered, including an activation or inactivation, in, e.g., normal versus angiogenic tissue. Genes may be turned on or turned off in a particular state, relative to another state thus permitting comparison of two or more statese. A qualitatively regulated gene will exhibit an expression pattern within a state or cell type which is detectable by standard techniques. Some genes will be expressed in one state or cell type, but not in both. Alternatively, the difference in expression may be quantitative, e.g., in that

expression is increased or decreased; i.e., gene expression is either upregulated, resulting in an increased amount of transcript, or downregulated, resulting in a decreased amount of transcript. The degree to which expression differs need only be large enough to quantify via standard characterization techniques as outlined below, such as by use of Affymetrix GeneChipTM expression arrays, Lockhart, Nature Biotechnology, 14:1675-1680 (1996), hereby expressly incorporated by reference. Other techniques include, but are not limited to, quantitative reverse transcriptase PCR, Northern analysis and RNase protection. As outlined above, preferably the change in expression (i.e., upregulation or downregulation) is at least about 50%, more preferably at least about 150%, more preferably at least about 150%, with from 300 to at least 1000% being especially preferred.

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Evaluation may be at the gene transcript, or the protein level. The amount of gene expression may be monitored using nucleic acid probes to the DNA or RNA equivalent of the gene transcript, and the quantification of gene expression levels, or, alternatively, the final gene product itself (protein) can be monitored, e.g., with antibodies to the angiogenesis protein and standard immunoassays (ELISAs, etc.) or other techniques, including mass spectroscopy assays, 2D gel electrophoresis assays, etc. Proteins corresponding to angiogenesis genes, i.e., those identified as being important in an angiogenesis phenotype, can be evaluated in an angiogenesis diagnostic test.

In a preferred embodiment, gene expression monitoring is performed simultaneously on a number of genes. Multiple protein expression monitoring can be performed as well. Similarly, these assays may be performed on an individual basis as well.

In this embodiment, the angiogenesis nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of angiogenesis sequences in a particular cell. The assays are further described below in the example. PCR techniques can be used to provide greater sensitivity.

In a preferred embodiment nucleic acids encoding the angiogenesis protein are detected. Although DNA or RNA encoding the angiogenesis protein may be detected, of particular interest are methods wherein an mRNA encoding an angiogenesis protein is detected. Probes to detect mRNA can be a nucleotide/deoxynucleotide probe that is complementary to and hybridizes with the mRNA and includes, but is not limited to, oligonucleotides, cDNA or RNA. Probes also should contain a detectable label, as defined herein. In one method the mRNA is detected after immobilizing the nucleic acid to be examined on a solid support such as nylon membranes and hybridizing the probe with the sample. Following washing to remove the non-specifically bound probe, the label is

detected. In another method detection of the mRNA is performed in situ. In this method permeabilized cells or tissue samples are contacted with a detectably labeled nucleic acid probe for sufficient time to allow the probe to hybridize with the target mRNA. Following washing to remove the non-specifically bound probe, the label is detected. For example a digoxygenin labeled riboprobe (RNA probe) that is complementary to the mRNA encoding an angiogenesis protein is detected by binding the digoxygenin with an anti-digoxygenin secondary antibody and developed with nitro blue tetrazolium and 5-bromo-4-chloro-3-indoyl phosphate.

In a preferred embodiment, various proteins from the three classes of proteins as described herein (secreted, transmembrane or intracellular proteins) are used in diagnostic assays. The angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing angiogenesis sequences are used in diagnostic assays. This can be performed on an individual gene or corresponding polypeptide level. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes and/or corresponding polypeptides.

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As described and defined herein, angiogenesis proteins, including intracellular, transmembrane or secreted proteins, find use as markers of angiogenesis. Detection of these proteins in putative angiogenesis itssue allows for detection or diagnosis of angiogenesis. In one embodiment, antibodies are used to detect angiogenesis proteins. A preferred method separates proteins from a sample by electrophoresis on a gel (typically a denaturing and reducing protein gel, but may be another type of gel, including isoelectric focusing gels and the like). Following separation of proteins, the angiogenesis protein is detected, e.g., by immunoblotting with antibodies raised against the angiogenesis protein. Methods of immunoblotting are well known to those of ordinary skill in the art.

In another preferred method, antibodies to the angiogenesis protein find use in in situ imaging techniques, e.g., in histology (e.g., Methods in Cell Biology: Antibodies in Cell Biology, volume 37 (Asai, ed. 1993)). In this method cells are contacted with from one to many antibodies to the angiogenesis protein(s). Following washing to remove non-specific antibody binding, the presence of the antibody or antibodies is detected. In one embodiment the antibody is detected by incubating with a secondary antibody that contains a detectable label. In another method the primary antibody to the angiogenesis protein(s) contains a detectable label, for example an enzyme marker that can act on a substrate. In another preferred embodiment each one of multiple primary antibodies contains a distinct and

detectable label. This method finds particular use in simultaneous screening for a plurality of angiogenesis proteins. As will be appreciated by one of ordinary skill in the art, many other histological imaging techniques are alsoprovided by the invention.

In a preferred embodiment the label is detected in a fluorometer which has the ability to detect and distinguish emissions of different wavelengths. In addition, a fluorescence activated cell sorter (FACS) can be used in the method.

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In another preferred embodiment, antibodies find use in diagnosing angiogenesis from biological samples, such as blood, urine, sputum, or other bodily fluids. As previously described, certain angiogenesis proteins are secreted/circulating molecules. Blood samples, therefore, are useful as samples to be probed or tested for the presence of secreted angiogenesis proteins. Antibodies can be used to detect an angiogenesis protein by previously described immunoassay techniques including ELISA, immunoblotting (Western blotting), immunoprecipitation, BIACORE technology and the like. Conversely, the presence of antibodies may indicate an immune response against an endogenous angiogenesis protein.

In a preferred embodiment, in situ hybridization of labeled angiogenesis nucleic acid probes to tissue arrays is done. For example, arrays of tissue samples, including angiogenesis tissue and/or normal tissue, are made. In situ hybridization (see, e.g., Ausubel, supra) is then performed. When comparing the fingerprints between an individual and a standard, the skilled artisan can make a diagnosis, a prognosis, or a prediction based on the findings. It is further understood that the genes which indicate the diagnosis may differ from those which indicate the prognosis and molecular profiling of the condition of the cells may lead to distinctions between responsive or refractory conditions or may be predictive of outcomes.

In a preferred embodiment, the angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing angiogenesis sequences are used in prognosis assays. As above, gene expression profiles can be generated that correlate to angiogenesis severity, in terms of long term prognosis. Again, this may be done on either a protein or gene level, with the use of genes being preferred. As above, angiogenesis probes may be attached to biochips for the detection and quantification of angiogenesis sequences in a tissue or patient. The assays proceed as outlined above for diagnosis. PCR method may provide more sensitive and accurate quantification.

In a preferred embodiment members of the three classes of proteins as described herein are used in drug screening assays. The angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing angiogenesis sequences are used in drug

screening assays or by evaluating the effect of drug candidates on a "gene expression profile" or expression profile of polypeptides. In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent (e.g., Zlokarnik, et al., Science 279, 84-8 (1998); Heid, Genome Res 6:986-94, 1996).

In a preferred embodiment, the angiogenesis proteins, antibodies, nucleic acids, modified proteins and cells containing the native or modified angiogenesis proteins are used in screening assays. That is, the present invention provides novel methods for screening for compositions which modulate the angiogenesis phenotype or an identified physiological function of an angiogenesis protein. As above, this can be done on an individual gene level or by evaluating the effect of drug candidates on a "gene expression profile". In a preferred embodiment, the expression profiles are used, preferably in conjunction with high throughput screening techniques to allow monitoring for expression profile genes after treatment with a candidate agent, see Zlokamik, supra.

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Having identified the differentially expressed genes herein, a variety of assays may be executed. In a preferred embodiment, assays may be run on an individual gene or protein level. That is, having identified a particular gene as up regulated in angiogenesis, test compounds can be screened for the ability to modulate gene expression or for binding to the angiogenic protein. "Modulation" thus includes both an increase and a decrease in gene expression. The preferred amount of modulation will depend on the original change of the gene expression in normal versus tissue undergoing angiogenesis, with changes of at least 10%, preferably 50%, more preferably 100-300%, and in some embodiments 300-1000% or greater. Thus, if a gene exhibits a 4-fold increase in angiogenic tissue compared to normal tissue, a decrease of about four-fold is often desired; similarly, a 10-fold decrease in angiogenic tissue compared to normal tissue often provides a target value of a 10-fold increase in expression to be induced by the test compound.

The amount of gene expression may be monitored using nucleic acid probes and the quantification of gene expression levels, or, alternatively, the gene product itself can be monitored, e.g., through the use of antibodies to the angiogenesis protein and standard immunoassays. Proteomics and separation techniques may also allow quantification of expression.

In a preferred embodiment, gene expression or protein monitoring of a number of entitities, i.e., an expression profile, is monitored simultaneously. Such profiles will typically invove a plurality of those entitites described herein..

In this embodiment, the angiogenesis nucleic acid probes are attached to biochips as outlined herein for the detection and quantification of angiogenesis sequences in a particular cell. Alternatively, PCR may be used. Thus, a series, e.g., of microtiter plate, may be used with dispensed primers in desired wells. A PCR reaction can then be performed and analyzed for each well.

Modulators of angiogenesis

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Expression monitoring can be performed to identify compounds that modify the expression of one or more angiogenesis-associated sequences, e.g., a polynucleotide sequence set out in Tables 1-8. Generally, in a preferred embodiment, a test modulator is added to the cells prior to analysis. Moreover, screens are also provided to identify agents that modulate angiogenesis, modulate angiogenesis proteins, bind to an angiogenesis protein, or interfere with the binding of an angiogenesis protein and an antibody or other binding partner.

The term "test compound" or "drug candidate" or "modulator" or grammatical equivalents as used herein describes any molecule, e.g., protein, oligopeptide, small organic molecule, polysaccharide, polynucleotide, etc., to be tested for the capacity to directly or indirectly alter the angiogenesis phenotype or the expression of an angiogenesis sequence, e.g., a nucleic acid or protein sequence. In preferred embodiments, modulators alter expression profiles, or expression profile nucleic acids or proteins provided herein. In one embodiment, the modulator suppresses an angiogenesis phenotype, for example to a normal tissue fingerprint. In another embodiment, a modulator induced an angiogenesis phenotype. Generally, a plurality of assay mixtures are run in parallel with different agent concentrations to obtain a differential response to the various concentrations. Typically, one of these concentrations serves as a negative control, i.e., at zero concentration or below the level of detection.

In one aspect, a modulator will neutralize the effect of an angiogenesis protein.

By "neutralize" is meant that activity of a protein is inhibited or blocked and thereby has substantially no effect on a cell.

In certain embodiments, combinatorial libraries of potential modulators will be screened for an ability to bind to an angiogenesis polypeptide or to modulate activity.

Conventionally, new chemical entities with useful properties are generated by identifying a chemical compound (called a "lead compound") with some desirable property or activity, e.g., inhibiting activity, creating variants of the lead compound, and evaluating the property

and activity of those variant compounds. Often, high throughput screening (HTS) methods are employed for such an analysis.

In one preferred embodiment, high throughput screening methods involve providing a library containing a large number of potential therapeutic compounds (candidate compounds). Such "combinatorial chemical libraries" are then screened in one or more assays to identify those library members (particular chemical species or subclasses) that display a desired characteristic activity. The compounds thus identified can serve as conventional "lead compounds" or can themselves be used as potential or actual therapeutics.

A combinatorial chemical library is a collection of diverse chemical compounds generated by either chemical synthesis or biological synthesis by combining a number of chemical "building blocks" such as reagents. For example, a linear combinatorial chemical library, such as a polypeptide (e.g., mutein) library, is formed by combining a set of chemical building blocks called amino acids in every possible way for a given compound length (i.e., the number of amino acids in a polypeptide compound). Millions of chemical compounds can be synthesized through such combinatorial mixing of chemical building blocks (Gallop et al. (1994) J. Med. Chem. 37(9): 1233-1251).

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Preparation and screening of combinatorial chemical libraries is well known to those of skill in the art. Such combinatorial chemical libraries include, but are not limited to, peptide libraries (see, e.g., U.S. Patent No. 5.010,175, Furka (1991) Int. J. Pept. Prot. Res., 37: 487-493, Houghton et al. (1991) Nature, 354: 84-88), peptoids (PCT Publication No WO 20 91/19735, 26 Dec. 1991), encoded peptides (PCT Publication WO 93/20242, 14 Oct. 1993), random bio-oligomers (PCT Publication WO 92/00091, 9 Jan. 1992), benzodiazepines (U.S. Pat. No. 5,288,514), diversomers such as hydantoins, benzodiazepines and dipeptides (Hobbs et al., (1993) Proc. Nat. Acad. Sci. USA 90: 6909-6913), vinylogous polypeptides (Hagihara et al. (1992) J. Amer. Chem. Soc. 114: 6568), nonpeptidal peptidomimetics with a Beta-D-25 Glucose scaffolding (Hirschmann et al., (1992) J. Amer. Chem. Soc. 114: 9217-9218), analogous organic syntheses of small compound libraries (Chen et al. (1994) J. Amer. Chem. Soc. 116; 2661), oligocarbamates (Cho, et al., (1993) Science 261:1303), and/or peptidyl phosphonates (Campbell et al., (1994) J. Org. Chem. 59: 658). See, generally, Gordon et al., (1994) J. Med. Chem. 37:1385, nucleic acid libraries (see, e.g., Strategene, Corp.), peptide 30 nucleic acid libraries (see, e.g., U.S. Patent 5,539,083), antibody libraries (see, e.g., Vaughn et al. (1996) Nature Biotechnology, 14(3): 309-314), and PCT/US96/10287), carbohydrate libraries (see, e.g., Liang et al., (1996) Science, 274: 1520-1522, and U.S. Patent No. 5.593,853), and small organic molecule libraries (see, e.g., benzodiazepines, Baum (1993)

C&EN, Jan 18, page 33; isoprenoids, U.S. Patent No. 5,569,588; thiazolidinones and metathiazanones, U.S. Patent No. 5,549,974; pyrrolidines, U.S. Patent Nos. 5,525,735 and 5,519,134; morpholino compounds, U.S. Patent No. 5,506,337; benzodiazepines, U.S. Patent No. 5,288,514; and the like).

Devices for the preparation of combinatorial libraries are commercially available (see, e.g., 357 MPS, 390 MPS, Advanced Chem Tech, Louisville KY, Symphony, Rainin, Woburn, MA, 433A Applied Biosystems, Foster City, CA, 9050 Plus, Millipore, Bedford, MA).

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A number of well known robotic systems have also been developed for solution phase chemistries. These systems include automated workstations like the automated synthesis apparatus developed by Takeda Chemical Industries, LTD. (Osaka, Japan) and many robotic systems utilizing robotic arms (Zymate II, Zymark Corporation, Hopkinton, Mass.; Orca, Hewlett-Packard, Palo Alto, Calif.), which mimic the manual synthetic operations performed by a chemist. Any of the above devices are suitable for use with the present invention. The nature and implementation of modifications to these devices (if any) so that they can operate as discussed herein will be apparent to persons skilled in the relevant art. In addition, numerous combinatorial libraries are themselves commercially available (see, e.g., ComGenex, Princeton, N.J., Asinex, Moscow, Ru, Tripos, Inc., St. Louis, MO, ChemStar, Ltd, Moscow, RU, 3D Pharmaceuticals, Exton, PA, Martek Biosciences, Columbia, MD, etc.).

The assays to identify modulators are amenable to high throughput screening. Preferred assays thus detect enhancement or inhibition of angiogenesis gene transcription, inhibition or enhancement of polypeptide expression, and inhibition or enhancement of polypeptide activity.

High throughput assays for the presence, absence, quantification, or other properties of particular nucleic acids or protein products are well known to those of skill in the art. Similarly, binding assays and reporter gene assays are similarly well known. Thus, for example, U.S. Patent No. 5,559,410 discloses high throughput screening methods for proteins, U.S. Patent No. 5,585,639 discloses high throughput screening methods for nucleic acid binding (i.e., in arrays), while U.S. Patent Nos. 5,576,220 and 5,541,061 disclose high throughput methods of screening for ligand/antibody binding.

In addition, high throughput screening systems are commercially available (see, e.g., Zymark Corp., Hopkinton, MA; Air Technical Industries, Mentor, OH; Beckman Instruments. Inc. Fullerton, CA; Precision Systems. Inc., Natick, MA, etc.). These systems

typically automate entire procedures, including all sample and reagent pipetting, liquid dispensing, timed incubations, and final readings of the microplate in detector(s) appropriate for the assay. These configurable systems provide high throughput and rapid start up as well as a high degree of flexibility and customization. The manufacturers of such systems provide detailed protocols for various high throughput systems. Thus, for example, Zymark Corp. provides technical bulletins describing screening systems for detecting the modulation of gene transcription, ligand binding, and the like.

In one embodiment, modulators are proteins, often naturally occurring proteins or fragments of naturally occurring proteins. Thus, e.g., cellular extracts containing proteins, or random or directed digests of proteinaceous cellular extracts, may be used. In this way libraries of proteins may be made for screening in the methods of the invention. Particularly preferred in this embodiment are libraries of bacterial, fungal, viral, and mammalian proteins, with the latter being preferred, and human proteins being especially preferred. Paticularly useful test compound will be directed to the class of proteins to which the target belongs, e.g., substrates for enzymes or ligands and receptors.

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In a preferred embodiment, modulators are peptides of from about 5 to about 30 amino acids, with from about 5 to about 20 amino acids being preferred, and from about 7 to about 15 being particularly preferred. The peptides may be digests of naturally occurring proteins as is outlined above, random peptides, or "biased" random peptides. By "randomized" or grammatical equivalents herein is meant that each nucleic acid and peptide consists of essentially random nucleotides and amino acids, respectively. Since generally these random peptides (or nucleic acids, discussed below) are chemically synthesized, they may incorporate any nucleotide or amino acid at any position. The synthetic process can be designed to generate randomized proteins or nucleic acids, to allow the formation of all or most of the possible combinations over the length of the sequence, thus forming a library of randomized acididate bioactive proteinaceous agents.

In one embodiment, the library is fully randomized, with no sequence preferences or constants at any position. In a preferred embodiment, the library is biased. That is, some positions within the sequence are either held constant, or are selected from a limited number of possibilities. For example, in a preferred embodiment, the nucleotides or amino acid residues are randomized within a defined class, for example, of hydrophobic amino acids, hydrophilic residues, sterically biased (either small or large) residues, towards the creation of nucleic acid binding domains, the creation of cysteines, for cross-linking,

prolines for SH-3 domains, serines, threonines, tyrosines or histidines for phosphorylation sites, etc., or to purines, etc.

Modulators of angiogenesis can also be nucleic acids, as defined above.

As described above generally for proteins, nucleic acid modulating agents may be naturally occurring nucleic acids, random nucleic acids, or "biased" random nucleic acids. For example, digests of procaryotic or eucaryotic genomes may be used as is outlined above for proteins.

In a preferred embodiment, the candidate compounds are organic chemical mojeties, a wide variety of which are available in the literature.

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After the candidate agent has been added and the cells allowed to incubate for some period of time, the sample containing a target sequence to be analyzed is added to the biochip. If required, the target sequence is prepared using known techniques. For example, the sample may be treated to lyse the cells, using known lysis buffers, electroporation, etc., with purification and/or amplification such as PCR performed as appropriate. For example, an *in vitro* transcription with labels covalently attached to the nucleotides is performed. Generally, the nucleic acids are labeled with biotin-FITC or PE, or with cy3 or cy5.

In a preferred embodiment, the target sequence is labeled with, for example, a fluorescent, a chemiluminescent, a chemical, or a radioactive signal, to provide a means of detecting the target sequence's specific binding to a probe. The label also can be an enzyme, such as, alkaline phosphatase or horseradish peroxidase, which when provided with an appropriate substrate produces a product that can be detected. Alternatively, the label can be a labeled compound or small molecule, such as an enzyme inhibitor, that binds but is not catalyzed or altered by the enzyme. The label also can be a moiety or compound, such as, an epitope tag or biotin which specifically binds to streptavidin. For the example of biotin, the streptavidin is labeled as described above, thereby, providing a detectable signal for the bound target sequence. Unbound labeled streptavidin is typically removed prior to analysis.

As will be appreciated by those in the art, these assays can be direct hybridization assays or can comprise "sandwich assays", which include the use of multiple probes, as is generally outlined in U.S. Patent Nos. 5,681,702, 5,597,909, 5,545,730, 5,594,117, 5,591,584, 5,571,670, 5,580,731, 5,571,670, 5,591,584, 5,624,802, 5,635,352, 5,594,118, 5,359,100, 5,124,246 and 5,681,697, all of which are hereby incorporated by reference. In this embodiment, in general, the target nucleic acid is prepared as outlined above, and then added to the biochip comprising a plurality of nucleic acid probes, under conditions that allow the formation of a hybridization complex.

A variety of hybridization conditions may be used in the present invention, including high, moderate and low stringency conditions as outlined above. The assays are generally run under stringency conditions which allows formation of the label probe hybridization complex only in the presence of target. Stringency can be controlled by altering a step parameter that is a thermodynamic variable, including, but not limited to, temperature, formamide concentration, salt concentration, chaotropic salt concentration pH, organic solvent concentration, etc.

These parameters may also be used to control non-specific binding, as is generally outlined in U.S. Patent No. 5,681,697. Thus it may be desirable to perform certain steps at higher stringency conditions to reduce non-specific binding.

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The reactions outlined herein may be accomplished in a variety of ways. Components of the reaction may be added simultaneously, or sequentially, in different orders, with preferred embodiments outlined below. In addition, the reaction may include a variety of other reagents. These include salts, buffers, neutral proteins, e.g. albumin, detergents, etc. which may be used to facilitate optimal hybridization and detection, and/or reduce non-specific or background interactions. Reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may also be used as appropriate, depending on the sample preparation methods and purity of the target.

The assay data are analyzed to determine the expression levels, and changes in expression levels as between states, of individual genes, forming a gene expression profile.

Screens are performed to identify modulators of the angiogenesis phenotype. In one embodiment, screening is performed to identify modulators that can induce or suppress a particular expression profile, thus preferably generating the associated phenotype. In another embodiment, e.g., for diagnostic applications, having identified differentially expressed genes important in a particular state, screens can be performed to identify modulators that alter expression of individual genes. In an another embodiment, screening is performed to identify modulators that alter a biological function of the expression product of a differentially expressed gene. Again, having identified the importance of a gene in a particular state, screens are performed to identify agents that bind and/or modulate the biological activity of the gene product.

In addition screens can be done for genes that are induced in response to a candidate agent. After identifying a modulator based upon its ability to suppress an angiogenesis expression pattern leading to a normal expression pattern, or to modulate a single angiogenesis gene expression profile so as to mimic the expression of the gene from

normal tissue, a screen as described above can be performed to identify genes that are specifically modulated in response to the agent. Comparing expression profiles between normal tissue and agent treated angiogenesis tissue reveals genes that are not expressed in normal tissue or angiogenesis tissue, but are expressed in agent treated tissue. These agent-specific sequences can be identified and used by methods described herein for angiogenesis genes or proteins. In particular these sequences and the proteins they encode find use in marking or identifying agent treated cells. In addition, antibodies can be raised against the agent induced proteins and used to target novel therapeutics to the treated angiogenesis tissue sample.

Thus, in one embodiment, a test compound is administered to a population of angiogenic cells, that have an associated angiogenesis expression profile. By "administration" or "contacting" herein is meant that the candidate agent is added to the cells in such a manner as to allow the agent to act upon the cell, whether by uptake and intracellular action, or by action at the cell surface. In some embodiments, nucleic acid encoding a proteinaceous candidate agent (i.e., a peptide) may be put into a viral construct such as an adenoviral or retroviral construct, and added to the cell, such that expression of the peptide agent is accomplished, e.g., PCT US97/01019. Regulatable gene therapy systems can also be used

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Once the test compound has been administered to the cells, the cells can be washed if desired and are allowed to incubate under preferably physiological conditions for some period of time. The cells are then harvested and a new gene expression profile is generated, as outlined herein.

Thus, for example, angiogenesis tissue may be screened for agents that modulate, e.g., induce or suppress the angiogenesis phenotype. A change in at least one gene, preferably many, of the expression profile indicates that the agent has an effect on angiogenesis activity. By defining such a signature for the angiogenesis phenotype, screens for new drugs that alter the phenotype can be devised. With this approach, the drug target need not be known and need not be represented in the original expression screening platform, nor does the level of transcript for the target protein need to change.

Measure of angiogenesis polypeptide activity, or of angiogenesis or the angiogenic phenotype can be performed using a variety of assays. For example, the effects of the test compounds upon the function of the anagiogenesis polypeptides can be measured by examining parameters described above. A suitable physiological change that affects activity can be used to assess the influence of a test compound on the polypeptides of this invention.

When the functional consequences are determined using intact cells or animals, one can also measure a variety of effects such as, in the case of angiogenesis associated with tumors, tumor growth, neovascularization, hormone release, transcriptional changes to both known and uncharacterized genetic markers (e.g., northern blots), changes in cell metabolism such as cell growth or pH changes, and changes in intracellular second messengers such as cGMP. In the assays of the invention, mammalian angiogenesis polypeptide is typically used, e.g., mouse, preferably human.

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A variety of angiogenesis assays are known to those of skill in the art. Various models have been employed to evaluate angiogenesis (e.g., Croix et al., Science 289:1197-1202, 2000 and Kahn et al., Amer. J. Pathol. 156:1887-1900). Assessement of angiogenesis in the presence of a potential modulator of angiogenesis can be performed using cell-cultrebased angiogenesis assays, e.g., endothelial cell tube formation assays, as well as other bioassays such as the chick CAM assay, the mouse corneal assay, and assays measuring the effect of administering potential modulators on implanted tumors. The chick CAM assay is described by O'Reilly, et al. Cell 79: 315-328, 1994. Briefly, 3 day old chicken embryos with intact volks are separated from the egg and placed in a petri dish. After 3 days of incubation, a methylcellulose disc containing the protein to be tested is applied to the CAM of individual embryos. After about 48 hours of incubation, the embryos and CAMs are observed to determine whether endothelial growth has been inhibited. The mouse corneal assay involves implanting a growth factor-containing pellet, along with another pellet containing the suspected endothelial growth inhibitor, in the cornea of a mouse and observing the pattern of capillaries that are elaborated in the cornea. Angiogenesis can also be measured by determining the extent of neovascularization of a tumor. For example, carcinoma cells can be subcutaneously inoculated into athymic nude mice and tumor growth then monitored. The cancer cells are treated with an angiogenesis inhibitor, such as an antibody, or other compound that is exogenously administered, or can be transfected prior to inoculation with a polynucleotide inhibitor of angiogenesis. Immunoassays using endothelial cell-specific antibodies are typically used to stain for vascularization of tumor and the number of vessels in the tumor.

Assays to identify compounds with modulating activity can be performed in vitro. For example, an angiogenesis polypeptide is first contacted with a potential modulator and incubated for a suitable amount of time, e.g., from 0.5 to 48 hours. In one embodiment, the angiogenesis polypeptide levels are determined in vitro by measuring the level of protein or mRNA. The level of protein is measured using immunoassays such as western blotting,

ELISA and the like with an antibody that selectively binds to the angiogenesis polypeptide or a fragment thereof. For measurement of mRNA, amplification, e.g., using PCR, LCR, or hybridization assays, e.g., northern hybridization, RNAse protection, dot blotting, are preferred. The level of protein or mRNA is detected using directly or indirectly labeled detection agents, e.g., fluorescently or radioactively labeled nucleic acids, radioactively or enzymatically labeled antibodies, and the like, as described herein.

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Alternatively, a reporter gene system can be devised using the angiogenesis protein promoter operably linked to a reporter gene such as luciferase, green fluorescent protein, CAT, or β -gal. The reporter construct is typically transfected into a cell. After treatment with a potential modulator, the amount of reporter gene transcription, translation, or activity is measured according to standard techniques known to those of skill in the art.

In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular differentially expressed gene as important in a particular state, screening of modulators of the expression of the gene or the gene product itself can be done. The gene products of differentially expressed genes are sometimes referred to herein as "angiogenesis proteins". In preferred embodiments the angiogenesis protein comprises a sequence shown in Table 8. The angiogenesis protein may be a fragment, or alternatively, be the full length protein to a fragment shown herein.

Preferably, the angiogenesis protein is a fragment of approximately 14 to 24 amino acids long. More preferably the fragment is a soluble fragment. In one embodiment an angiogenesis protein is conjugated or fused to an immunogenic agent or BSA.

In one embodiment, screening for modulators of expression of specific genes is performed. Typically, the expression of only one or a few genes are evaluated. In another embodiment, screens are designed to first find compounds that bind to differentially expressed proteins. These compounds are then evaluated for the ability to modulate differentially expressed activity. Moreover, once initial candidate compounds are identified, variants can be further screened to better evaluate strucutre activity relationships.

In a preferred embodiment, binding assays are done. In general, purified or isolated gene product is used; that is, the gene products of one or more differentially expressed nucleic acids are made. For example, antibodies are generated to the protein gene products, and standard immunoassays are run to determine the amount of protein present. Alternatively, cells comprising the angiogenesis proteins can be used in the assays.

Thus, in a preferred embodiment, the methods comprise combining an angiogenesis protein and a candidate compound, and determining the binding of the compound to the angiogenesis protein. Preferred embodiments utilize the human angiogenesis protein, although other mammalian proteins may also be used, for example for the development of animal models of human disease. In some embodiments, as outlined herein, variant or derivative angiogenesis proteins may be used.

Generally, in a preferred embodiment of the methods herein, the angiogenesis protein or the candidate agent is non-diffusably bound to an insoluble support having isolated sample receiving areas (e.g. a microtiter plate, an array, etc.). The insoluble supports may be made of any composition to which the compositions can be bound, is readily separated from soluble material, and is otherwise compatible with the overall method of screening. The surface of such supports may be solid or porous and of any convenient shape. Examples of suitable insoluble supports include microtiter plates, arrays, membranes and beads. These are typically made of glass, plastic (e.g., polystyrene), polysaccharides, nylon or nitrocellulose, teflonTM, etc. Microtiter plates and arrays are especially convenient because a large number of assays can be carried out simultaneously, using small amounts of reagents and samples. The particular manner of binding of the composition is not crucial so long as it is compatible with the reagents and overall methods of the invention, maintains the activity of the composition and is nondiffusable. Preferred methods of binding include the use of antibodies (which do not sterically block either the ligand binding site or activation sequence when the protein is bound to the support), direct binding to "sticky" or ionic supports, chemical crosslinking, the synthesis of the protein or agent on the surface, etc. Following binding of the protein or agent, excess unbound material is removed by washing. The sample receiving areas may then be blocked through incubation with bovine serum albumin (BSA), casein or other innocuous protein or other moiety.

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In a preferred embodiment, the angiogenesis protein is bound to the support, and a test compound is added to the assay. Alternatively, the candidate agent is bound to the support and the angiogenesis protein is added. Novel binding agents include specific antibodies, non-natural binding agents identified in screens of chemical libraries, peptide analogs, etc. Of particular interest are screening assays for agents that have a low toxicity for human cells. A wide variety of assays may be used for this purpose, including labeled in vitro protein-protein binding assays, electrophoretic mobility shift assays, immunoassays for protein binding. functional assays (phosphorylation assays, etc.) and the like.

The determination of the binding of the test modulating compound to the angiogenesis protein may be done in a number of ways. In a preferred embodiment, the compound is labelled, and binding determined directly, e.g., by attaching all or a portion of the angiogenesis protein to a solid support, adding a labelled candidate agent (e.g., a fluorescent label), washing off excess reagent, and determining whether the label is present on the solid support. Various blocking and washing steps may be utilized as appropriate.

By "labeled" herein is meant that the compound is either directly or indirectly labeled with a label which provides a detectable signal, e.g. radioisotope, fluorescers, enzyme, antibodies, particles such as magnetic particles, chemiluminescers, or specific binding molecules, etc. Specific binding molecules, etc. Specific binding molecules, such as biotin and streptavidin, digoxin and antidigoxin, etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for detection, in accordance with known procedures, as outlined above. The label can directly or indirectly provide a detectable signal.

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In some embodiments, only one of the components is labeled, e.g., the proteins (or proteinaceous candidate compounds) can be labeled. Alternatively, more than one component can be labeled with different labels, e.g., 1²⁵I for the proteins and a fluorophor for the compound. Proximity reagents, e.g., quenching or energy transfer reagents are also useful.

In one embodiment, the binding of the test compound is determined by competitive binding assay. The competitor is a binding moiety known to bind to the target molecule (i.e. an angiogenesis protein), such as an antibody, peptide, binding partner, ligand, etc. Under certain circumstances, there may be competitive binding between the compound and the binding moiety, with the binding moiety displacing the compound. In one embodiment, the test compound is labeled. Either the compound, or the competitor, or both, is added first to the protein for a time sufficient to allow binding, if present. Incubations may be performed at a temperature which facilitates optimal activity, typically between 4 and 40°C. Incubation periods are typically optimized, e.g., to facilitate rapid high throughput screening. Typically between 0.1 and 1 hour will be sufficient. Excess reagent is generally removed or washed away. The second component is then added, and the presence or absence of the labeled component is followed, to indicate binding.

In a preferred embodiment, the competitor is added first, followed by the test compound. Displacement of the competitor is an indication that the test compound is binding to the angiogenesis protein and thus is capable of binding to, and potentially modulating, the

activity of the angiogenesis protein. In this embodiment, either component can be labeled. Thus, for example, if the competitor is labeled, the presence of label in the wash solution indicates displacement by the agent. Alternatively, if the test compound is labeled, the presence of the label on the support indicates displacement.

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In an alternative embodiment, the test compound is added first, with incubation and washing, followed by the competitor. The absence of binding by the competitor may indicate that the test compound is bound to the angiogenesis protein with a higher affinity. Thus, if the test compound is labeled, the presence of the label on the support, coupled with a lack of competitor binding, may indicate that the test compound is capable of binding to the angiogenesis protein.

In a preferred embodiment, the methods comprise differential screening to identity agents that are capable of modulating the activitity of the angiogenesis proteins. In this embodiment, the methods comprise combining an angiogenesis protein and a competitor in a first sample. A second sample comprises a test compound, an angiogenesis protein, and a competitor. The binding of the competitor is determined for both samples, and a change, or difference in binding between the two samples indicates the presence of an agent capable of binding to the angiogenesis protein and potentially modulating its activity. That is, if the binding of the competitor is different in the second sample relative to the first sample, the agent is capable of binding to the angiogenesis protein.

Alternatively, differential screening is used to identify drug candidates that bind to the native angiogenesis protein, but cannot bind to modified angiogenesis proteins. The structure of the angiogenesis protein may be modeled, and used in rational drug design to synthesize agents that interact with that site. Drug candidates that affect the activity of an angiogenesis protein are also identified by screening drugs for the ability to either enhance or reduce the activity of the protein.

Positive controls and negative controls may be used in the assays. Preferably control and test samples are performed in at least triplicate to obtain statistically significant results. Incubation of all samples is for a time sufficient for the binding of the agent to the protein. Following incubation, samples are washed free of non-specifically bound material and the amount of bound, generally labeled agent determined. For example, where a radiolabel is employed, the samples may be counted in a scintillation counter to determine the amount of bound compound.

A variety of other reagents may be included in the screening assays. These include reagents like salts, neutral proteins, e.g. albumin, detergents, etc. which may be used

to facilitate optimal protein-protein binding and/or reduce non-specific or background interactions. Also reagents that otherwise improve the efficiency of the assay, such as protease inhibitors, nuclease inhibitors, anti-microbial agents, etc., may be used. The mixture of components may be added in an order that provides for the requisite binding.

In a preferred embodiment, the invention provides methods for screening for a compound capable of modulating the activity of an angiogenesis protein. The methods comprise adding a test compound, as defined above, to a cell comprising angiogenesis proteins. Preferred cell types include almost any cell. The cells contain a recombinant nucleic acid that encodes an angiogenesis protein. In a preferred embodiment, a library of candidate agents are tested on a plurality of cells.

In one aspect, the assays are evaluated in the presence or absence or previous or subsequent exposure of physiological signals, for example hormones, antibodies, peptides, antigens, cytokines, growth factors, action potentials, pharmacological agents including chemotherapeutics, radiation, carcinogenics, or other cells (i.e. cell-cell contacts). In another example, the determinations are determined at different stages of the cell cycle process.

In this way, compounds that modulate angiogenesis agents are identified.

Compounds with pharmacological activity are able to enhance or interfere with the activity of the angiogenesis protein. Once identified, similar structures are evaluated to identify critical structural feature of the compound.

In one embodiment, a method of inhibiting angiogenic cell division is provided. The method comprises administration of an angiogenesis inhibitor. In another embodiment, a method of inhibiting angiogenesis is provided. The method comprises administration of an angiogenesis inhibitor. In a further embodiment, methods of treating cells or individuals with angiogenesis are provided. The method comprises administration of an angiogenesis inhibitor.

In one embodiment, an angiogenesis inhibitor is an antibody as discussed above. In another embodiment, the angiogenesis inhibitor is an antisense molecule.

Polynucleotide modulators of angiogenesis

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Antisense Polynucleotides

In certain embodiments, the activity of an angiogenesis-associated protein is downregulated, or entirely inhibited, by the use of antisense polynucleotide, i.e., a nucleic acid complementary to, and which can preferably hybridize specifically to, a coding mRNA nucleic acid sequence, e.g., an angiogenesis protein mRNA, or a subsequence thereof.

Binding of the antisense polynucleotide to the mRNA reduces the translation and/or stability of the mRNA.

In the context of this invention, antisense polynucleotides can comprise naturally-occurring nucleotides, or synthetic species formed from naturally-occurring subunits or their close homologs. Antisense polynucleotides may also have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other sulfur containing species which are known for use in the art. Analogs are comprehended by this invention so long as they function effectively to hybridize with the angiogenesis protein mRNA. See, e.g., Isis Pharmaceuticals, Carlsbad, CA; Scouttor, Inc., Natick, MA.

Such antisense polynucleotides can readily be synthesized using recombinant means, or can be synthesized in vitro. Equipment for such synthesis is sold by several vendors, including Applied Biosystems. The preparation of other oligonucleotides such as phosphorothioates and alkylated derivatives is also well known to those of skill in the art.

Antisense molecules as used herein include antisense or sense

oligonucleotides. Sense oligonucleotides can, e.g., be employed to block trancription by binding to the anti-sense strand. The antisense and sense oligonucleotide comprise a single-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target mRNA (sense) or DNA (antisense) sequences for angiogenesis molecules. A preferred antisense molecule is for an angiogenesis sequences in Tables 1-8, or for a ligand or activator thereof. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment generally at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

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Ribozymes

In addition to antisense polynucleotides, ribozymes can be used to target and inhibit transcription of angiogenesis-associated nucleotide sequences. A ribozyme is an RNA molecule that catalytically cleaves other RNA molecules. Different kinds of ribozymes have been described, including group I ribozymes, hammerhead ribozymes, hairpin ribozymes, RNase P, and axhead ribozymes (see, e.g., Castanotto et al. (1994) Adv. in Pharmacology 25: 289-317 for a general review of the properties of different ribozymes).

The general features of hairpin ribozymes are described, e.g., in Hampel et al. (1990) Nucl. Acids Res. 18: 299-304; Hampel et al. (1990) European Patent Publication No. 0

360 257; U.S. Patent No. 5,254,678. Methods of preparing are well known to those of skill in the art (see, e.g., Wong-Staal et al., WO 94/26877; Ojwang et al. (1993) Proc. Natl. Acad. Sci. USA 90: 6340-6344; Yamada et al. (1994) Human Gene Therapy 1: 39-45; Leavitt et al. (1995) Proc. Natl. Acad. Sci. USA 92: 699-703; Leavitt et al. (1994) Human Gene Therapy 5: 1151-120: and Yamada et al. (1994) Virology 205: 121-126).

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Polynucleotide modulators of angiogenesis may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell. Alternatively, a polynucleotide modulator of angiogenesis may be introduced into a cell containing the target nucleic acid sequence, e.g., by formation of an polynucleotide-lipid complex, as described in WO 90/10448. It is understood that the use of antisense molecules or knock out and knock in models may also be used in screening assays as discussed above, in addition to methods of treatment.

Thus, in one embodiment, methods of modulating angiogenesis in cells or organisms are provided. In one embodiment, the methods comprise administering to a cell an anti-angiogenesis antibody that reduces or eliminates the biological activity of an endogeneous angiogenesis protein. Alternatively, the methods comprise administering to a cell or organism a recombinant nucleic acid encoding an angiogenesis protein. This may be accomplished in any number of ways. In a preferred embodiment, for example when the angiogenesis sequence is down-regulated in angiogenesis, such state may be reversed by increasing the amount of angiogenesis gene product in the cell. This can be accomplished, e.g., by overexpressing the endogeneous angiogenesis gene or administering a gene encoding the angiogenesis sequence, using known gene-therapy techniques, for example. In a preferred embodiment, the gene therapy techniques include the incorporation of the exogenous gene using enhanced homologous recombination (EHR), for example as described in PCT/US93/03868, hereby incorporated by reference in its entireity. Alternatively, for example when the angiogenesis sequence is up-regulated in angiogenesis, the activity of the endogeneous angiogenesis gene is decreased, for example by the administration of a angiogenesis antisense nucleic acid or other inhibitor, such as RNAi.

In one embodiment, the angiogenesis eproteins of the present invention may be used to generate polyclonal and monoclonal antibodies to angiogenesis proteins. Similarly, the angiogenesis proteins can be coupled, using standard technology, to affinity chromatography columns. These columns may then be used to purify angiogenesis antibodies useful for production, diagnostic, or therapeutic purposes. In a preferred embodiment, the antibodies are generated to epitopes unique to a angiogenesis protein; that is, the antibodies show little or no cross-reactivity to other proteins. The angiogenesis antibodies may be coupled to standard affinity chromatography columns and used to purify angiogenesis proteins. The antibodies may also be used as blocking polypeptides, as outlined above, since they will specifically bind to the angiogenesis protein.

Methods of identifying variant angiogenesis-associated sequences

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Without being bound by theory, expression of various angiogenesis sequences is correlated with angiogenesis. Accordingly, disorders based on mutant or variant angiogenesis genes may be determined. In one embodiment, the invention provides methods for identifying cells containing variant angiogenesis genes, e.g., determining all or part of the sequence of at least one endogeneous angiogenesis genes in a cell. This may be accomplished using any number of sequencing techniques. In a preferred embodiment, the invention provides methods of identifying the angiogenesis genotype of an individual, e.g., determining all or part of the sequence of at least one angiogenesis gene of the individual. This is generally done in at least one tissue of the individual, and may include the evaluation of a number of tissues or different samples of the same tissue. The method may include comparing the sequence of the sequenced angiogenesis gene to a known angiogenesis gene, i.e., a wild-type gene.

The sequence of all or part of the angiogenesis gene can then be compared to the sequence of a known angiogenesis gene to determine if any differences exist. This can be done using any number of known homology programs, such as Bestfit, etc. In a preferred embodiment, the presence of a a difference in the sequence between the angiogenesis gene of the patient and the known angiogenesis gene correlates with a disease state or a propensity for a disease state, as outlined herein.

In a preferred embodiment, the angiogenesis genes are used as probes to determine the number of copies of the angiogenesis gene in the genome.

In another preferred embodiment, the angiogenesis genes are used as probes to determine the chromosomal localization of the angiogenesis genes. Information such as

chromosomal localization finds use in providing a diagnosis or prognosis in particular when chromosomal abnormalities such as translocations, and the like are identified in the angiogenesis gene locus.

5 Administration of pharmaceutical and vaccine compositions

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In one embodiment, a therapeutically effective dose of an angiogenesis protein or modulator thereof, is administered to a patient. By "therapeutically effective dose" herein is meant a dose that produces effects for which it is administered. The exact dose will depend on the purpose of the treatment, and will be ascertainable by one skilled in the art using known techniques (e.g., Ansel et al., Pharmaceutical Dosage Forms and Drug Delivery, Lippincott, Williams & Wilkins Publishers, ISBN:0683305727; Lieberman (1992)
Pharmaceutical Dosage Forms (vols. 1-3), Dekker, ISBN 0824770846, 082476918X, 0824716992, 0824716981; Lloyd (1999) The Art, Science and Technology of Pharmaceutical Compounding, Amer. Pharmaceutical Assn, ISBN 0917330889; and Pickar (1999) Dosage Calculations, Delmar Pub, ISBN 0766805042). As is known in the art, adjustments for angiogenesis degradation, systemic versus localized delivery, and rate of new protease synthesis, as well as the age, body weight, general health, sex, diet, time of administration, drug interaction and the severity of the condition may be necessary, and will be ascertainable with routine experimentation by those skilled in the art.

A "patient" for the purposes of the present invention includes both humans and other animals, particularly mammals. Thus the methods are applicable to both human therapy and veterinary applications. In the preferred embodiment the patient is a mammal, preferably a primate, and in the most preferred embodiment the patient is human.

The administration of the angiogenesis proteins and modulators thereof of the present invention can be done in a variety of ways as discussed above, including, but not limited to, orally, subcutaneously, intravenously, intranasally, transdermally, intrapelmonary, vaginally, rectally, or intraocularly. In some instances, for example, in the treatment of wounds and inflammation, the angiogenesis proteins and modulators may be directly applied as a solution or spray.

The pharmaceutical compositions of the present invention comprise an angiogenesis protein in a form suitable for administration to a patient. In the preferred embodiment, the pharmaceutical compositions are in a water soluble form, such as being present as pharmaceutically acceptable salts, which is meant to include both acid and base addition salts. "Pharmaceutically acceptable acid addition salt" refers to those salts that retain

the biological effectiveness of the free bases and that are not biologically or otherwise undesirable, formed with inorganic acids such as hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid, phosphoric acid and the like, and organic acids such as acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, maleic acid, malonic acid, succinic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methanesulfonic acid, ethanesulfonic acid, p-toluenesulfonic acid, salicylic acid and the like. "Pharmaceutically acceptable base addition salts" include those derived from inorganic bases such as sodium, potassium, lithium, ammonium, calcium, magnesium, iron, zinc, copper, manganese, aluminum salts and the like. Particularly preferred are the ammonium, potassium, sodium, calcium, and magnesium salts. Salts derived from pharmaceutically acceptable organic non-toxic bases include salts of primary, secondary, and tertiary amines, substituted amines including naturally occurring substituted amines, cyclic amines and basic ion exchange resins, such as isopropylamine, trimethylamine, diethylamine, triethylamine, tripropylamine, and ethanolamine,

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The pharmaceutical compositions may also include one or more of the following: carrier proteins such as serum albumin; buffers; fillers such as microcrystalline cellulose, lactose, corn and other starches; binding agents; sweeteners and other flavoring agents; coloring agents; and polyethylene glycol.

The pharmaceutical compositions can be administered in a variety of unit 20 dosage forms depending upon the method of administration. For example, unit dosage forms suitable for oral administration include, but are not limited to, powder, tablets, pills, capsules and lozenges. It is recognized that angiogenesis protein modulators (e.g., antibodies, antisense constructs, ribozymes, small organic molecules, etc.) when administered orally, should be protected from digestion. This is typically accomplished either by complexing the molecule(s) with a composition to render it resistant to acidic and enzymatic hydrolysis, or by packaging the molecule(s) in an appropriately resistant carrier, such as a liposome or a protection barrier. Means of protecting agents from digestion are well known in the art.

The compositions for administration will commonly comprise an angiogenesis protein modulator dissolved in a pharmaceutically acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers can be used, e.g., buffered saline and the like. These solutions are sterile and generally free of undesirable matter. These compositions may be sterilized by conventional, well known sterilization techniques. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions such as pH adjusting and buffering agents, toxicity adjusting agents

and the like, for example, sodium acetate, sodium chloride, potassium chloride, calcium chloride, sodium lactate and the like. The concentration of active agent in these formulations can vary widely, and will be selected primarily based on fluid volumes, viscosities, body weight and the like in accordance with the particular mode of administration selected and the patient's needs (e.g., Remington's Pharmaceutical Science, 15th cd., Mack Publishing Company, Easton, Pennsylvania (1980) and Goodman and Gillman, The Pharmacologial Basis of Therapeutics, (Hardman, J.G, Limbird, L.E, Molinoff, P.B., Ruddon, R.W, and Gilman, A.G., eds) The McGraw-Hill Companies. Inc., 1996).

Thus, a typical pharmaceutical composition for intravenous administration would be about 0.1 to 10 mg per patient per day. Dosages from 0.1 up to about 100 mg per patient per day may be used, particularly when the drug is administered to a secluded site and not into the blood stream, such as into a body cavity or into a lumen of an organ. Substantially higher dosages are possible in topical administration. Actual methods for preparing parenterally administrable compositions will be known or apparent to those skilled in the art, e.g., Remington's Pharmaceutical Science and Goodman and Gillman, The Pharmacologial Basis of Therapeutics, supra.

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The compositions containing modulators of angiogenesis proteins can be administered for therapeutic or prophylactic treatments. In therapeutic applications, compositions are administered to a patient suffering from a disease (e.g., a cancer) in an amount sufficient to cure or at least partially arrest the disease and its complications. An amount adequate to accomplish this is defined as a "therapeutically effective dose." Amounts effective for this use will depend upon the severity of the disease and the general state of the patient's health. Single or multiple administrations of the compositions may be administered depending on the dosage and frequency as required and tolerated by the patient. In any event, the composition should provide a sufficient quantity of the agents of this invention to effectively treat the patient. An amount of modulator that is capable of preventing or slowing the development of cancer in a mammal is referred to as a "prophylactically effective dose." The particular dose required for a prophylactic treatment will depend upon the medical condition and history of the mammal, the particular cancer being prevented, as well as other factors such as age, weight, gender, administration route, efficiency, etc. Such prophylactic treatments may be used, e.g., in a mammal who has previously had cancer to prevent a recurrence of the cancer, or in a mammal who is suspected of having a significant likelihood of developing cancer.

It will be appreciated that the present angiogenesis protein-modulating compounds can be administered alone or in combination with additional angiogenesis modulating compounds or with other therapeutic agent, e.g., other anti-cancer agents or treatments

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In numerous embodiments, one or more nucleic acids, e.g., polynucleotides comprising nucleic acid sequences set forth in Tables 1-8, such as antisense polynucleotides or ribozymes, will be introduced into cells, in vitro or in vivo. The present invention provides methods, reagents, vectors, and cells useful for expression of angiogenesis-associated polypeptides and nucleic acids using in vitro (cell-free), ex vivo or in vivo (cell or organism-based) recombinant expression systems.

The particular procedure used to introduce the nucleic acids into a host cell for expression of a protein or nucleic acid is application specific. Many procedures for introducing foreign nucleotide sequences into host cells may be used. These include the use of calcium phosphate transfection, spheroplasts, electroporation, liposomes, microinjection, plasma vectors, viral vectors and any of the other well known methods for introducing cloned genomic DNA, cDNA, synthetic DNA or other foreign genetic material into a host cell (see, e.g., Berger and Kimmel, Guide to Molecular Cloning Techniques, Methods in Enzymology volume 152 Academic Press, Inc., San Diego, CA (Berger), F.M. Ausubel et al., eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (supplemented through 1999), and Sambrook et al., Molecular Cloning - A Laboratory Manual (2nd Ed.), Vol. 1-3, Cold Spring Harbor Laboratory, Cold Spring Harbor New York, 1989.

In a preferred embodiment, angiogenesis proteins and modulators are administered as therapeutic agents, and can be formulated as outlined above. Similarly, angiogenesis genes (including both the full-length sequence, partial sequences, or regulatory sequences of the angiogenesis coding regions) can be administered in a gene therapy application. These angiogenesis genes can include antisense applications, either as gene therapy (i.e. for incorporation into the genome) or as antisense compositions, as will be appreciated by those in the art.

Angiogenesis polypeptides and polymucleotides can also be administered as vaccine compositions to stimulate HTL, CTL and antibody responses.. Such vaccine compositions can include, for example, lipidated peptides (e.g., Vitiello, A. et al., J. Clin. Invest. 95:341, 1995), peptide compositions encapsulated in poly(DL-lactide-co-glycolide) ("PLG") microspheres (see, e.g., Eldridge, et al., Molec. Immunol. 28:287-294, 1991: Alonso

et al., Vaccine 12:299-306, 1994; Jones et al., Vaccine 13:675-681, 1995), peptide compositions contained in immune stimulating complexes (ISCOMS) (see, e.g., Takahashi et al., Nature 344:873-875, 1990; Hu et al., Clin Exp Immunol. 113:235-243, 1998), multiple antigen peptide systems (MAPs) (see e.g., Tam, J. P., Proc. Natl. Acad. Sci. U.S.A. 85:5409-5413, 1988; Tam, J.P., J. Immunol. Methods 196:17-32, 1996), peptides formulated as multivalent peptides; peptides for use in ballistic delivery systems, typically crystallized peptides, viral delivery vectors (Perkus, M. E. et al., In: Concepts in vaccine development, Kaufmann, S. H. E., ed., p. 379, 1996; Chakrabarti, S. et al., Nature 320:535, 1986; Hu, S. L. et al., Nature 320:537, 1986; Kieny, M.-P. et al., AIDS Bio/Technology 4:790, 1986; Top, F. H. et al., J. Infect. Dis. 124:148, 1971; Chanda, P. K. et al., Virology 175:535, 1990), particles of viral or synthetic origin (e.g., Kofler, N. et al., J. Immunol. Methods. 192:25, 1996; Eldridge, J. H. et al., Sem. Hematol. 30:16, 1993; Falo, L. D., Jr. et al., Nature Med. 7:649, 1995), adjuvants (Warren, H. S., Vogel, F. R., and Chedid, L. A. Annu. Rev. Immunol. 4:369, 1986; Gupta, R. K. et al., Vaccine 11:293, 1993), liposomes (Reddy, R. et al., J. Immunol, 148:1585, 1992; Rock, K. L., Immunol, Today 17:131, 1996), or, naked or particle absorbed cDNA (Ulmer, J. B. et al., Science 259:1745, 1993; Robinson, H. L., Hunt, L. A., and Webster, R. G., Vaccine 11:957, 1993; Shiver, J. W. et al., In: Concepts in vaccine development, Kaufmann, S. H. E., ed., p. 423, 1996; Cease, K. B., and Berzofsky, J. A., Annu. Rev. Immunol. 12:923, 1994 and Eldridge, J. H. et al., Sem. Hematol. 30:16, 1993). Toxin-targeted delivery technologies, also known as receptor mediated targeting, such as those of Avant Immunotherapeutics, Inc. (Needham, Massachusetts) may also be used.

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Vaccine compositions often include adjuvants. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, Bortadella pertussis or Mycobacterium tuberculosis derived proteins. Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difoc Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Vaccines can be administered as nucleic acid compositions wherein DNA or RNA encoding one or more of the polypeptides, or a fragment thereof, is administered to a patient. This approach is described, for instance, in Wolff et. al., Science 247:1465 (1990) as well as U.S. Patent Nos. 5,580,859; 5,589,466; 5,804,566; 5,739,118; 5,736,524; 5,679,647; WO 98/04720; and in more detail below. Examples of DNA-based delivery technologies include "naked DNA", facilitated (bupivicaine, polymers, peptide-mediated) delivery, cationic lipid complexes, and particle-mediated ("gene gun") or pressure-mediated delivery (see, e.g., U.S. Patent No. 5,922,687).

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For therapeutic or prophylactic immunization purposes, the peptides of the 10 invention can be expressed by viral or bacterial vectors. Examples of expression vectors include attenuated viral hosts, such as vaccinia or fowlpox. This approach involves the use of vaccinia virus, for example, as a vector to express nucleotide sequences that encode angiogenic polypeptides or polypeptide fragments. Upon introduction into a host, the recombinant vaccinia virus expresses the immunogenic peptide, and thereby elicits an immune response. Vaccinia vectors and methods useful in immunization protocols are described in, e.g., U.S. Patent No. 4,722,848. Another vector is BCG (Bacille Calmette Guerin). BCG vectors are described in Stover et al., Nature 351:456-460 (1991). A wide variety of other vectors useful for therapeutic administration or immunization e.g. adeno and adeno-associated virus vectors, retroviral vectors, Salmonella typhi vectors, detoxified anthrax toxin vectors, and the like, will be apparent to those skilled in the art from the description herein (see, e.g., Shata et al. (2000) Mol Med Today, 6: 66-71; Shedlock et al., J Leukoc Biol 68,:793-806, 2000; Hipp et al., In Vivo 14:571-85, 2000).

Methods for the use of genes as DNA vaccines are well known, and include placing an angiogenesis gene or portion of an angiogenesis gene under the control of a regulatable promoter or a tissue-specific promoter for expression in an angiogenesis patient. 2.5 The angiogenesis gene used for DNA vaccines can encode full-length angiogenesis proteins, but more preferably encodes portions of the angiogenesis proteins including peptides derived from the angiogenesis protein. In one embodiment, a patient is immunized with a DNA vaccine comprising a plurality of nucleotide sequences derived from an angiogenesis gene. For example, angiogenesis-associated genes or sequence encoding subfragments of an 30 angiogenesis protein are introduced into expression vectors and tested for their immunogenicity in the context of Class I MHC and an ability to generate cytotoxic T cell responses. This procedure provides for production of cytotoxic T cell responses against cells which present antigen, including intracellular epitopes.

In a preferred embodiment, the DNA vaccines include a gene encoding an adjuvant molecule with the DNA vaccine. Such adjuvant molecules include cytokines that increase the immunogenic response to the angiogenesis polypeptide encoded by the DNA vaccine. Additional or alternative adjuvants are available.

In another preferred embodiment angiogenesis genes find use in generating animal models of angiogenesis. When the angiogenesis gene identified is repressed or diminished in angiogenesic tissue, gene therapy technology, e.g., wherein antisense RNA directed to the angiogenesis gene will also diminish or repress expression of the gene. Animal models of angiogenesis find use in screening for modulators of an angiogenesis-associated sequence or modulators of angiogenesis. Similarly, transgenic animal technology including gene knockout technology, for example as a result of homologous recombination with an appropriate gene targeting vector, will result in the absence or increased expression of the angiogenesis protein. When desired, tissue-specific expression or knockout of the angiogenesis protein may be necessary.

It is also possible that the angiogenesis protein is overexpressed in angiogenesis. As such, transgenic animals can be generated that overexpress the angiogenesis protein. Depending on the desired expression level, promoters of various strengths can be employed to express the transgene. Also, the number of copies of the integrated transgene can be determined and compared for a determination of the expression level of the transgene. Animals generated by such methods find use as animal models of angiogenesis and are additionally useful in screening for modulators to treat angiogenesis or to evaluate a therapeutic entity.

Kits for Use in Diagnostic and/or Prognostic Applications

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For use in diagnostic, research, and therapeutic applications suggested above, kits are also provided by the invention. In the diagnostic and research applications such kits may include any or all of the following: assay reagents, buffers, angiogenesis-specific nucleic acids or antibodies, hybridization probes and/or primers, antisense polynucleotides, ribozymes, dominant negative angiogenesis polypeptides or polynucleotides, small molecules inhibitors of angiogenesis-associated sequences etc. A therapeutic product may include sterile saline or another pharmaceutically acceptable emulsion and suspension base.

In addition, the kits may include instructional materials containing directions (i.e., protocols) for the practice of the methods of this invention. While the instructional materials typically comprise written or printed materials they are not limited to such. Any

medium capable of storing such instructions and communicating them to an end user is contemplated by this invention. Such media include, but are not limited to electronic storage media (e.g., magnetic discs, tapes, cartridges, chips), optical media (e.g., CD ROM), and the like. Such media may include addresses to internet sites that provide such instructional materials.

The present invention also provides for kits for screening for modulators of angiogenesis-associated sequences. Such kits can be prepared from readily available materials and reagents. For example, such kits can comprise one or more of the following materials: an angiogenesis-associated polypeptide or polynucleotide, reaction tubes, and instructions for testing angiogenic-associated activity. Optionally, the kit contains biologically active angiogenesis protein. A wide variety of kits and components can be prepared according to the present invention, depending upon the intended user of the kit and the particular needs of the user. Diagnosis would typically involve evaluation of a plurality of genes or products. The genes will be selected based on correlations with important parameters in disease which may be identified in historical or outcome data.

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

EXAMPLES

25 Example 1: Tissue Preparation, Labeling Chips, and Fingerprints

Purify total RNA from tissue using TRIzol Reagent

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Homogenize tissue samples in 1ml of TRIzol per 50mg of tissue using a Polytron 3100 homogenizer. The generator/probe used depends upon the tissue size. A generator that is too large for the amount of tissue to be homogenized will cause a loss of sample and lower RNA yield. TRIzol is added directly to frozen tissue, which is then homogenize. Following homogenization, insoluble material is removed by centrifugation at 7500 x g for 15 min in a Sorvall superspeed or 12,000 x g for 10 min. in an Eppendorf centrifuge at 4°C. The clear homogenate is transferred to a new tube for use. The samples may be frozen now at -60° to -70°C (and kept for at least one month). The homogenate is

mixed with 0.2ml of chloroform per 1ml of TRIzol reagent used in the original homogenization and incubated at room temp. for 2-3 minutes. The aqueous phase is then separated by centrifugation and transferred to a fresh tube and the RNA precipitated using isopropyl alcohol. The pellet is isolated by centrifugation, washed, air-dried, resuspended in an appropriate volume of DEPC H₂0, and the absorbance measured.

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Purification of poly A+mRNA from total RNA is performed as follows. Heat an oligotex suspension to 37°C and mixing immediately before adding to RNA. The Elution Buffer is heated at 70°C. Warm up 2 x Binding Buffer at 65°C if there is precipitate in the buffer. Mix total RNA with DEPC-treated water, 2 x Binding Buffer, and Oligotex according to Table 2 on page 16 of the Oligotex Handbook. Incubate for 3 minutes at 65°C. Incubate for 10 minutes at room temperature. Centrifuge for 2 minutes at 14,000 to 18,000 g. Remove supernatant without disturbing Oligotex pellet. A little bit of solution can be left behind to reduce the loss of Oligotex. Gently resuspend in Wash Buffer OW2 and pipet onto spin column. Centrifuge the spin column at full speed for 1 minute. Transfer spin column to a new collection tube and gently resuspend in Wash Buffer OW2 and centrifuge as describe herein. Transfer spin column to a new tube and elute with 20 to 100 ul of preheated (70oC) Elution Buffer. Gently resuspend Oligotex resin by pipetting up and down. Centrifuge as above. Repeat elution with fresh elution buffer or use first eluate to keep the elution volume low. Read absorbance, using diluted Elution Buffer as the blank. Before proceeding with cDNA synthesis, precipitate the mRNA as follows: add 0.4 vol. of 7.5 M NH4OAc + 2.5 vol. of cold 100% ethanol. Precipitate at -20oC 1 hour to overnight (or 20-30 min. at -70oC). Centrifuge at 14,000-16,000 x g for 30 minutes at 4oC. Wash pellet with 0.5ml of 80%ethanol (-20oC) then centrifuge at 14,000-16,000 x g for 5 minutes at room temperature. Repeat 80% ethanol wash. Air dry the ethanol from the pellet in the hood. Suspend pellet in DEPC H20 at 1ug/ul concentration.

To further Clean up total RNA using Qiagen's RNeasy kit, add no more than 100ug to an RNeasy column. Adjust sample to a volume of 100ul with RNase-free water. Add 350ul Buffer RLT then 250ul ethanol (100%) to the sample. Mix by pipetting (do not centrifuge) then apply sample to an RNeasy mini spin column. Centrifuge for 15 sec at >10,000rpm. Transfer column to a new 2-ml collection tube. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough. Add 500ul Buffer RPE and centrifuge for 15 sec at >10,000rpm. Discard flowthrough then centrifuge for 2 min at maximum speed to dry column membrane. Transfer column to a new 1.5-ml collection tube

and apply 30-50ul of RNase-free water directly onto column membrane. Centrifuge 1 min at >10,000pm. Repeat elution, and read absorbance.

cDNA synthesis using Gibco's "SuperScript Choice System for cDNA Synthesis" kit

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First Strand cDNA synthesis is performed as follows. Use 5ug of total RNA or lug of polyA+ mRNA as starting material. For total RNA, use 2ul of SuperScript RT. For polyA+ mRNA, use 1ul of SuperScript RT. Final volume of first strand synthesis mix is 20ul. RNA must be in a volume no greater than 10ul. Incubate RNA with 1ul of 100pmol T7-T24 oligo for 10 min at 70C. On ice, add 7 ul of: 4ul 5X 1st Strand Buffer, 2ul of 0.1M DTT, and 1 ul of 10mM dNTP mix. Incubate at 37C for 2 min then add SuperScript RT. Incubate at 37C for 1 hour.

For the second strand synthesis, place 1st strand reactions on ice and add: 91ul DEPC H₂0; 30ul 5X 2nd Strand Buffer; 3ul 10mM dNTP mix; 1ul 10U/ul E.coli DNA Ligase; 4ul 10U/ul E.coli DNA Polymerase; and 1ul 2U/ul RNase H. Mix and incubate 2 hours at 16C. Add 2ul T4 DNA Polymerase. Incubate 5 min at 16C. Add 10ul of 0.5M EDTA. A further clean-up of DNA is performed using phenol:chloroform:isoamyl Alcohol (25:24:1) purification.

In vitro Transcription (IVT) and labeling with biotin is performed as follows: Pipet 1.5ul of cDNA into a thin-wall PCR tube. Make NTP labeling mix by combining 2ul T7 10xATP (75mM) (Ambion); 2ul T7 10xGTP (75mM) (Ambion); 1.5ul T7 10xUTP (75mM) (Ambion); 3.75ul 10mM Bio-11-UTP (Boehringer-Mannheim/Roche or Enzo); 3.75ul 10mM Bio-16-CTP (Enzo); 2ul 10x T7 transcription buffer (Ambion); and 2ul 10x T7 enzyme mix (Ambion). The final volume is 20ul. Incubate 6 hours at 37°C in a PCR machine. The RNA can be furthered cleaned.

Fragmentation is performed as follows. 15 ug of labeled RNA is usually fragmented. Try to minimize the fragmentation reaction volume; a 10 ul volume is recommended but 20 ul is all right. Do not go higher than 20 ul because the magnesium in the fragmentation buffer contributes to precipitation in the hybridization buffer. Fragment RNA by incubation at 94 C for 35 minutes in 1 x Fragmentation buffer (5 x Fragmentation buffer is 200 mM Tris-acetate, pH 8.1; 500 mM KOAc; 150 mM MgOAc). The labeled RNA transcript can be analyzed before and after fragmentation. Samples can be heated to 65°C for 15 minutes and electrophoresed on 1% agarose/TBE gels to get an approximate idea of the transcript size range

For hybridization, 200 ul (10ug cRNA) of a hybridization mix is put on the chip. If multiple hybridizations are to be done (such as cycling through a 5 chip set), then it is recommended that an initial hybridization mix of 300 ul or more be made. The hybridization mix is: fragment labeled RNA (50ng/ul final conc.); 50 pM 948-b control oligo; 1.5 pM BioB; 5 pM BioC; 25 pM BioD; 100 pM CRE; 0.1mg/ml herring sperm DNA; 0.5mg/ml acetylated BSA; and 300 ul with 1xMES hyb buffer.

Labeling is performed as follows: The hybridization reaction includes non-biotinylated IVT (purified by RNeasy columns); IVT antisense RNA 4 µg:µl; random Hexamers (1 µg/µl) 4 µl and water to 14 ul. The reaction is incubated at 70°C, 10 min. Reverse transcriptionis performed in the following reaction: 5X First Strand (BRL) buffer, 6 µl; 0.1 M DTT, 3 µl; 50X dNTP mix, 0.6 µl; H₂O, 2.4 µl; Cy3 or Cy5 dUTP (1mM), 3 µl; SS RT II (BRL), 1 µl in a final volume of 16 µl. Add to hybridization reaction. Incubate 30 min., 42°C. Add 1 µl SSII and incubate another hour. Put on ice. 50X dNTP mix (25mM of cold dATP, dCTP, and dGTP, 10mM of dTTP: 25 µl each of 100mM dATP, dCTP, and dGTP: 10 µl of 100mM dTTP to 15 µl H2O. dNTPs from Pharmacia)

RNA degradation is performed as follows. Add 86 µl H2O, 1.5 µl 1M NaOH/2mM EDTA and incubate at 65°C, 10 min. For U-Con 30, 500 µl TE/sample spin at 7000g for 10 min, save flow through for purification. For Qiagen purification, suspend u-con recovered material in 500µl buffer PB and proceed using Qiagen protocol. For DNAse digestion, add 1 ul of 1/100 dil of DNAse/30ul Rx and incubate at 37°C for 15 min. Incubate at 5 min 95°C to denature the DNAse/

For sample preparation, add Cot-1 DNA, 10 µl; 50X dNTPs, 1 µl; 20X SSC, 2.3 µl; Na pyro phosphate, 7.5 µl; 10mg/ml Herring sperm DNA; 1ul of 1/10 dilution to 21.8 final vol. Dry in speed vac. Resuspend in 15 µl H20. Add 0.38 µl 10% SDS. Heat 95°C, 2 min and slow cool at room temp. for 20 min. Put on slide and hybridize overnight at 64°C. Washing after the hybridization: 3X SSC/0.03% SDS: 2 min., 37.5 mls 20X SSC+0.75mls 10% SDS in 250mls H2O; 1X SSC: 5 min., 12.5 mls 20X SSC in 250mls H2O; 0.2X SSC: 5 min., 2.5 mls 20X SSC in 250mls H2O. Dry slides and scan at appropriate PMT's and channels.

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Example 2. A model of angiogenesis is used to determine expression in angiogenesis

In the model of angiogenesis used to determine expression of angiogenesisassociated sequences, human umbilical vein endothelial cells (HUVEC) were obtained, e.g.,

as passage 1 (p1) frozen cells from Cascade Biologies (Oregon) and grown in maintenance medium: Medium 199 (Life Technologies) supplemented with 20% pooled human serum, 100 mg/ml heparin and 75 mg/ml endothelial cell growth supplements (Sigma) and gentamicin (Life Technologies). An *in vitro* cell system model was used in which 2x10⁵ HUVECs were cultured in 0.5 ml 3 mgs/ml plasminogen-depleted fibrinogen (Calbiochem, San Diego, CA) that was polymerized by the addition of 1 unit of maintenance medium supplemented with 100 ng/ml VEGF and HGF and 10 ng/ml TGF-a (R&D Systems, Minneapolis,MN) added (growth medium). The growth medium was replaced every 2 days. Samples for RNA were collected, e.g., at 0, 2, 6, 15, 24, 48, and 96 hours of culture. The fibrin clots were placed in Trizol (Life Technologies) and disrupted using a Tissuemizer. Thereafter standard procedures were used for extracting the RNA (e.g., Example 1).

As indicated, some of the Accession numbers include expression sequence tags (ESTs).

Thus, in one embodiment herein, genes within an expression profile, also termed expression
profile genes, include ESTs and are not necessarily full length.

Angiogenesis associated sequences thus identified are shown in Tables 1-8.

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TABLE 1:

5	Pkey: Accession: ExAccn: UnigeneID: Unigene Title:		Unique Eos probeset identifier number Accession numbru usod for providus petent filings Ezemplar Accession number, Genbank accession number Unigere en umber Unigere en umber				
10	Pkey	Accession	ExAcon	UnigenelD	UnigeneTitle		
15	121443 100082 132817 130150	AB000450 AB002380 AB003103 AB004884 AF000573_a AF008937	AB000450 AF180681 AA130080 N27852 na1 BE094848 AF008937	Hs.82771 Hs.6582 Hs.4295 Hs.57553 Hs.15113 Hs.102178	vaccinia related kinase 2 Rito grantine exchange factor (GEE) 12 protessome (procone, micropain) 265 subvais, non-ATPase, 12 protessome (procone, micropain) 265 subvais, non-ATPase, 12 homogenisales 1,2-dioxygenase (homogenisale oxidate) symbol 16		
20	130839 427064 100113 133980	AF009301 AF009368 D00591 D00760 D11139	AB011169 AF029674 NM_001269 AA294921 AA469369	Hs.20141 Hs.173422 Hs.84746 Hs.250811 Hs.5831	symbol or Scorovisiae SSM4 KIAA 1616 proteh - chromosome condensation 1 - v-al strain leukema krail oncogene homolog B (ras related; GTP binding protein) - tissue inhibitor or healblogrobelmase 1 (erythroid potentiating activity, collagemase inhibitor)		
25	100154 100169 101956 100190	D14657 D14878 D17716 D21090	H60720 AL037228 NM_002410 M91401	Hs.81892 Hs.82043 Hs.121502 Hs.178658	KIAA0101 gene product D123 gene product manncoy (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase RAD23 (S. cerevisiae) homolog B		
30	100211 100238	D26135 D26528 D30742 D31762 D31765	NM_001346 D26528 L24959 NM_012288 D31765	Hs.89462 Hs.123058 Hs.348 Hs.153954 Hs.170114	diacytglycerol kinsas, gamma (SOMD) DEADH (Aps-Disub-As-sphile) box polypeptide 7 (RNA helicase, 52xC) calcium/calmodulin-dependent protein kinase IV TRAIAMse protein KIAA0061 protein		
35	100248 100256	D31888 D38128 D38500 D38551	NM_015156 D25418 D38500 N92036 AF091035	Hs.78398 Hs.393 Hs.278468 Hs.81848 Hs.184627	KIAA007 i protein prostaglandin 12 (proslacyclin) receptor (IP) postmeticio: segregation increased 2-like 4 RAD21 (S. pombe) homolog KIAA0118 (protein in KIAA0118 (protein in KIAA018 (protein in KIAA018 (protein in KIAA018 (protein in KIAA018 (protein in		
40	100294 100327 100335 134495	D49396 D55640 D63391	AA331881 D55640 AW247529 D63477 D86864	Hs.6793 Hs.84087 Hs.57735	peroxitedoxin 3 gb-Human monocyte PABL (pseudoautosomal boundary-like sequence) mRNA, clone Mo2. plateiet-advalleg lactor acetylinydrolase, isoform ib, gamma subun't (2902) KIAAO143 probin acetyl LDL receptor, SPEC		
45	135152 134269 100372 134304	D64015 D79990 D79997 D80010 D84276	M96954 NM_014737 NM_014791 BE613486 D84284	Hs.182741 Hs.80905 Hs.184339 Hs.81412 Hs.66052	Tháf of pichoicí granú-e-associated RNA-binding protein-like 1 Ras association (RaúCSNAF-6) domain familly 2 KUA/0175 gene product lipin 1 C038 antisen (p45)		
50	100405 100418 133154 134347 128653	D86425 D86978 D87012 D87075 D87432	AW291587 D86978 D87012 AF164142 D87432	Hs.82733 Hs.84790 Hs.194685 Hs.82042 Hs.10315	nidogna 2 protein topoliscenerase (DNA) III befa soluble carrier farmly 23 (nucleobase transporters), member 1 soluble carrier farmly 7 cettoric amino acid transporter, y-e system), member 6		
55	134593 100481 100552 100591	HG2167-HT	AA013051 NM_000437 1098 X70377 2237 AA019521 2511 NM_004091	Hs.91417 Hs.234392 Hs.121489 Hs.301946 Hs.231444	topoisomenses (DNA) Il binding protein platalet activating factor acolyfinydralese 2 (4/0kD) cystalin D (4/0kD) ysacomal Homo sapions, Similar to hypothetical protein PRO1722, done MGC:15992, mRNA, complete Homo sapions, Similar to hypothetical protein PRO1722, done MGC:15992, mRNA, complete		
60	100662 100899	HG2887-HT HG4660-HT	5073 AL039123 5146 L12260	Hs.142653 Al368680 Hs.103042 Hs.172816	ret finger protein Hs.816 SRY (sex determining region Y)-box 2 microtibute-associated protein 1B neuregulin 1		
65	100950 100964 135407	HG884-HT8 HG919-HT9 J00212_f J04029 J04031		Hs.180686 Hs.166846 Hs.99936 Hs.172665	ubiquifin protein lipase ESA (human popilloma virus E6 associated protein, Angelman syndrome) polymerase (DNA directed), epaillom Empirically selected from AFFX, single probeset loaratin 10 (polciemolytic hyperteratiosis, koratosis palmaris et plantaris) methylemetetatyloidate delytydegosae (NADP v dependent), methenyltetahydrotolate		
70	131877 101016 134786 134100 134078	J04038 J04543 L06139 L07540 L08895	J04068 J04543 T29618 AA460085 L08895	Hs.156346 Hs.78637 Hs.89640 Hs.171075 Hs.78995	bopoismerase (DNA) II alpha (170kD) annecin A7 TEK tyrosine kinase, endothelial (venous malformations, multiple cutaneous and mucosal) replication factor C (activator 1) 5 (35.5kD) MADS box transcription enhancer factor 2, polypeptide C (myocyte enhancer factor 2c)		
75	134849	L11239 L11353 L13773	L11239 BE409525 AK000310	Hs.36993 Hs.902 Hs.17138	gastrulation brain homeo box 1 neurofibromin 2 (bilateral acoustic neuroma) hypothetical protein FLJ23033		

	101152 L13800	AI984625	Hs.9884	spindle pole body protein
	135397 L14922	L14922	Hs.166563	replication factor C (activator 1) 1 (145kD)
	131687 L15189	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)
-	101168 L15388	NM_005308	Hs.211569	G protein-coupled receptor kinase 5
5	421155 L16895	H87879	Hs.102267	lysyl oxidase
	101226 L27476	AF083892	Hs.75608	tight junction protein 2 (zona occludens 2)
	133975 L27624	C18356	Hs.295944	tissue factor pathway inhibitor 2
	134739 L32976	NM_002419	Hs.89449	mitogen-activated protein kinase kinase kinase 11
10	130155 L33404	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum comeum)
10	440538 L35263	W76332	Hs.79107	mitogen-activated protein kinase 14 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2
	132813 L37347	BE313625 AF168418	Hs.57435 Hs.116784	thyroid hormone receptor interactor 4
	101294 L40371 101300 L40391	BE535511	Hs.74137	transmembrane trafficking protein
	101310 L41607	L41607	Hs.934	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme
15	130344 L77566	AW250122	Hs.154879	DiGeorge syndrome critical region gene DGSI; likely ortholog of mouse expressed sequence 2
15	embryonic lethal	A WZJO IZZ	18.10-013	Discouge syndrous cases region gains poor, andy draining or money are seen and
	101381 M13928	AW675039	Hs.1227	aminolevulinate, delta-, dehydratase
	101668 M14016	AW005903	Hs.78601	uroporphyrinogen decarboxylase
	133780 M14219	AA557660	Hs.76152	decorin
20	101396 M15796	BE267931	Hs.78996	proliferating cell nuclear antigen
	101447 M21305	M21305		gb:Human alpha satellite and satellite 3 junction DNA sequence.
	101458 M22092	M22092		gb:Human neural cell adhesion molecule (N-CAM) gene, exon SEC and partial cds.
	101470 M22898	NM_000546	Hs.1846	tumor protein p53 (LI-Fraumeni syndrome)
	134604 M22995	NM_002884	Hs.865	RAP1A, member of RAS oncogene family
25	101478 M23379	NM_002890	Hs.758	RAS p21 protein activator (GTPase activating protein) 1
	406698 M24364	X03068	Hs.73931	major histocompatibility complex, class II, DQ beta 1
	133519 M24400	AW583062	Hs.74502	chymotrypsinogen B1
	131185 M25753	BE280074	Hs.23960	cyclin B1
••	134116 M27691	R84694	Hs.79194	cAMP responsive element binding protein 1
30	133999 M2B213	AA535244	Hs.78305	RAB2, member RAS oncogene family
	130174 M29550	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)
	129963 M29971 132983 M30269	M29971 M30269	Hs.1384 Hs.62041	O-6-methylguanine-DNA methyltransferase ntdogen (enactin)
	133900 M31158	M31158	Hs.77439	protein kinase, cAMP-dependent, regulatory, type II, beta
35	101543 M31166	M31166	Hs.2050	pentaxin-related gene, rapidly induced by IL-1 beta
33	101545 M31210	BE246154	Hs.154210	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	101620 M55420	855271	Hs.247930	Epsilon , IgE
	134691 M59979	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
	133595 M62810	AA393273	Hs.75133	transcription factor 6-like 1 (mitochondrial transcription factor 1-like)
40	130425 M63838	AA243383	Hs.155530	interferon, gamma-inducible protein 16
	101700 M64710	D90337	Hs.247916	natriuretic peptide precursor C
	101714 M68874	M68874	Hs.211587	phospholipase A2, group IVA (cylosolic, calcium-dependent)
	134246 M74524	D28459	Hs.80612	ublquitin-conjugating enzyme E2A (RAD6 homolog)
4.5	101760 M80254	M80254	Hs.173125	peptidylprolyl isomerase F (cyclophilin F)
45	133948 M81780_cds3	X59980	Hs.77813	sphingomyelin phosphodiesterase 1, acid lysosomal (acid sphingomyelinase)
	101791 M83822	MB3822	Hs.62354	cell division cycle 4-like
	101812 M86934	BE439894	Hs.78991	DNA segment, numerous copies, expressed probes (GS1 gene)
	101813 M87338 133396 M96326_ma1	NM_002914 M96328	Hs.139226 Hs.72885	reptication factor C (activator 1) 2 (40kD) azurocidin 1 (cationic antimicrobial protein 37)
50	135152 M96954	M96954	Hs.182741	TIA1 cytotoxic granule-associated RNA-binding protein-like 1
30	130152 M96954 129026 M98833	AL120297	Hs.108043	Friend leukemia virus integration 1
	101901 S66793	H38026	Hs.308	arrestin 3, retinal (X-arrestin)
	134831 S72370	AA853479	Hs.89890	pyruvate carboxylase
	134039 878569	NM_002290	Hs.78672	laminin, alpha 4
55	134395 S79873	AA456539	Hs.8262	lysosomal
	101975 S83325	AA079717	Hs.283664	aspartate beta-hydroxylase
	101977 S83364	AF112213	Hs.184062	putative Rab5-interacting protein
	101978 S83365	BE561610	Hs.5809	putative transmembrane protein; homolog of yeast Golgi membrane protein Yif1p (Yip1p-
	interacting factor)			
60	101998 U01212	U01212	Hs.248153	olfactory marker protein
	102003 U01922	U01922	Hs.125565	translocase of inner mitochondrial membrane 8 (yeast) homolog A
	102007 U02556	U02556	Hs.75307	t-complex-associated-testis-expressed 1-like
	102009 U02630	BE245149	Hs.82643	protein tyrosine kinase 9
	416658 U03272	U03272	Hs.79432	fibrillin 2 (congenital contractural arachnodactyly)
65	132951 U04209	AW821182	Hs.61418	microfibrillar-associated protein 1
	135389 U05237	U05237	Hs.99872	fetal Alzheimer antigen
	102048 U07225 130145 U07620	U07225 U34820	Hs.339 Hs.151051	purinergic receptor P2Y, G-protein coupled, 2 mitogen-activated protein kinase 10
	303153 U09759	U09759	Hs. 131051 Hs. 246857	mitogen-activated protein kinase 9
70	420269 U09820	U72937	Hs.96264	alpha thatassemia/mental retardation syndrome X-linked (RAD54 (S. cerevisiae) homolog)
, 0	102095 U11313	U11313	Hs.75760	sterol carrier protein 2
	102123 U14518	NM_001809	Hs.1594	centromere protein A (17kD)
	102126 U14575	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhibitor) subunit 8
	102133 U15173	AU076845	Hs.155596	BCL2/adenovirus E1B 19kD interacting protein 2
75	102139 U15932	NM_004419	Hs.2128	dual specificity phosphatase 5
	102162 U18291	AA450274	Hs.1592	CDC16 (cell division cycle 16, S. cerevisiae, homolog)

	102164 U18300	NM_000107	Hs.77602	damage-specific DNA binding protein 2 (48kD)
	427653 U18383	AA159001	Hs.180069	nuclear respiratory factor 1
	131817 U20536	U20536	Hs.3280	caspase 6, apoptosis-related cysteine protease
	102200 U21551	AA232362	Hs.157205	branched chain aminotransferase 1, cytosolic
5	102210 U23028	EE619413	Hs.2437	eukaryotic translation initiation factor 2B, subunit 5 (epsilon, 82kD)
	102214 U23752	U23752	Hs.32964	SRY (sex determining region Y)-box 11
	132811 U25435	U25435	Hs.57419	CCCTC-binding factor (zinc finger protein)
	131319 U25997	NM_003155	Hs.25590	stanniocaldin 1
	102256 U28251_cds2	U28251	Hs.53237	ESTs, Highly simitar to Z169_HUMAN ZINC FINGER PROTEIN 169 [H.sapiens]
10	132316 U28831	U28831	Hs.44566	KIAA1641 protein
	102269 U30245	U30245		gb:Human myelomonocytic specific protein (MNDA) gene, 5' flanking sequence and complete
	exon 1.			
	134365 U32315	AA568906	Hs.82240	syntaxin 3A
	102293 U32439	AF090116	Hs.79348	regulator of G-protein signalling 7
15	102298 U32849	AA382169	Hs.54483	N-myc (and STAT) interactor
	102325 U35139	AI815867	Hs.50130	necdin (mouse) homolog
	302344 U36764	BE303044	Hs.192023	eukaryotic translation initiation factor 3, subunit 2 (beta, 36kD)
	102361 U39400	AA223616	Hs.75859	chromosome 11 open reading frame 4
	102367 U39657	U39656	Hs.118825	mitogen-activated protein kinase kinase 6
20	102388 U41344	AA362907	Hs.76494	proline arginine-rich end leucine-rich repeat protein
	102394 U41766	NM_003816	Hs.2442	a disintegrin and metalloproteinase domain 9 (meltrin gamma)
	129829 U41813	AF010258	Hs.127428	homeo box A9
	102251 U41815	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase)
	102409 U43286	BE300330	Hs.118725	selenophosphate synthetase 2
25	133746 U44378	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Drosophila) homolog 4
	102423 U44754	Z47542	Hs.179312	small nuclear RNA activating complex, polypeptide 1, 43kD
	132828 U47011_cds1	AB014615	Hs.57710	fibroblast growth factor 8 (androgen-induced)
	130441 U47077	U63630	Hs.155637	protein kinase, DNA-activated, catalytic polypeptide
	102450 U48251	U48251	Hs.75871	protein kinase C binding protein 1
30	129350 U50535	U50535	Hs.110630	Human BRCA2 region, mRNA sequence CG006
	102534 U56833	U96759	Hs.198307	von Hippel-Lindau binding protein 1
	130457 U58091	AB014595	Hs.155976	cullin 48
	135065 U58837	AA019401	Hs.93909	cyclic nucleotide gated channel beta 1
	102560 U59289	R97457	Hs.63984	cadhenn 13, H-cadhenn (heart)
35	102567 U59863	U63830	Hs.146847	TRAF family member-associated NFKB activator
	134305 U67122	U61397	Hs.81424	ubiquitin-like 1 (sentrin)
	102638 U67319	U67319	Hs.9216	caspase 7, apoptosis-related cysteine protease
	132736 U68019	AW081883	Hs.288261	Homo sapiens cDNA: FLJ23037 fis, clone LNG02036, highly similar to HSU68019 Homo
	sapiens mad protein hom		nRNA	
40	133070 U69611	U92649	Hs.64311	a disintegrin and metalloproteinase domain 17 (tumor necrosis factor, alpha, converting enzyme)
	102663 U70322	NM_002270	Hs.168075	karyophenn (importin) beta 2
	134660 U73524	U73524	Hs.87465	ATP/GTP-binding protein
	102735 U79267	AF111106	Hs.3382	protein phosphatase 4, regulatory subunit 1
45	102741 U79291	AW959829	Hs.83572	hypothetical protein MGC14433
45	101175 U82671_cds2	U82671	Hs.36980	melanoma antigen, family A, 2
	132164 U84573	AI752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2
	102823 U90914	D85390	Hs.5057	carboxypeptidase D
	102826 U91316	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydrolase
50	102831 U91932	AA262170	Hs.80917	adaptor-related protein complex 3, sigma 1 subunit
30	102846 U96131	BE264974	Hs.6566	thyroid hormone receptor interactor 13
	129777 U97018	U97018	Hs.12451 Hs.79440	echinoderm microtubule-associated protein-like
	134161 U97188	AA634543 J03464	Hs.179440 Hs.179573	IGF-II mRNA-binding protein 3
	134854 V00503 302363 X04327	AW163799	Hs.179373 Hs.198365	collagen, type I, alpha 2 2,3-bisphosphoglycerate mutase
- 55	133708 X06389	AW103799 AI018666	Hs.75667	z,3-dispriceprogrycerate masses synaptophysin
33	125708 X05369 125701 X07496	T72104	Hs.93194	apolipoprotein A-I
	102915 X07820	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin 2)
			Hs.87409	
	134656 X14787	AI750878	Hs.75589	thrombospondin 1 acid phosphatase 2, lysosomal
60	413858 X15525_ma1	NM_001610 AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase (NAD+dependent), methenyltetrahydrofolate
00	102968 X16396 cyclohydrolase	AU0/0011	ns.104012	tilatilikata tatatilangarangarangarangarangarangarangaranga
	102971 X16609	X16609	Hs.183805	ankyrin 1, erythrocytic
	134037 X53586_ma1	AI808780	Hs.227730	integrin, alpha 6
	103023 X53793	AW500470	Hs.117950	multifunctional polypeptide similar to SAICAR synthetase and AIR carboxylase
65	103023 A55793 103037 X54936	BE018302	Hs.2894	placental growth factor, vascular endothelial growth factor-related protein
0.5		BE245380	Hs.153952	5' nucleotidase (CD73)
	130282 X55740 134542 X57025	M14156	Hs.85112	insulin-like growth factor 1 (somatomedin C)
	134542 A57025 128568 X60673 ma1	H12912	Hs.274691	adenylate kinase 3
	128568 X60673_ma1 103093 X60708	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine deaminase complexing protein 2)
70		U10564	Hs.75188	wee1+(S. pombe) homolog
70	133606 X62048 129063 X63097	X63094	Hs.283822	Rhesus blood group, D antigen
	129063 X63097 424460 X63563	BE275979	Hs.296014	polymerase (RNA) II (DNA directed) polypeptide B (140kD)
	133227 X64037	AW977263	Hs.68257	general transcription factor IIF, polypeptide 1 (74kD subunit)
			Hs.334731	Homo sapiens, clone IMAGE:3448306, mRNA, partial cds
75	103181 X69636	X69636		
75	103181 X69636 103184 X69878 103194 X70649	U43143 NM_004939	Hs.74049 Hs.78580	ms-related tyrosine kinase 4 DEADM (Asp.Glu-Ala-Asp/tis) box polypeptide 1

	103208		AW411340		retinoblastoma-binding protein 7
	129698				ATP-binding cassette, sub-family E (OABP), member 1
	131486			Hs.27372	BMX non-receptor tyrosine kinase
-	130729	X84194	Al963747	Hs.18573	acylphosphalase 1, erythrocyle (common) type
5	103334				cyclin-dependent kinase 8
	132645 135094	X8787U	A1654712 NM 003304	Hs.54424 Hs.250687	hepatocyte nuclear factor 4, alpha transient receptor potential channel 1
		X89066 X89398 cds2	NM_003304 H09366	Hs.78853	transient receptor potential channel i uracil-DNA glycosylase
	103352		X89399		RAS p21 protein activator (GTPase activating protein) 3 (Ins(1,3,4,5)P4-binding protein)
10	132173		X89426	Hs.41716	endothelial cell-specific molecule 1
10	103371		X91247	Hs.13046	thioredoxin reductase 1
	131584		AA598509		purine-rich element binding protein A
	103376		AL036166	Hs.323378	coated vesicle membrane protein
	103378	X92110	AL119690		HCGVIII-1 protein
15	128510			Hs.296371	RAB28, member RAS oncogene family
	103410		AA158294	Hs.334879	DR1-associated protein 1 (negative cofactor 2 alpha)
		X97230_f	AF022044	Hs.274601	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tall, 1
	103438	X98263	AW175781	Hs.152720	M-phase phosphoprotein 6
	103440		X98296	Hs.77578	ubiquitin specific protease 9, X chromosome (Drosophila fat facets related)
20	103452	X99584	NM_006936	Hs.85119	SMT3 (suppressor of mif two 3, yeast) homolog 1
	133536	Y00264	W25797.comp	Hs.177486	amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)
	135185	Y07566	AW404908	Hs.96038	Ric (Drosophila)-like, expressed in many tissues
	118523		Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myoxin)
25	134662		NM_007048	Hs.284283	butyrophilin, subfamily 3, member A1
25	132083		BE386490	Hs.279663	Pirin
	103500		AW408009	Hs.22580	alkylglycerone phosphate synthase
	134389		Y09858	Hs.82577	spindin-like
	132084	Y12394	NM_002267 NM_002197	Hs.3886 Hs.154721	karyopherin alpha 3 (importin alpha 4) acontrase 1, soluble
30	103540 133152		Z11695	Hs.324473	mitogen-activated protein kinase 1
30	103548		Z15005	Hs.75573	centromere protein E (312kD)
	103612		BE336654	Hs.70937	H3 histone family, member A
		AA011243_s	D56365	Hs.63525	poly(rC)-binding protein 2
		AA018418	AW137912	Hs.227583	Homo sapiens chromosome X map Xp11.23 L-type calcium channel alpha-1 subunit
35	(CACNA	1F) gene, complet	e cds: HSP27 p	seudogene, con	mplete sequence; and JM1 protein, JM2 protein, and Hb2E genes, complete cds
		AA018758	AW207152	Hs.186600	ESTs
		AA018804	BE218319	Hs.5807	GTPase Rab14
		AA031993	AA306325	Hs.4311	SUMO-1 activating enzyme subunit 2
		AA044217	BE264633	Hs.143638	WD repeat domain 4
40		AA046548	W17064	Hs.332848	SWIJSNF related, matrix associated, actin dependent regulator of chromatin, subfamily e,
	member	1	DE024040		No DNA EL MARAGE UEADA 1005780
	103723	AA057447_s	BE274312	Hs.214783	Homo sapiens cDNA FLJ14041 fis, clone HEMBA1005780 Homo sapiens cDNA FLJ11968 fis, clone HEMBB1001133
	453308	AA058376	W20296 AA403045	Hs.288178 Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone REC00917
45	100200	AA083572 AA085696	AA085696	Hs.169600	KIAA0826 protein
73		AA088744	AI920783	Hs.191435	ESTs .
		AA089688	BE244667	Hs.296155	CGI-100 protein
		AA091284	AA393968	Hs.180145	HSPC030 protein
	103773	AA092700	Al219323	Hs.101077	ESTs, Weakly similar to T22363 hypothetical protein F47G9.4 - Caenorhabditis elegans
50	[C.elega				
	135289	AA092968	AW372569	Hs.9788	hypothetical protein MGC10924 similar to Nedd4 WW-binding protein 5
	132729	AA094800	AW970843	Hs.55682	eukaryotic translation initiation factor 3, subunit 7 (zeta, 66/67kD)
	103794	AA100219	AF244135	Hs.30670	hepatocellular cardnoma-associated antigen 66
	131471	AA114885	AA164842	Hs.192619	KIAA1600 protein
55		AA129547	BE304999	Hs.75653	furnarate hydratase
		AA133016	AW958264	Hs.103832	similar to yeast Upf3, variant B
	119159	AA149507	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain RNA binding protein)
		AA151005	BE379765	Hs.129872	sperm associated antigen 9
60		AA187101	AA187101	Hs.213194 Hs.302267	hypothetical protein MGC10895
00		AA195179_s	W02363 AW024973	Hs.283675	hypothetical protein FLJ10330 NPD009 protein
		AA203138 AA203645	AA142922	Hs.278626	Arg/Abl-interacting protein ArgBP2
		AA206236	AA206236	Hs.4944	hypothetical protein FLJ12783
	100001	AA227621	AI769067	Hs.127824	ESTs. Weakly similar to T28770 hypothetical protein W03D2.1 - Caenorhabdilis elegans
65	[C.elega		Allosoon	110.12.024	LOTS, HOURY CHARGE TO TEOTIC HYPORICION PROTOST TO SOLETI
05	447735	AA248283	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone LNG00943
		AA249611	AA249611	Hs.47438	SH3 domain binding glutamic acid-rich protein
		AA282640	AF043117	Hs.24594	ubiquitination factor E4B (homologous to yeast UFD2)
		AA287199	D42039	Hs.78871	mesoderm development candidate 2
70	129013	AA313990	AA371156	Hs.107942	DKFZP564M112 protein
-	129435	AA314256	AF151852	Hs.111449	CGI-94 protein
	103988	AA314389	AA314389	Hs.42500	ADP-ribosylation factor-like 5
	104000	AA324364	Al146527	Hs.80475	polymerase (RNA) II (DNA directed) polypeptide J (13.3 kD)
75		AA329211_s	AF155568	Hs.155489	NS1-associated protein 1
75		AA399187	AL096748	Hs.102708	DKFZP434A043 protein
	133281	AA421079	AK001601	Hs.69594	high-mobility group 20A

	104104 AA422029	AA422029	Hs.143640	ESTs, Weakly similar to hyperpolarization-activated cyclic nucleotide-gated channel hHCN2
	[H.sapiens] 108154 AA425230	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain-binding protein
	132091 AA447052	AW954243	Hs.170218	KIAA0251 protein
5	135073 AA452000	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from done DKFZp586E1624)
	131367 AA456687	Al750575	Hs.173933	nuclear factor I/A
	129593 AA487015_s	Al338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (from done DKFZp586L0120)
	135266 AB002326 133505 C01527	R41179 Al630124	Hs.97393 Hs.324504	KIAA0328 protein Homo sapiens mRNA; cDNA DKFZp586J0720 (from clone DKFZp586J0720)
10	132064 C01714	AA121098	Hs.3838	serum-indudible kinase
	134393 C01811 f	W52642	Hs.8261	hypothetical protein FLJ22393
	131427 C02352_s	AF151879	Hs.28706	CGI-121 protein
	133435 C02375	Al929357	Hs.323966	Homo sapiens clone H63 unknown mRNA
15	104282 C14448 134827 D16611_s	C14448 BE314037	Hs.332338 Hs.89866	EST coproporphyrinogen oxidase (coproporphyria, harderoporphyria)
13	130443 D25216	D25216	Hs.155650	KIAA0014 gene product
	131742 D31352	AA961420	Hs.31433	ESTs
	132637 D58024_s	AA370362	Hs.57958	EGF-TM7-latrophilin-related protein
20	130377 D80897	NM_014909	Hs.155182	KIAA1036 protein
20	104334 D82614	D82614 NM_000437	Hs.78771 Hs.234392	phosphoglycerate kinase 1 platelet-activating factor acetylhydrolase 2 (40kD)
	134593 D87845 134731 D89377_i	D89377	Hs.234392 Hs.89404	msh (Drosophila) homeo box homolog 2
	129913 H06583	NM_001310	Hs.13313	cAMP responsive element binding protein-like 2
	131670 H40732	H03514	Hs.10130	ESTs
25	104394 H46617	AA129551	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone COL03924
	104402 H56731	H56731 AA306090	Hs.132956 Hs.124707	ESTs ESTs
	129781 H75570 129077 H78886	N74724	Hs.108479	ESTs
	104417 H81241	Al819448	Hs.320861	Kruppel-like factor 8
30	134927 L36531	L36531	Hs.91296	integrin, alpha 8
	129280 M63154	M63154	Hs.110014	gastric intrinsic factor (vitamin B synthesis)
	134498 M63180	AW248273	Hs.84131	threonyl-IRNA synthetase Homo saplens, clone IMAGE:4299322, mRNA, partial cds
	104460 M91504 104488 N56191	AW955705 N56191	Hs.62604 Hs.106511	protocadherin 17
35	131248 N78483	Al038989	Hs.332633	Bardet-Biedi syndrome 2
	129214 N79268	AL044335	Hs.109526	zinc finger protein 198
	130017 R14652	AK000096	Hs.143198	inhibitor of growth family, member 3
	104530 R20459 104534 R22303	AK001676 R22303	Hs.12457	hypothetical protein FLJ10814 gb:yh26b09.r1 Soares placenta Nb2HP Homo sapiens cDNA clone !MAGE:130841 5', mRNA
40	SEQUENCE.	NZ2303		go./ii/20009.11 30ales piacella 1922 il Tiorio sapiero conte inicola 1904 i 5 ; il 1917
	104544 R33779	Al091173	Hs.222362	ESTs, Weakly similar to p40 [H.sapiens]
	133328 R36553	AW452738	Hs.265327	hypothetical protein DKFZp761I141
	104567 R64534	AA040620	Hs.5672	hypothetical protein AF140225
45	128562 R66475 129575 R70821	AA923382 F08282	Hs.101490 Hs.278428	ESTs progestin induced protein
73	130776 R79356	AF167706	Hs.19280	cysteine-rich motor neuron 1
	104599 R84933	AW815036	Hs.151251	ESTs
	104660 RC_AA007160	BE298665	Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (from clone DKFZp564D016)
50	104667 RC_AA007234_s	AI239923 AI143020	Hs.30098 Hs.36250	ESTs ESTs, Weakly similar to 138022 hypothetical protein [H.saplens]
30	104718 RC_AA018409 104764 RC_AA025351	AI 143020 AI 039243	Hs.278585	ESTs, (Yearly similar to 130022 hypothetical protein (H.Saprens)
	104786 RC_AA027168	AA027167	Hs.10031	KIAA0955 protein
	104787 RC_AA027317	AA027317		gb:ze97d11.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366933 3'
ée	similar to contains Alu repa			
55	134079 RC_AA029423 104804 RC_AA031357	AK001751 Al858702	Hs.171835 Hs.31803	hypothetical protein FLJ10889 ESTs, Weakly similar to N-WASP [H.saplens]
	104865 RC_AA045136	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc finger protein)
	130828 RC_AA053400	AW631469	Hs.203213	ESTs
	104907 RC_AA055829	AA055829	Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
60	WARNING ENTRY [H.sap			(t-t-1/2
	104943 RC_AA065217 105013 RC_AA116054	AF072873 H63789	Hs.114218 Hs.296288	frizzled (Drosophila) homolog 6 ESTs, Weakly similar to KIAA0638 protein [H.sapiens]
	105024 RC_AA126311	AA126311	Hs.9879	ESTs
	132592 RC_AA129390	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone HRC12825
65	105038 RC_AA130273	AW503733	Hs.9414	KIAA1488 protein
	105077 RC_AA142919 105096 RC_AA150205	W55946	Hs.234863 Hs.21599	Homo sapiens cDNA FLJ12082 fis, clone HEMBB1002492 Kruppel-like factor 7 (ubiquitous)
	129215 RC_AA176867	AL042506 AB040930	Hs.126085	KIAA1497 protein
	105169 RC_AA180321	BE245294	Hs.180789	S164 protein
70	132796 RC_AA180487	NM_006283	Hs.173159	transforming, acidic coiled-coll containing protein 1
	130401 RC_AA187634	BE396283	Hs.173987	eukaryotic translation initiation factor 3, subunit 1 (alpha, 35kD)
	105200 RC_AA195399	AA328102	Hs.24641 Hs.14992	cytoskeleton associated protein 2 hypothetical protein FLJ11151
	130114 RC_AA234717 105330 RC_AA234743	AA233393 AW338625	Hs.14992 Hs.22120	ESTs .
75	105337 RC_AA234743	A1468789	Hs.23200	myotubularin related protein 1
, .	129385 RC_AA235604	AA172106	Hs.110950	Rag C protein
				· ·

	105376 RC_AA236559	AW994032	Hs.8768	hypothetical protein FLJ10849
	105397 RC_AA242868	AA814807	Hs.7395	hypothetical protein FLJ23182
	131962 RC_AA251776	AK000046	Hs.267448	hypothetical protein FLJ20039 budding uninhibited by benzimidazoles 1 (yeast homolog), beta
5	131991 RC_AA251909 128658 RC_AA252672_s	AF053306	Hs.36708 Hs.324830	diptheria toxin resistance protein required for diphthemide biosynthesis (Saccharomyces)-like 2
,	105489 RC_AA256157	AA256157	Hs.24115	Homo saplens cDNA FLJ14178 fis, clone NT2RP2003339
	105508 RC_AA256680	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (from clone DKFZp564H1916)
	105539 RC_AA258873	AB040884	Hs.109694	KIAA1451 protein
	135172 RC_AA262727	AB026956	Hs.12144	KIAA1033 protein
10	131569 RC_AA281451	AL389951	Hs.271623	nucleoponin 50kD
	132542 RC_AA281545	AL137751	Hs.263671 Hs.173802	Homo sapiens mRNA; cDNA DKFZp434l0612 (from clone DKFZp434l0612); partial cds KIAA0603 gene product
	105643 RC_AA262069 105659 RC_AA263044	BE621719 AA283044	Hs.25625	hypothetical protein FLJ11323
	105666 RC_AA263930	AA426234	Hs.34906	ESTs. Weakly similar to T17210 hypothetical protein DKFZp434N041.1 [H.sapiens]
15	105674 RC_AA284755	AI609530	Hs.279789	histone deacelylase 3
	105709 RC_AA291268	AI928962	Hs.26761	DKFZP586L0724 protein
	105722 RC_AA291927	AI922821	Hs.32433	ESTs
	105765 RC_AA343514	AA299688	Hs.24183	ESTs
20	115951 RC_AA398109	BE546245	Hs.301048	sec13-like protein
20	105962 RC_AA405737	AW880358	Hs.339808	hypothetical protein FLJ10120 gb:zv15b10.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:753691 3' similar to
	105985 RC_AA406610 ab:X02067	AA406610		gu.zv13010.31 30ales_nairimir o_31 Florito sapieis dellar delle liar-oc.103031 3 annian to
	106008 RC_AA411465	AB033888	Hs.8619	SRY (sex determining region Y)-box 18
	131216 RC_AA416886	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HEP08257
25	134222 RC_AA424013	AW855861	Hs.8025	Homo sapiens clone 23767 and 23782 mRNA sequences
	113689 RC_AA424148	AB037850	Hs.16621	DKFZP434l116 protein
	106141 RC_AA424558	AF031463	Hs.9302	phosducin-like
	130639 RC_AA424961_	s AB011169	Hs.20141	similar to S. cerevisiae SSM4
30	106157 RC_AA425367	W37943	Hs.34892 Hs.285418	KIAA1323 protein Homo sapiens cDNA FLJ10643 fis, clone NT2RP2005753, highly similar to Homo sapiens I-1
30	130777 RC_AA425921 receptor	AW135049	HS.200410	Fullio Sapielis CDIVA PLU 10040 ils, Golie 1412/142000100, rigitiy sittilai 10 110110 sapielio 1-1
	130561 RC_AA426220	AB011095	Hs.16032	KJAA0523 protein
	106196 RC_AA427735	AA525993	Hs.173699	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
	WARNING			
35	131878 RC_AA430673	AA083764	Hs.6101	hypothetical protein MGC3178
	133200 RC_AA432248	AB037715	Hs.183639	hypothetical protein FLJ10210
	106302 RC_AA435896	AA398859	Hs.18397	hypothetical protein FLJ23221
	106328 RC_AA436705 450534 RC_AA446561	AL079559 Al570189	Hs.28020 Hs.25132	KIAA0766 gene product KIAA0470 gene product
40	106423 RC_AA448238	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15
70	133442 RC_AA448688	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (from clone DKFZp434G227)
	439608 RC_AA449756	AW864696	Hs.301732	hypothetical protein MGC5306
	106477 RC_AA450303	R23324	Hs.41693	DnaJ (Hsp40) homolog, subfamily B, member 4
4.5	106503 RC_AA452411	AB033042	Hs.29679	cofactor required for Sp1 transcriptional activation, subunit 3 (130kD)
45	446999 RC_AA454566	AA151520	Hs.334822	hypothetical protein MGC4485
	106543 RC_AA454667 130010 RC_AA456437	AA676939 AA301116	Hs.69285 Hs.142838	neuropilin 1 nucleolar phosphoprotein Nopp34
	106589 RC_AA456646	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HEMBA1001702
	106593 RC_AA456826	AW296451	Hs.24605	ESTS
50	106596 RC_AA456981	AA452379	Hs.293552	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE
	CONTAMINATION			
	134655 RC_AA458959	AF265208	Hs.123090	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily f,
	member 1	AW958037	Hs.286	ribosomal protein L4
55	106636 RC_AA459950 106654 RC_AA460449	AW075485	Hs.286049	phosphoserine aminotransferase
55	131353 RC_AA463910	AW754182	115.200045	gb:RC2-CT0321-131199-011-c01 CT0321 Homo saplens cDNA, mRNA sequence
	106707 RC_AA464603	AK000566	Hs.98135	hypothetical protein FLJ20559
	131710 RC AA464606	NM_015368	Hs.30985	pannexin 1
	106717 RC_AA465093	AA600357	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein
60	131775 RC_AA465692	AB014548	Hs.31921	KIAA0648 protein
	106747 RC_AA476473	NM_007118	Hs.171957	triple functional domain (PTPRF interacting)
	106773 RC_AA478109	AA478109	Hs.188833	ESTs
	106781 RC_AA478474	AA330310 D61216	Hs.24181 Hs.18672	ESTs ESTs
65	106817 RC_AA480889 106846 RC_AA485223	AB037744	Hs.34892	KIAA1323 protein
05	106848 RC_AA485254	AA449014	Hs.121025	chromosome 11 open reading frame 5
	106856 RC_AA486183	W58353	Hs.285123	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2005779
	418699 RC_AA496936	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION
	WARNING			
70	107001 RC_AA598589	Al926520	Hs.31016	putative DNA binding protein
	130638 RC_AA598831_		Hs.17121	ESTs MAA4079 pertain
	107054 RC_AA600150	AI076459 BE614410	Hs.15978 Hs.23044	KIAA1272 protein RAD51 (S. cerevisiae) homolog (E coli RecA homolog)
	107059 RC_AA608545 107080 RC_AA609210	AL122043	Hs.19221	hypothetical protein DKFZp566G1424
75	107115 RC_AA610108	BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-like 1
, ,	107130 RC_AA620582	AB033106	Hs.12913	KIAA1280 protein

	107156 RC AA621239	AA137043	Hs.9663	programmed cell death 6-interacting protein
	107174 RC_AA621714	BE122762	Hs.25338	ESTs
		AW513087	Hs. 16803	LUC7 (S. cerevisiae)-like
	130621 RC_AA621718	AA836401	Hs.5103	ESTs
5	107190 RC_D19673 132626 RC_D25755_s	AW504732	Hs.21275	hypothetical protein FLJ11011
,	107217 RC_D51095	AL080235	Hs.21275 Hs.35861	DKFZP586E1621 protein
	131610 RC_D60272_i	AA357879	Hs.29423	scavenger receptor with C-type lectin
		AF088886	Hs.11590	cathensin F
	129604 T08879	AA186629	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyliransferase 1
10	107295 T34527 (GalNAc-T1)	AA 1000Z9	NS.00120	ODF-14-acetyr-alpha-D-galactusainii ecpotypeptide 14-acetyrgalactusainii yii ansienase 1
10	107299 T40327_s	BE277457	Hs.30661	hypothetical protein MGC4606
		AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3
	107315 T62771_s	T63174	Hs.193700	Homo sapiens mRNA; cDNA DKFZp586i0324 (from clone DKFZp586i0324)
	107316 T63174_s '		Hs.76591	KIAA0887 protein
15	107328 T83444	AW959891		
13	107334 T93641	T93597	Hs.187429 Hs.89040	ESTs prepronociceptin
	134715 U48263 128636 U49065	U48263 U49065	Hs.102865	interleukin 1 receptor-like 2
	120636 U49U65 129938 U79300	AW003668	Hs.102860 Hs.135587	Human clone 23629 mRNA sequence
20	107375 U88573	BE011845	Hs.251064	high-mobility group (nonhistone chromosomal) protein 14
20	130074 U93867	AL038596	Hs.250745 Hs.118893	polymerase (RNA) III (DNA directed) (62kD)
	107387 W01094 132036 W01568	D86983 AL157433	Hs.37706	Metanoma associated gene hypothetical protein DKFZp434E2220
	107426 W26853	W26853	Hs.291003	hypothetical protein MGC4707
25	113857 W27179	AW243158	Hs.5297	DKFZP564A2416 protein
23	135388 W27965	W27965	Hs.99865	epimorphin
	130419 W36280_s	AF037448	Hs.155489	NS1-associated protein 1
	107469 W47063	W47063	Hs.94668 Hs.283558	ESTs
	132616 W79060	BE262677		hypothetical protein PRO1855
30	107506 W88550	AB028981	Hs.8021	KIAA1058 protein
30	132358 X60486	NM_003542	Hs.46423	H4 histone family, member G
	107522 X78931_s	X78931	Hs.99971	zinc finger protein 272
	125827 Z14077_s	NM_003403	Hs.97498	YY1 transcription factor EST
	107582 RC_AA002147	AA002147	Hs.59952	
35	107609 RC_AA004711	R75654	Hs.164797	hypothetical protein FLJ13693
30	107861 RC_AA010383	AA010383	Hs.60389	ESTs
	107714 RC_AA015761	AA015761	Hs.60642	ESTs
	107775 RC_AA018772	AW008846	Hs.60857	ESTS
	107832 RC_AA021473_	r AAU214/3		gb:ze66c11.s1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:363956 3', mRNA
40	sequence.			and the second s
40	107859 RC_AA024835	AW732573	Hs.47584	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3
	124337 RC_AA025858	N23541	Hs.281561	Homo sapiens cDNA: FLJ23582 fis, clone LNG13759
	107914 RC_AA027229	AA027229	Hs.61329	ESTs, Weakly similar to T16370 hypothetical protein F45E12.5 - Caenorhebditis elegans
	[C.elegans]			
4.5	107935 RC_AA029428	AA029428	Hs.61555	ESTs
45	118262 RC_AA035143	Al936442	Hs.59838	hypothetical protein FLJ 10808
	131461 RC_AA035237	AA992841	Hs.27263	KIAA1458 protein
	108007 RC_AA039347	AA039347	Hs.61916	EST
	108029 RC_AA040740	AA040740	Hs.62007	ESTs
50	108040 RC_AA041551	AL121031	Hs.159971	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b,
50	member 1		440000	The state that MA OF MEMORS would available to
	108084 RC_AA045513	AA058944	Hs.116602	Homo sapiens, clone IMAGE:4154008, mRNA, partial cds
	108088 RC_AA045745	AA045745	Hs.62886	ESTs
	108168 RC_AA055348	Al453137	Hs.63176	ESTs
	130719 RC_AA056582_	s AA679262	Hs.14235	hypothelical protein FLJ20008; K/AA1839 protein
55	108189 RC_AA056697	AW376061	Hs.63335	ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]
	108190 RC_AA056746	AA056746	Hs.63338	EST
	108203 RC_AA057678	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone COL06049
	108216 RC_AA058681	AA524743	Hs.44883	ESTs
	108217 RC_AA058686	AA058686	Hs.62588	ESTs
60	108245 RC_AA062840	BE410285	Hs.89545	proteasome (prosome, macropain) subunit, beta type, 4
	108277 RC_AA064859	AA064859		gb:zm50f03.s1 Stratagene fibroblast (937212) Homo sapiens cDNA clone IMAGE:529085 3°,
	mRNA			
	108280 RC_AA065069	AA065069		gb:zm12e11.s1 Stratagene pancreas (937208) Homo sapiens cDNA clone 3', mRNA sequence
	108309 RC_AA069923	AA069818		gb:zm67e03.r1 Stratagene neuroepithelium (937231) Homo sapiens cDNA clone 5' similar to
65	133739 RC_AA070799_	s BE536554	Hs.278270	unactive progesterone receptor, 23 kD
	108340 RC_AA070815	AA069820	Hs.180909	peroxiredoxin 1
	108403 RC_AA075374	AA075374		gb:zm87a01.s1 Stratagene ovarian cancer (937219) Homo sapiens cDNA clone IMAGE:544872
	3', mRNA sequence.			
	108427 RC_AA076382	AA076382		gb:zm91g08.s1 Stratagene ovarian cancer (937219) Homo sapiens cDNA clone IMAGE:545342
70	3', mRNA sequence.			
	108435 RC_AA078787	T82427	Hs.194101	Homo saplens cDNA: FLJ20869 fis, clone ADKA02377
	108439 RC_AA078986	AA078986		gb:zm92h01.s1 Stratagene ovarian cancer (937219) Homo sapiens cDNA clone IMAGE:545425
	3', mRNA sequence.			•
	108465 RC_AA079393	AA079393	Hs.3462	cytochrome c oxidase subunit VIIc
75	108469 RC_AA079487	AA079487		gb:zm97f08.s1 Stratagene colon HT29 (937221) Homo saplens cDNA clone 3', mRNA
, 5	sequence			

	108500	RC_AA083207	AA083207	Hs.68270	EST
	108501	RC_AA083256	AA083256		gb:zn08g12.s1 Stratagene hNT neuron (937233) Homo sapiens cDNA clone 3' similar to
	gb:M333		11001115		gb:zn06g09.s1 Stratagene hNT neuron (937233) Homo sapiens cDNA clone IMAGE:546688 3',
5	mRNA	RC_AA084415	AA084415		gbizhogue.s1 Siłaggere niv1 neglon (95/255) nono sapiens colvis done instruction of
		RC_AA085274	AA100796		gb:zm26c06.s1 Stratagene pancreas (937208) Homo sapiens cDNA clone 3' similar to
	gb:X153				
	130890	RC_AA088678 RC_AA100925	AI732404 AI907537	Hs.68846 Hs.76698	ESTs stress-associated endoplasmic reticulum protein 1; ribosome associated membrane protein 4
10	134585	RC_AA101255	D14041	Hs.278573	H-2K binding factor-2
	130385	RC. AA126474	AW067800	Hs.155223	stanniocalcin 2
	108749	RC_AA127017	AA127017	Hs.71052	ESTS
		RC_AA129968 RC_AA130240	Al652236 AA045088	Hs.49376 Hs.62738	hypothetical protein FLJ20644 ESTs
15		RC_AA131866	AF188527	Hs.61661	ESTs, Weakly similar to AF174605 1 F-box protein Fbx25 [H.saplens]
	107290	RC_AA132039	W27740	Hs.323780	ESTs
	108846	RC_AA132983 RC_AA133250	AL117452 AK001468	Hs.44155 Hs.62180	DKFZP586G1517 protein anilfin (Drosophila Scraps homolog), actin binding protein
	131474	RC_AA133583_s		Hs.2726	high-mobility group (nonhistone chromosomal) protein isoform I-C
20	108894	RC_AA135941	AK001431	Hs.5105	hypothetical protein FLJ10569
	108941	RC_AA148650	AA148650		gb:zo09e06.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapians cDNA clone
	108068	67202 3', RC_AA151110	AI304870	Hs.188680	ESTs
	108996	RC_AA155754	AW995610	Hs.332436	EST
25	109001	RC_AA156125	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to hedgehog-interacting protein
		RC_AA156289	AI611807 AA156755	Hs.285107 · Hs.72150	hypothetical protein FLJ13397 ESTs
	109019	RC_AA156997 RC_AA157291	AA157291	Hs.21479	ubinuclein 1
	109023	RC_AA157293	AA157293	Hs.72168	ESTs
30	109068	RC_AA164293_f		Hs.72545	ESTs
	129072	RC_AA164676 RC_AA167375	AI732585 AL044675	Hs.22394 Hs.173081	hypothetical protein FLJ10893 KIAA0530 protein
	130346	RC_AA167550	H05769	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, complete cds
26		RC_AA176589	AA176589	Hs.142078	EST
35		RC_AA180448 RC_AA187144_s	AA180448 NM 004066	Hs.144300 Hs.2271	EST endothelin 1
		RC_AA189170_f		Hs.109441	MSTP033 protein
	109222	RC_AA192757	AA192833	Hs.333512	similar to rat myomegalin
40	109300	RC_AA205650	AA418276	Hs.170142	ESTs hypothetical protein FLJ21016
40		RC_AA233342 RC_AA233472	AA878923 BE619092	Hs.289069 Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP02442
	109516	RC_AA234110	Al471839	Hs.71913	ESTs
	109537	RC_D80981	AI858695	Hs.34898	ESTs
45		RC_F01660 RC_F02206	AI925294 F02206	Hs.87385 Hs.296639	ESTs Homo sapiens potassium channel subunit (HERG-3) mRNA, complete cds
10		RC_F02208	F02208	Hs.27214	ESTs
	109595	RC_F02544	AA078629	Hs.27301	ESTs
	109625	RC_F03918 RC_F04258_s	H29490 AF119665	Hs.22697 Hs.184011	ESTs pyrophosphatase (Inorganic)
50		RC_F04600	H17800	Hs.7154	ESTs
	109671	RC_F08998	R59210	Hs.26634	ESTs
		RC_F09605	H18013 AW016809	Hs.167483 Hs.323795	ESTs ESTs
	109020	RC_F11115 RC_H06371	R52417	Hs.20945	Homo sapiens clone 24993 mRNA sequence
55	110014	RC_H10995	AL109666	Hs.7242	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 35907
	110039	RC_H11938	H11938	Hs.21907	histone acetyltransferase ESTs
	110099	RC_H16568 RC_H16772	R44557 AW151660	Hs.23748 Hs.31444	ESTs
		RC_H18951	Al559626	Hs.93522	Homo sapiens mRNA for KIAA1647 protein, partial cds
60	110197	RC_H20859	AW090386	Hs.112278	arrestin, beta 1
		RC_H23747 RC_H38087	H19836 H38087	Hs.31697 Hs.105509	ESTs CTL2 gene
	110335	RC_H40331	H65490	Hs.18845	ESTS
	110342	RC_H40567	H40961	Hs.33008	ESTS
65		RC_H46966	AA025116	Hs.33333	ESTs
		RC_H56640_i RC_H57154	H56640 Al040384	Hs.221460 Hs.19102	ESTs ESTs, Weakly similar to organic anion transporter 1 [H.sapiens]
		RC_H96712	H96712	Hs.269029	ESTs
70	110754	RC_N20814	AW302200	Hs.6336	KIAA0672 gene product
70		RC_N25249 RC_N27100	U55936 NM_016569	Hs.184376 Hs.267182	synaptosomal-associated protein, 23kD TBX3-iso protein
		RC_N39616	AW973443	Hs.8086	RNA (guanine-7-) methyltransferase
	110938	RC_N48982	N48982	Hs.38034	Homo sapiens cDNA FLJ12924 fis, clone NT2RP2004709
75		RC_N51957	NM_015367	Hs.10267 Hs.154103	MiL1 protein LIM protein (similar to rat protein kinase C-binding enigma)
13		RC_N52271 RC_N59435	AA253314 AI146349	Hs.271614	CGI-112 protein
	111001				and the process

```
111128 RC N64139
                                AW505364
                                             Hs 19074
                                                            LATS (large tumor suppressor, Drosophila) homolog 2
                                AI834273
         135244 RC_N66981
                                              Hs.9711
                                                            novel protein
         111216 RC N68640
                                AW/139408
                                              He 152940
                                                            ESTs
         437562 RC N69352
                                AB001636
                                              Hs.5683
                                                            DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15
         131002 RC_N95226
                                AL 050295
                                                            KIAA0758 protein
                                              Hs 22039
         111399 RC_R00138
                                AW270776
                                              Hs.18857
                                                            ESTS
         111514 RC R07998
                                R07998
                                                            abovf16g11.s1 Soares fetal liver spicen 1NFLS Homo sapiens cDNA clone IMAGE;127076 31
         similar to
                                              Hs.192853
                                                            ubiquitin-conjugating enzyme E2G 2 (homologous to yeast UBC7)
         130182 RC R08929
                                BF267033
10
         111574 RC_R10307
                                Al024145
                                              Hs.188526
                                                            ESTs
         111804 RC_R33354
                                AA482478
                                              Hs.181785
                                                            ESTS
         111831 RC_R36083
                                R36095
                                              Hs.268695
                                                            ESTs
         129675 RC R37938 f
                                                            KIAA0440 protein
                                NM 015556 Hs.172180
         111904 RC R39330
                                741572
                                                            gb:HSCZYB122 normalized infant brain cDNA Homo sapiens cDNA clone c-zyb12, mRNA
         secuence
         133868 RC_R40816_s
                                AB012193
                                              Hs.183874
                                                           cuttin 4A
         112033 RC R43162 s
                                R49031
                                              He 22627
                                                            FST<sub>e</sub>
         130987 RC R45698
                                BE613269
                                              Hs.21893
                                                            hypothetical protein DKFZp761N0624
         112300 RC R54554
                                H24334
                                              Hs.26125
                                                            ESTs.
         112513 RC_R68425
                                                           hypothetical protein FLJ10648
20
                                R68425
                                              Hs.13809
         112514 RC R68568
                                R68568
                                              He 183373
                                                            src homology 3 domain-containing protein HIP-55
         112522 RC R68763
                                R68857
                                              Hs.265499
                                                            gbyk40a10.s1 Soares placenta Nb2HP Homo saplens cDNA clone 3', mRNA sequence
         112540 RC_R70467
                                R69751
         130346 RC_R73565
                                H05769
                                              Hs.188757
                                                            Homo sapiens, clone MGC:5564, mRNA, complete cds
25
         129534 RC R73640
                                AK002126
                                              Hs.11260
                                                            hypothetical protein FLJ11264
         112597 RC R78376
                                R78376
                                              Hs.29733
                                                            EST
         112732 RC_R92453
                                R92453
                                              Hs.34590
                                                            ESTS
                                                            hypothetical protein FLJ20392
         131458 RC_T03865
                                BE297567
                                              Hs.27047
         112888 RC T03872
                                AW195317
                                              Hs.107716
                                                            hypothetical protein FLJ22344
30
         131863 RC T10072
                                A)656378
                                              He 33461
                                                            ESTs
         112911 RC T10080
                                AW732747
                                              Hs 13493
                                                            like mouse brain protein E46
         132215 RC_T10132
                                AL035703
                                              Hs.4236
                                                            KIAA0478 gene product
         112931 RC T15343
                                T02966
                                              Hs.167428
                                                           ESTs
         112984 RC_T23457
112998 RC_T23555
                                T16971
                                              He 289014
                                                            ESTs. Weakly similar to A43932 mucin 2 precursor, intestinal [H.saplens]
35
                                H11257
                                              Hs 22968
                                                            Homo sapiens clone IMAGE:451939, mRNA sequence
         133376 RC_T23670
                                BE618768
                                              Hs.7232
                                                            acetyl-Coenzyme A carboxylase alpha
         113026 RC_T23948
113070 RC_T33464
                                AA376654
                                              Hs. 183684
                                                            eukarvotic translation initiation factor 4 gamma, 2
                                AB032977
                                              Hs 6298
                                                            KIAA1151 protein
         128970 RC_T34413
                                A1375672
                                              Hs.165028
                                                            FSTs
40
         113074 RC_T34611
113095 RC_T40920
                                AK001335
                                              Hs.31137
                                                            protein tyrosine phosphatase, receptor type, E
                                AA828380
                                              Hs.126733
         113179 RC_T55182
                                RF622021
                                              He 152571
                                                            ESTs. Highly similar to IGF-II mRNA-binding protein 2 [H.sapiens]
         113337 RC_T77453
113421 RC_T84039
                                T77453
                                              Hs.302234
                                                            ESTs
                                A1769400
                                              Hs.189729
                                                            ESTs
         113454 RC_T86458
                                              Hs.16188
                                                            ESTo
                                AI022166
         113481 RC T87693
                                TR7693
                                              He 201327
                                AA302862
                                                           neurocalcin delta
         131441 RC T89350 s
                                              Hs.90063
         113557 RC_T90945
                                H66470
                                              Hs 16004
                                                            FSTs
         113559 RC_T90987
                                T70763
                                              Hs.14514
                                                            ESTe
50
         113589 RC T91863
                                41078554
                                              He 15682
        113591 RC_T91881
113619 RC_T93783_s
113683 RC_T96687
                                T91881
                                              Hs.200597
                                                            KIAA0563 gene product
                                R08665
                                              Hs 17244
                                                            hypothetical protein FLJ13605
                                                            T-cell leukernia/lymphoma 6
                                AB035335
                                              He 144519
         113692 RC_T96944
                                AL 360143
                                              Hs.17936
                                                            DKFZP434H132 protein
55
                                                            gb:ve53h05.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:121497 31
         113702 RC T97307
                                T97307
         mRNA
                                              Hs.187447
         113717 RC_T97764
                                T99513
                                                            ESTs
         113824 RC_W48817
                                AI631964
                                              Hs.34447
                                                            ESTs
         113840 RC_W58343
                                R72137
                                              Hs.7949
                                                            DKFZP586B2420 protein
                                                           Homo sagiens cDNA FLJ14445 fis, clone HEMBB1001294, highly similar to GTP-BINDING
60
         113844 RC_W59949
                                              Hs 243010
                                A1369275
         PROTEIN TC10
         113902 RC W74644
                                AA340111
                                              Hs.100009
                                                            acyl-Coenzyme A oxidase 1, palmitoyl
         113904 RC W74761
                                AF125044
                                              Hs.19196
                                                            ubiquitin-conjugating enzyme HBUCE1
         113905 RC W74802
                                R81733
                                              Hs.33106
                                                            FSTs
                                                            hypothetical protein MGC15749
         113931 RC_W81205
                                BE255499
                                              Hs.3496
         113932 RC W81237
                                AA256444
                                              Hs.126485
                                                            hypothetical protein FLJ12604; KIAA1692 protein
         131965 RC_W90146_f
                                W79283
                                              Hs.35962
                                                            FSTe
         114035 RC_W92798
                                W92798
                                              Hs.269181
                                                            FST<sub>8</sub>
         114106 RC_Z38412
                                AW602528
                                                            gb:RC5-BT0562-260100-011-A02 BT0562 Homo sapiens cDNA, mRNA sequence
70
         133593 RC_Z38709
114161 RC_Z38904
                                A1416988
                                              Hs.238272
                                                            inositol 1.4.5-triphosphate receptor, type 2
                                                            hypothetical protein FLJ23399
                                 RF548222
                                              He 200883
         424949 RC Z39103
                                AF052212
                                              Hs 153934
                                                            core-binding factor, runt domain, alpha subunit 2; translocated to, 2
                                              Hs.279583
         129059 RC_Z39930_f
                                AW069534
         128937 RC_Z39939
                                AA251380
                                              Hs.10726
                                                            ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
75
         WARNING
         130983 RC_Z40012_i
                                AI479813
                                              Hs.278411
                                                            NCK-associated protein 1
```

	114277 RC_Z40377_s	AI052229	Hs.25373	ESTs, Weakly similar to T20410 hypothetical protein E02A10.2 - Caenorhabditis elegans
	[C.elegans]			
	114304 RC_Z40820	A1934204	Hs.16129	ESTs
5	114364 RC_Z41680 132900 RC_AA005112	AL117427 AA777749	Hs.172778 Hs.5978	Homo sapiens mRNA; cDNA DKFZp566P013 (from clone DKFZp566P013) LIM domain only 7
J	129034 RC AA005432	AA481157	Hs.108110	DKFZP547E2110 protein
	131881 RC_AA010163	AW361018	Hs.3383	upstream regulatory element binding protein 1
	452461 RC_AA026356	N78223	Hs.108106	transcription factor
	114465 RC_AA026901	BE621056	Hs. 131731	hypothetical protein FLJ11099
10	131376 RC_AA036867	AK001644	Hs.26156	hypothetical protein FLJ10782
	101567 RC_AA044644	M33552	Hs.56729	lysosomal
	431555 RC_AA046426 132944 RC_AA054515	AI815470 T96641	Hs.260024 Hs.6127	Cdo42 effector protein 3 Homo saptens cDNA: FLJ23020 fis, clone LNG00943
	114618 RC_AA084162	AW979261	Hs.291993	ESTs
15	130274 RC_AA085749	AA128376	Hs.153884	ATP binding protein associated with cell differentiation
	110330 RC_AA098874	AJ288666	Hs.16621	DKFZP434I116 prolein
	114648 RC_AA101056	AA101056		gb:zn25b03.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapians cDNA clone
	IMAGE:548429 3'		11.040400	
20	114658 RC_AA102746	AA102383	Hs.249190 Hs.48924	lumor necrosis factor receptor superfamily, member 10a
20	132456 RC_AA114250_ 131319 RC_AA126561_	6 NM 002155	Hs.25590	KIAA0512 gene product; ALEX2 stanniocalcin 1
	132225 RC_AA128980_	AA128980	110.2000	gb:zo09a11.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone
	IMAGE:567164 3'	7177120000		gancoon in the contract of the
	132669 RC_AA129757	W38586	Hs.293981	guanine nucleotide binding protein (G protein), gamma 3, linked
25	114709 RC_AA129921	AA397651	Hs.301959	proline synthetase co-transcribed (bacterial homolog)
	131973 RC_AA133331	AB018284	Hs.158688	KIAA0741 gene product
	114750 RC_AA135958	AA887211	Hs.129467	ESTs
	115714 RC_AA136524_ 114763 RC_AA147044	AA810755	Hs.172572 Hs.88977	hypothefical protein FLJ20093 hypothefical protein dJ511E16.2
30	114767 RC_AA148885	A1859865	Hs.154443	minichromosome maintenance deficient (S. cerevisiae) 4
50	114774 RC_AA150043	AV656017	Hs.184325	CGI-76 protein
	129388 RC_AA151621	AA662477	Hs.110964	hypothetical protein FLJ23471
	129183 RC_AA155743	BE561824	Hs.273369	uncharacterized hematopoietic stem/progenitor cells protein MDS027
	128869 RC_AA156335	AA768242	Hs.80618	hypothetical protein
35	130207 RC_AA156336	AF044209	Hs.144904	nuclear receptor co-repressor 1
	114798 RC_AA159181	AA159181	Hs.54900	serologically defined colon cancer antigen 1
	114800 RC_AA159825	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypothetical protein T03F6.2 - Caenorhabditis elegans
	[C.elegans] 114828 RC_AA234185	AA252937	Hs.283522	Homo sapiens mRNA; cDNA DKFZp434J1912 (from clone DKFZp434J1912)
40	114846 RC_AA234929	BE018682	Hs.166196	ATPase, Class I, type 8B, member 1
	114848 RC_AA234935	BE614347	Hs.169615	hypothetical protein FLJ20989
	114902 RC_AA236359	AW275480	Hs.39504	hypothetical protein MGC4308
	132271 RC_AA236466	AB030034	Hs.115175	sterile-alpha molif and leucine zipper containing kinase AZK
4.5	114907 RC_AA236535	N29390	Hs.13804	hypothetical protein dJ462O23.2
45	135159 RC_AA236935_	s U43374	Hs.95631 Hs.42265	Human normal keratinocyte mRNA ESTs
	132204 RC_AA236942 114928 RC_AA237018	AA235827 AA237018	Hs.94869	ESTs
	132481 RC_AA237025	W93378	Hs.49614	ESTs
	114932 RC_AA242751	AA971436	Hs.16218	KIAA0903 protein
50	314162 RC_AA242760	BE041820	Hs.38516	Homo sapiens, clone MGC:15887, mRNA, complete cds
	131006 RC_AA242763	AF064104	Hs.22116	CDC14 (cell division cycle 14, S. carevisiae) homolog B
	114935 RC_AA242809	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
	WARNING		Hs.250822	
55	132454 RC_AA243133	BE296227 R60366	Hs.250822 Hs.5822	serine/threonine kinase 15 Homo sapiens cDNA: FLJ22120 fis, clone HEP18874
55	437754 RC_AA243495 114957 RC_AA243706	AW170425	Hs.87680	ESTs
	114974 RC_AA250848	AW966931	Hs.179662	nucleosome assembly protein 1-like 1
	114977 RC_AA250868	AW296978	Hs.87787	ESTs
	114995 RC_AA251152	AA769266	Hs.193657	ESTs
60	115005 RC_AA251544_		Hs.111339	ESTs
	417177 RC_AA251792	NM_004458	Hs.81452	fatty-acid-Coenzyme A ligase, long-chain 4
	131889 RC_AA252063	NM_002589	Hs.34073	BH-protocadherin (brain-heart)
	115026 RC_AA252144 115045 RC_AA252524	AA251972 AW014549	Hs.188718 Hs.58373	ESTs ESTs
65	115068 RC_AA253461	AW512260	Hs.87767	ESTs
03	133138 RC_AA255522	AV657594	Hs.181161	Homo sapiens cDNA FLJ14643 fis, clone NT2RP2001597, weakly similar to RYANODINE
	RECEPTOR,			
	115114 RC_AA256468	AA527548	Hs.7527	small fragment nuclease
	129584 RC_AA256528	AV656017	Hs.184325	CGI-76 protein
70	115137 RC_AA257976	AW968304	Hs.56156	ESTs
	134312 RC_AA258296	AB011151	Hs.334659	hypothetical protein MGC14139
	115166 RC_AA258409	AF095727	Hs.287832 Hs.43728	myelin protein zero-like 1
	115167 RC_AA258421 129807 RC_AA262077	AA749209 Y11192	Hs.43728 Hs.5299	hypothetical protein aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase)
75	129807 RC_AA262077 115239 RC_AA278650	BE251328	Hs.73291	hypothetical protein FLJ10881
, 3	115243 RC_AA278766	009908VV	Hs.116665	KIAA1842 protein

	100850 RC_AA279667_s		Hs.297939	cathepsin B
	126884 RC_AA280791	U49436	Hs.286236	KIAA1856 protein
	115322 RC_AA280819	L08895	Hs.78995	MADS box transcription enhancer factor 2, polypeptide C (myccyte enhancer factor 2C)
5	133626 RC_AA280828	AW836130	Hs.75277	hypothetical protein FLJ13910
,	115372 RC_AA282195 132825 RC_AA283127_s	AW014385	Hs.88678 Hs.57698	ESTs, Weakly similar to Unknown [H.sapiens] Emptrically selected from AFFX single probeset
	130269 RC_AA284694	F05422	Hs.168352	nucleoporin-like protein 1
	129192 RG_AA291137	AA286914	Hs.183299	ESTs
	452598 RC_AA291708	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION
10	WARNING	711001004	110.000,11	EUR, House, Galley Bracot _ House House God Hallon Galley
	132131 RC_AA293495	AF069291	Hs.40539	chromosome 8 open reading frame 1
	115536 RC_AA347193	AK001468	Hs.62180	anillin (Drosophila Scraps homolog), actin binding protein
	132411 RC_AA398474_s	AA059412	Hs.47986	hypothetical protein MGC10940
	115575 RC_AA398512	AA393254	Hs.43619	ESTs
15	115601 RC_AA400277	AA148984	Hs.48849	ESTs, Weakly similar to ALU4_HUMAN ALU SUBFAMILY SB2 SEQUENCE CONTAMINATION
	WARNING			
	103928 RC_AA400896	D14540	Hs.199160	myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog)
	125819 RC_AA404494	AA044840	Hs.251871	CTP synthase junctional adhesion molecule 2
20	115683 RC_AA410345	AF255910 BE395161	Hs.54650 Hs.1390	protessome (prosome, macropain) subunit, beta type, 2
20	115715 RC_AA416733 132952 RC_AA425154	AI658580	Hs.61426	Homo sapiens mesenchymal stem cell protein DSC96 mRNA, partial cds
	115819 RC_AA426573	AA486620	Hs.41135	endomucin-2
	132525 RC_AA431418	AW292809	Hs.50727	N-acetylglucosaminidase, alpha- (Sanfilippo disease IIIB)
	115895 RC_AA436182	AB033035	Hs.51965	KIAA1209 protein
25	132333 RC_AA437099	AA 192669	Hs.45032	ESTs
	115962 RC_AA446585	AI636361	Hs.179520	hypothetical protein MGC10702
	115967 RC_AA446887	Al745379	Hs.42911	ESTs
	115974 RC_AA447224	BE513442	Hs.238944	hypothetical protein FLJ10631
••	115985 RC_AA447709	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable transcription factor CA150 [H.sapiens]
30	129254 RC_AA453624	AA252468	Hs.1098	DKFZp434J1813 protein
	133071 RC_AA455044	BE384932	Hs.64313	ESTs, Weakly similar to AF257182 1 G-protein-coupled receptor 48 [H.sapiens]
	116095 RC_AA456045	AA043429	Hs.62618 Hs.172788	ESTs ALCY2 ametric
	122691 RC_AA460454_8 116210 RC_AA476494	BE622792	Hs.172788	ALEX3 protein ALEX3 protein
35	116213 RC_AA476738	AA292105	Hs.326740	hypothetical protein MGC10947
55	134585 RC_AA481422	D14041	Hs.278573	H-2K binding factor-2
	134790 RC_AA482269	BE002798	Hs.287850	integral membrane protein 1
	116265 RC_AA482595	BE297412	Hs.55189	hypothetical protein
	129334 RC_AA485084_s		Hs.4947	hypothetical protein FLJ22584
40	116274 RC_AA485431_s	AI129767	Hs.182874	guanine nucleotide binding protein (G protein) alpha 12
	303150 RC_AA489057	AA887146	Hs.8217	stromal antigen 2
	129945 RC_AA489638	BE514376	Hs.165998	PAI-1 mRNA-binding protein
	116331 RC_AA491000	N41300	Hs.71616	Homo sapiens mRNA; cDNA DKFZp586N1720 (from clone DKFZp586N1720)
45	116333 RC_AA491250	AF155827 AA112748	Hs.203963 Hs.279905	hypothetical protein FLJ10339 clone HQ0310 PRO0310p1
43	132994 RC_AA505133 134577 RC_AA598447	BE244323	Hs.85951	exportin, IRNA (nuclear export receptor for IRNAs)
	116391 RC_AA599243	T86558	Hs.75113	general transcription factor IIIA
	116394 RC_AA599574_i		Hs.65370	lipase, endothelial
	134531 RC_AA600153	A1742845	Hs.110713	DEK oncogene (DNA binding)
50	116417 RC_AA609309	AW/499664	Hs.12484	Human clone 23826 mRNA sequence
	116429 RC_AA609710	AF191018	Hs.279923	putative nucleotide binding protein, estradiol-induced
	116439 RC_AA610068	AA251594	Hs.43913	PIBF1 gene product
	116459 RC_AA621399	R80137	Hs.302738	Homo sapiens cDNA: FLJ21425 ffs, clone COL04162
	427505 RC_AA621752	AA361562	Hs.178761	26S proteasome-associated pad1 homolog
55	132699 RC_C21523	AW449822	Hs.55200	ESTs
	116541 RC_D12160 132557 RC_D19708	D12160	Hs.249212	polymerase (RNA) III (DNA directed) (155kD)
	112259 RC_D25801	AA114926 AA337548	Hs.5122 Hs.333402	ESTs hypothetical protein MGC12760
	116571 RC_D45652	D45652	HS.333402	gb:HUMGS02848 Human adult lung 3' directed Mbol cDNA Homo sapiens cDNA 3', mRNA
60	sequence.	D43002		ge. Tomocozono haman adat lang o discolor mon obra mon obpacto asi a co, ma a m
00	129815 RC_D60208_f	BE565817	Hs.26498	hypothetical protein FLJ21657
	421919 RC_D80504_s	AJ224901	Hs.109526	zinc finger protein 198
	116643 RC_F03010	AI367044	Hs.153638	myeloid/lymphoid or mixed-lineage leukemia 2
	116661 RC_F04247	R61504		gb:yh16a03.s1 Soares infant brain 1NIB Homo sapiens cDNA clone 3' similar to contains Alu
65	repetitive			
	116715 RC_F10966	AL117440	Hs.170263	turnor protein p53-binding protein, 1
	116729 RC_F13700	BE549407	Hs.115823	nbonuclease P, 40kD subunit
	318709 RC_H05063	R52576	Hs.285280	Homo saplens cDNA: FLJ22096 fis, clone HEP16953
70	134760 RC_H16758 116773 RC_H17315_s	NM_000121 Al823410	Hs.89548 Hs.169149	erythropoietin receptor karyopherin alpha 1 (importin alpha 5)
70	106425 RC_H22556	H24201	Hs.247423	adducin 2 (beta)
	116780 RC_H22566	H22566	Hs.30098	ESTs ESTS
	131978 RC_H48459_s	AA355925	Hs.36232	KIAA0186 gene product
	116819 RC_H53073	H53073	Hs.93698	EST
75	111428 RC_H56559_s	AL031428	Hs.174174	KIAA0601 protein
	133175 RC_H57957_s	AW955632	Hs.66666	ESTs, Weakly similar to \$19560 proline-rich protein MP4 - mouse [M.musculus]

	116844 RC H64938 s	H64938	Hs.337434	ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]
	116845 RC_H64973	AA649530		gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens cDNA clone, mRNA sequence
	116892 RC_H69535	AI573283	Hs.38458	ESTs
-	116925 RC_H73110	H73110	Hs.260603	ESTs, Moderately similar to A47582 B-cell growth factor precursor [H.saplens]
5	116981 RC_H81783	N29218	Hs.40290	ESTs
	131768 RC_H86259	AC005757	Hs.31809	hypothetical protein
	117031 RC_H88353	H88353		gb:yw21a02.s1 Morton Fetal Cochlea Homo sapiens cDNA clone IMAGE:252842 3' similar to
	contains L1 117034 RC_H88639	U72209	Hs.180324	YY1-associated factor 2
10	132542 RC_H88675	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434l0812 (from clone DKFZp434l0812); partial cds
10	134403 RC H93708 s	AA334551	Hs.82767	sperm specific antigen 2
	117280 RC_N22107	M18217	Hs.172129	Homo saplens cDNA: FLJ21409 fis, clone COL03924
	117344 RC_N24046	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT2RP3004070
	117422 RC_N27028	Al355562	Hs.43880	ESTs, Weakly similar to A46010 X-linked retinopathy protein [H,sapiens]
15	117475 RC_N30205	N30205	Hs.93740	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
	117487 RC_N30621	N30621	Hs.44203	ESTs
	130207 RC_N33258	AF044209	Hs.144904 Hs.44483	nuclear receptor co-repressor 1
	117549 RC_N33390	N33390 N40180	HS.44483	EST gb:yy44d02.s1 Soares_multiple_sclerosis_2NbHMSP Homo saplens cDNA clone
20	117683 RC_N40180 IMAGE:276387 3' similar t			gu.yy-retroz.s i oceres_intriupre_scierosis_zaronimor nonio sapiens curin ocire
20	117710 RC_N45198	N45198	Hs.47248	ESTs, Highly similar to similar to Cdc14B1 phosphatase [H.sapiens]
	104514 RC_N45979_s	AF164622	Hs.182982	golgin-67
	117791 RC_N48325	N48325	Hs.93956	EST
	117822 RC_N48913	AA706282	Hs.93963	ESTs
25	129647 RC_N49394	AB018259	Hs.118140	KIAA0716 gene product
	117895 RC_N50656	AW450348	Hs.93996	ESTs, Highly similar to SORL_HUMAN SORTILIN-RELATED RECEPTOR PRECURSOR
	[H.sapiens]			
	131557 RC_N50721	AA317439	Hs.28707 Hs.64001	signal sequence receptor, gamma (translocon-associated protein gamma) Homo sapiens clone 25218 mRNA sequence
30	133057 RC_N53143 118103 RC_N55326	AA465131 AA401733	Hs.184134	ESTs
30	118111 RC_N55493	N55493	115.104154	qb;w50c02.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:246146 31
	mRNA	1130400		go. yeocozo i con co i con mici chical i il i co i cino depicio con il cono il interiori e i
	118129 RC_N57493	N57493		gb:yy54c08.s1 Soares_multiple_sclerosis_2NbHMSP Homo saplens cDNA clone
	IMAGE:277358 3', mRNA			*" - 1
35	118278 RC_N62955	N82955	Hs.316433	Homo sapiens cDNA FLJ11375 fis, clone HEMBA1000411, weakly similar to ANKYRIN
	118329 RC_N63520	N63520		gb:yy62l01.s1 Soares_multiple_sclerosls_2NbHMSP Homo saplens cDNA clone IMAGE:278137
	3', mRNA			
	118336 RC_N83604	BE327311	Hs.47166	HT021
40	132457 RC_N64166	AB017365 Al183838	Hs.173859 Hs.48938	frizzled (Drosophila) homolog 7 hypothetical protein FLJ21802
+0	118363 RC_N64168 118364 RC_N64191	N46114	Hs.29169	hypothetical protein FLJ22623
	118475 RC_N66845	N66845	110.20100	gb:za46c11.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:295304 3
	similar to			
	118491 RC_N67135	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone HEP09071
45	118500 RC_N67295	W32889	Hs.154329	ESTs
	101663 RC_N68399	NM_003528	Hs.2178	H2B histone family, member Q
	118584 RC_N68963	AW136928		gb:UI-H-BI1-adp-d-08-0-UI.s1 NCI_CGAP_Sub3 Homo sapiens cDNA clone 3', mRNA
	sequence 421983 RC_N69331	Al252640	Hs.110364	peptidylprolyl isomerase C (cyclophilin C)
50	118661 RC_N70777	AL137554	Hs.49927	protein kinase NYD-SP15
50	118684 RC_N71364_s	N71313	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone KAIA1180
	118689 RC_N71545_s	AW390601	Hs.184544	Homo saplens, clone IMAGE:3355383, mRNA, partial cds
	118690 RC_N71571	N71571	Hs.269142	ESTs
	118766 RC_N74456	N74456	Hs.50499	EST
55	118793 RC_N75594	N75594	Hs.285921	ESTs, Moderately similar to T47135 hypothetical protein DKFZp761L0812.1 [H.sapiens]
	118817 RC_N79035	Al668658	Hs.50797	ESTs
	118844 RC_N80279	AL035364 AW452696	Hs.50891 Hs.130760	hypothetical protein myosin phosphalase, target subunit 2
	118919 RC_N91797 129558 RC_N92454	AW580922	Hs.180446	karyopherin (importin) bela 1
60	132692 RC_N94581	AW191962	Hs.249239	collegen, type VIII, alpha 2
00	118996 RC_N94746	N94746	Hs.274248	hypothetical protein FLJ20758
	119021 RC_N98238	N98238	Hs.55185	ESTs
	119039 RC_R02384	Al160570	Hs.252097	pregnancy specific beta-1-glycoprotein 6
	119063 RC_R16833	R16833	Hs.53106	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
65	WARNING			
	118523 RC_R41828_s	Y07759	Hs.170157	myosin VA (heavy polypeptide 12, myoxin)
	119111 RC_R43203 133970 RC R46395	T02865 AA214228	Hs.328321 Hs.127751	EST hypothetical protein
	133970 RC_R46395 119146 RC_R58863	R58863	Hs.91815	ESTs
70	120296 RC_R78248	AW995911	Hs.299883	hypothetical protein FLJ23399
, ,	119239 RC_T11483	T11483		gb:CHR90049 Chromosome 9 exon Homo sapiens cDNA clone 111-15 and 3', mRNA
	sequence.			
	119281 RC_T16896	Al692322	Hs.65373	ESTs, Weakly similar to T02345 hypothetical protein KIAA0324 [H.sapiens]
~~	119298 RC_T23820	NM_001241	Hs.155478	cyclin T2
75	126502 RC_T30222	T10077	Hs.13453	hypothetical protein FLJ14753
	135073 RC_W15275_s	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (from clone DKFZp586E1624)

	119558 RC_W38194	W38194		Empirically selected from AFFX single probeset
	132736 RC_W42414_s	AW081883	Hs.288261	Homo sapiens cDNA: FLJ23037 fis, clone LNG02036, highly similar to HSU68019 Homo
	sapiens mad protein			
5	132173 RC_W46577_s 134873 RC_W49632_s	X89426 AA884471	Hs.41716 Hs.90449	endothelial cell-specific molecule 1 Human clone 23908 mRNA sequence
,	119650 RC_W57613	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]
	119654 RC_W57759	W57759		gb:zd20g11.s1 Soares_fetal_heart_NbHH19W Homo saplens cDNA clone IMAGE:341252 3'
	similar to			FOT
10	119683 RC_W61118 119694 RC_W65344	W65379 AA041350	Hs.57835 Hs.57847	ESTs ESTs, Moderately similar to ICE4_HUMAN CASPASE-4 PRECURSOR [H.saplens]
10	119718 RC_W69216	W69216	Hs.92848	ESTs
	133010 RC_W69379	Al287518	Hs.62669	Homo sapiens mRNA; cDNA DKFZp586D0923 (from clone DKFZp586D0923)
	119938 RC_W86728	AW014862	Hs.58885	ESTs
15	120128 RC_Z38499 120130 RC_Z38630	BE379320 AA045767	Hs.91448 Hs.5300	MKP-1 like protein tyrosine phosphatase bladder cancer associated protein
13	120148 RC_Z39494	F02806	Hs.65765	ESTs
	120155 RC_Z39623	Z39623	Hs.65783	ESTs
	131486 RC_Z40071_s	F06972	Hs.27372	BMX non-receptor tyrosine kinase
20	120183 RC_Z40174	AW082866 Z40182	Hs.65882 Hs.65885	ESTs EST .
20	120184 RC_Z40182 120211 RC_Z40904	Z40904	Hs.66012	EST
	120245 RC_AA166965	AW959615	Hs.111045	ESTs
	120247 RC_AA167500	AA167500	Hs.103939	EST
25	120254 RC_AA169599_1 120259 RC_AA171724	AW014786	Hs.111054 Hs.192742	ESTs hypothetical protein FLJ12785
23	120260 RC_AA171739	AK000061	Hs.101590	hypothetical protein
	120275 RC_AA177105	AA177105	Hs.78457	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15
	120284 RC_AA182626	AA179656		gb:zp54e11.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 3' similar
30	to contains 114056 RC_AA186324	AA188175	Hs.82506	KIAA1254 protein
30	129507 RC_AA192099	AJ236885	Hs.112180	zinc finger protein 148 (pHZ-52)
	120302 RC_AA192173	AA837098	Hs.269933	ESTs
	120303 RC_AA192415	AI216292	Hs.96184	ESTs
35	120305 RC_AA192553	AW295096 T57776	Hs.101337 Hs.191094	uncoupiling protein 3 (mitochondrial, proton carrier) ESTs
33	120319 RC_AA194851 133389 RC_AA195520_		Hs.72639	ESTs
	120326 RC_AA196300	AA198300	Hs.21145	hypothetical protein RG083M05.2
	134272 RC_AA198517	X76040	Hs.278614	protease, serine, 15
40	133145 RC_AA196549	H94227 AK000292	Hs.6592 Hs.278732	Homo sapiens, clone IMAGE:2961368, mRNA, partial cds hypothetical protein FLJ20285
40	120327 RC_AA196721 106686 RC_AA196729_		Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT2RP3003071
	120328 RC_AA196979	AA923278	Hs.290905	ESTs. Weakly similar to protease [H.saplens]
	120340 RC_AA206828	AA206828		gb:zq80b08.s1 Stratagene hNT neuron (937233) Homo saplens cDNA done IMAGE:847895 31
45	similar to 134292 RC_AA207123	AI906291	Hs.81234	immunoglobulin superfamily, member 3
73	131522 RC AA214539	AI380040	Hs.239489	TIA1 cytotoxic granule-associated RNA-binding protein
	129051 RC_AA226914_	s AA227068	Hs.108301	nuclear receptor subfamily 2, group C, member 1
	120375 RC_AA227260	AF028706	Hs.111227	Zic family member 3 (odd-paired Drosophila homolog, heterotaxy 1)
50	120376 RC_AA227469 IMAGE:6637323', mRNA	AA227469		gb:zr18a07.s1 Stratagene NT2 neuronal precursor 937230 Homo saplens cDNA clone
30	120390 RC_AA233122	AA837093	Hs.111460	calcium/calmodulin-dependent protein kinase (CaM kinase) II delta
	303876 RC_AA233334_	s U64820	Hs.66521	Machado-Joseph disease (spinocerebellar ataxta 3, olivopontocerebellar ataxta 3, autosomal
	dominant, ataxin 3)			-1-6
55	132038 RC_AA233347 104463 RC_AA233519	AI825842 T85825	Hs.3776 Hs.246885	zinc finger protein 216 hypothetical protein FLJ20783
33	125750 RC_AA233714	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411 (from clone DKFZp761A0411)
	120396 RC_AA233796	AA134006	Hs.79306	eukaryotic translation initiation factor 4E
	120409 RC_AA235050_	F AA235050		gb:zs38e04.s1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:687486 3' similar to
60	gb:L07077 120414 RC_AA235704	AW137156	Hs.181202	hypothetical protein FLJ10038
00	120414 RC_AA236031	AV 137 150 Al128114	Hs.112885	spinal cord-derived growth factor-B
	120422 RC_AA236352	AL133097	Hs.301717	hypothetical protein DKFZp434N1928
	132221 RC_AA236390_	s W94915	Hs.42419	ESTs
65	120423 RC_AA236453 120435 RC_AA243370	AA236453 AA243370	Hs.18978 Hs.96450	Homo sapiens cDNA: FLJ22822 fis, clone KAIA3968 EST
05	120455 RC_AA245570 120453 RC_AA250947	AA250947	Hs.170263	tumor protein p53-binding protein, 1
	120455 RC_AA251083	AA251720	Hs.104347	ESTs, Wealdy similar to ALUC_HUMAN IIII ALU CLASS C WARNING ENTRY III [H.sapiens]
	120456 RC_AA251113	AA488750	Hs.88414	BTB and CNC homology 1, basic leucine zipper transcription factor 2
70	120473 RC_AA251973	AA251973 A1244901	Hs.269988 Hs.9589	ESTs ublquilin 1
/0	128922 RC_AA252023 120477 RC_AA252414	AA252414	Hs.43141	DKFZP727C091 protein
	120479 RC_AA252650	AF006689	Hs.110299	mitogen-activated protein kinase kinase 7
	120488 RC_AA255523	AW952916	Hs.63510	KIAA0141 gene product
75	120510 RC_AA258128	A1796395	Hs.111377 Hs.4094	ESTs Homo sapiens cDNA FLJ14208 fis, clone NT2RP3003264
13	120527 RC_AA262105 120528 RC_AA262107	AA262105 AI923511	Hs.104413	ESTs
		. 1020011		

	120529 RC_AA262235	AJ434823 W07318	Hs.104415 Hs.240	ESTs M-phase phosphoprolein 1
	120541 RC_AA278298 131445 RC_AA278529_i		Hs.172052	weptrase priosprioprotein i serine/threonine kinase 18
	120544 RC_AA278721	BE548277	Hs.103104	ESTS
5	120562 RC_AA280036	BE244580	Hs.302267	hypothetical protein FLJ10330
	120569 RC_AA280648	AA807544	Hs.24970	ESTs, Weakly similar to B34323 GTP-binding protein Rab2 [H.sapiens]
	120571 RC_AA280738	AB037744	Hs.34892	KIAA1323 protein
	120572 RC_AA260794	H39599	Hs.294008	ESTs
10	129434 RC_AA280837	AW967495	Hs.186644	ESTS
10	130529 RC_AA280886 repetitive	AA178953		gb:zp39e03.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 3' similar to contains Alu
	120575 RC_AA280934	AW978022	Hs.238911	hypolhetical protein DKFZp762E1511; KIAA1816 protein
	132635 RC AA281535	AB020686	Hs.54037	ectonucleotide pyrophosphalase/phosphodiesterase 4 (putative function)
	120591 RC_AA281797_s		Hs.191356	general transcription factor IIH, polypeptide 2 (44kD subunit)
15	120593 RC_AA282047	AA748355	Hs.193522	ESTs
	430275 RC_AA283002	Z11773	Hs.237786	zinc finger protein 187
	117729 RC_AA283709	AA306166	Hs.7145	colpain 7
	120609 RC_AA283902 132754 RC_AA284108	AW978721 AI752244	Hs.266076 Hs.75309	ESTs, Weakly simitar to A46010 X-linked retinopathy protein [H.saplens] eukaryotic translation elongation factor 2
20	130315 RC_AA284109	AI241084	Hs.154353	nonselective sodium potassium/proton exchanger
20	132614 RC_AA284371	AA284371	Hs.118064	similar to rat nuclear ubiquitous casein kinase 2
	447503 RC_AA284744_f		Hs.336898	Homo sapiens, Similar to RIKEN cDNA 1810038N03 gene, clone MGC:9890, mRNA, complete
	cds			
0.5	135376 RC_AA284784	BE617856	Hs.99756	mitochondrial ribosome recycling factor
25	120621 RC_AA284840	AW961294	Hs.143818	hypothetical protein FLJ23459
	107868 RC_AA286844	AA286844 AW172431	Hs.61260 Hs.13012	hypothetical protein FLJ13164 ESTs
	129868 RC_AA287032 120644 RC AA287038	AI869129	Hs.96616	ESTs
	120660 RC_AA287546	AA286785	Hs.99677	ESTs
30	135370 RC_AA287553_s		Hs.99670	ESTs, Weakly similar to I38022 hypothetical protein [H.saplens]
	120661 RC_AA287556	AA287556	Hs.263412	ESTs, Weakly similar to ALUB_HUMAN IIII ALU CLASS B WARNING ENTRY III [H.saplens]
	129116 RC_AA287564	AB019494	Hs.225767	IDN3 protein
	131567 RC_AA291015_6		Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1
35	120699 RC_AA291716	Al683243	Hs.97258 Hs.1657	ESTs, Moderately similar to \$29539 ribosomal protein L13a, cytosolic [H.sapiens] estrogen receptor 1
33	100690 RC_AA291749_s 120726 RC_AA293656	AA293655	Hs.97293	ESTs
	120737 RC_AA302430	AL049176	Hs.82223	chordin-like
	120745 RC_AA302809	AA302809		gb:EST10426 Adipose tissue, white I Homo saplens cDNA 3' end, mRNA sequence.
	135192 RC_AA302820_s	U83993	Hs.321709	purinergic receptor P2X, ligand-gated ion channel, 4
40	120750 RC_AA310499	Al191410	Hs.96693	ESTs, Moderately similar to 2109260A B cell growth factor [H.saplens]
	120761 RC_AA321890	AA321890	Hs.1265 Hs.104560	branched chain keto acid dehydrogenase E1, beta polypaptide (maple syrup urine disease) EST
	120768 RC_AA340589 120769 RC_AA340622	AA340589 AI769467	Hs.96769	ESTs
	135232 RC_AA342457_i		Hs.96800	ESTs, Moderately similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE
45	CONTAMINATION	7,2000012	115100000	
	133439 RC_AA342828_s	z23091	Hs.73734	glycoprotein V (platelet)
	120793 RC_AA342864	AA342864	Hs.96812	ESTs
	120796 RC_AA342973	AI247356	Hs.96820	ESTs
50	120809 RC_AA346495	AA346495		gb:EST52657 Fetal heart II Homo sapiens cDNA 3' end similar to EST containing O family
30	repeat, mRNA sequence. 132459 RC_AA347573	AL120071	Hs.48998	fibronectin leucine rich transmembrane protein 2
	120825 RC_AA347614	Al280215	Hs.96885	ESTs
	120827 RC_AA347717	AA382525	Hs.132967	Human EST clone 122887 mariner transposon Hsmar1 sequence
	120839 RC_AA348913	AA348913		gb:EST55442 Infant adrenal gland II Homo sapiens cDNA 3' end similar to EST containing Alu
55	repeat, mRNA sequence.			
	120850 RC_AA349647	AA349647	Hs.96927	Homo saplens cDNA FLJ12573 fis, clone NT2RM4000979
	120852 RC_AA349773	AA349773	Hs.191564 Hs.106601	ESTs ESTs
	128852 RC_AA350541_1 135240 RC_AA357159_i	A 4357150	Hs.96986	EST
60	120870 RC_AA357172_		Hs.292581	ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
00	WARNING			
	134637 RC_AA369856_s	s U87309	Hs.180941	vacuolar protein sorting 41 (yeast homolog)
	120894 RC_AA370132	AA370132	Hs.97063	ESTs
	131854 RC_AA370472_	s AF229839	Hs.173202	I-kappe-B-interacting Ras-like protein 1
65	120897 RC_AA370867	AA370867	Hs.97079	ESTs, Moderately similar to AF174605 1 F-box protein Fbx25 [H.sapiens] ESTs
	120915 RC_AA377296 120935 RC_AA383902	AL135556 AL048409	Hs.97104 Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
	WARNING	1120-10100	120.17	Cord ready sures and a series a
	120936 RC_AA385934	AA385934	Hs.97184	EST, Highly similar to (defline not available 7499603) [C.e/egans]
70	120937 RC_AA386255	AA386255	Hs.97186	EST
	120938 RC_AA386260	AA386260	Hs.104632	EST
	129722 RC_AA386266	R20855	Hs.5422	glycoprotein M6B
	120960 RC_AA398014 120985 RC_AA398222	AA398014 AI219896	Hs.104684 Hs.97592	EST ESTs
75	120988 RC_AA398235	AA398235	Hs.97631	ESTs
, ,	120000 1.0_1000000			

		AA398348	Hs.301720	Human DNA sequence from clone RP11-251J8 on chromosome 13 Contains ESTs, STSs,
	GSSs and a CpG 121029 RC_AA398482	AA398482	Hs.97641	EST
		AA393037	Hs.161798	ESTs
5	121033 RC_AA398505	AA398505	Hs.97360	ESTs
		AL389951	Hs.271623	nucleoporin 50kD
		AA398523	Hs.210579	ESTs
		AA398625	Hs.97391	ESTs
10		AA398632 AA393288	Hs.97395 Hs.97396	ESTs ESTs
10	121091 RC_AA398894	AA398894	Hs.97657	ESTs, Moderately similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE
	CONTAMINATION	701030034	110.01 001	Ecro, mondatoly difficult of the art and a constraint of t
		AA398895	Hs.97658	EST
	121094 RC_AA398900	AA402505		gb:zt62h10.r1 Soares_testis_NHT Homo sapiens cDNA clone 5', mRNA sequence
15		AA398904	Hs.332690	ESTs
	121115 RC_AA399122	AA398187	Hs.104682	ESTs, Weakly similar to mitochondrial citrate transport protein [H.saplens]
		AA399371 Al126713	Hs.189095 Hs.192233	simitar to SALL1 (sal (Drosophila)-like ESTs, Highly simitar to T00337 hypothetical protein KIAA0568 [H.sapiens]
	121125 RC_AA399441	AL042981	Hs.251278	KIAA1201 protein
20		AA399636	Hs.143629	ESTs
	121153 RC_AA399640	AA399640	Hs.97694	ESTs
	121163 RC_AA399680	AI676062	Hs.111902	ESTs
		AL121523	Hs.97774	ESTs
25		AA400262 Al002110	Hs.190093 Hs.97169	ESTs ESTs, Weakly similar to dJ667H12.2.1 [H.sapiens]
23		AA400748	Hs.97823	Homo sapiens mRNA; cDNA DKFZp434D024 (from clone DKFZp434D024)
		AA814948	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN IIII ALU CLASS C WARNING ENTRY III [H.sapiens]
	121278 RC_AA401631	AA037121	Hs.98518	Homo sapiens cDNA FLJ11490 fis, clone HEMBA1001918
	121279 RC_AA401688	AA292873	Hs.177996	ESTs
30		AA401695	Hs.97334	ESTs
		AA402227 NM_006202	Hs.22826 Hs.89901	tropomodulin 3 (ubiquitous) phosphodiesterase 4A, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E2)
	121301 RC_AA402329 121302 RC_AA402398	AA402587	Hs.325520	LAT1-3TM protein
		AA293863	Hs.97316	EST
35	121305 RC_AA402468	AA402468	Hs.291557	ESTs
	134721 RC_AA403268_s	AK000112	Hs.89306	hypothetical protein FLJ20105
		AA291411	Hs.97247	ESTs
	121324 RC_AA404229 129047 RC AA404260	AA404229 AI768623	Hs.97842 Hs.108264	EST ESTs
40	131074 RC AA404271	U16125	Hs.181581	glutamate receptor, ionotropic, kainate 1
	121344 RC_AA405026	AA405026	Hs.193754	ESTs
	121348 RC_AA405182	AA405182	Hs.97973	ESTs
	121350 RC_AA405237	AA405237		gb:zt06e10.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:712362 3' similar to
40	contains Alu			#OT
45		AA406061 AA406063	Hs.98001 Hs.98003	EST ESTs
	121402 RC_AA406063 121403 RC_AA406070	AA406070	Hs.98004	EST EST
	121408 RC_AA406137	AA406137	Hs.96019	EST
	121431 RC_AA406335	AA035279	Hs.176731	ESTs
50	132936 RC_AA411801	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear translocator 2
	121471 RC_AA411804	AA411804	Hs.261575	ESTs
	121474 RC_AA411833 121526 RC AA412219	AA402335 AW665325	Hs.188760 Hs.98120	ESTs, Highly similar to Trad [H.sapiens] ESTs
	121530 RC_AA412259	AA778658	Hs.98122	ESTS
55	121558 RC_AA412497	AA412497		gb:zt95g12.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:730150 3' similar to
	contains L1.t3 L1			• • • • • • • • • • • • • • • • • • • •
	121559 RC_AA412498	Al192044	Hs.104778	ESTs
	121584 RC_AA416586	AI024471	Hs.98232	ESTs
60	121609 RC_AA416867	AA416867 AA416874	Hs.98185 Hs.98168	EST ESTs
UU	121612 RC_AA416874 121737 RC_AA421133	AA421133	Hs.104671	erythrocyte transmembrane protein
	121740 RC_AA421138	AA421138	Hs.98334	EST
	129194 RC_AA422079 .	AA150797	Hs.109276	latexin protein
	121784 RC_AA423837	T90789	Hs.94308	RAB35, member RAS oncogene family
65	121802 RC_AA424328	Al251870	Hs.188898	ESTs
		Al338371	Hs.157173	ESTs ESTs
	121803 RC_AA424339	VIVIU-33/183		
	135286 RC_AA424469_s	AW023482	Hs.97849 Hs.98402	
	135286 RC_AA424469_s 121806 RC_AA424502	AW023482 AA424313 AW972853	Hs.98402 Hs.112237	ESTS ESTS
70	135286 RC_AA424469_s 121806 RC_AA424502 129517 RC_AA425004	AA424313	Hs.98402	ESTs
70	135286 RC_AA424469_s 121806 RC_AA424502	AA424313 AW972853 AI732692	Hs.98402 Hs.112237 Hs.165066	ESTS ESTS, Moderately similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE
70	135286 RC_AA424469_s 121806 RC_AA424602 129517 RC_AA42504 121845 RC_AA425734 CONTAMINATION 121853 RC_AA425887	AA424313 AW972853 AI732692 AA425887	Hs.98402 Hs.112237 Hs.165066 Hs.98502	EST's EST's EST's Moderately similar to ALUZ_HUMAN ALU SUBFAMILY SB SEQUENCE hypothetical protein FLJ 14303
70	135286 RC_AA42469_s 121806 RC_AA42502 129517 RC_AA425004 121845 RC_AA425734 CONTAMINATION 121853 RC_AA425887 121891 RC_AA426456	AA424313 AW972853 AI732692 AA425887 AA426456	Hs.98402 Hs.112237 Hs.165066	ESTs ESTs Moderately similar to ALUZ_HUMAN ALU SUBFAMILY SB SECUENCE hypothetical protein FLJ 14303 ESTs
	135286 RC_AA424469_s 121806 RC_AA42502 129517 RC_AA42502 129517 RC_AA42502 121845 RC_AA425734 CONTAMINATION 121853 RC_AA425887 121891 RC_AA42588 121895 RC_AA427396	AA424313 AW972853 AI732692 AA425887	Hs.98402 Hs.112237 Hs.165066 Hs.98502	EST's EST's EST's Moderately similar to ALUZ_HUMAN ALU SUBFAMILY SB SEQUENCE hypothetical protein FLJ 14303
70 75	135286 RC_AA42469_s 121806 RC_AA42502 129517 RC_AA425004 121845 RC_AA425734 CONTAMINATION 121853 RC_AA425887 121891 RC_AA426456	AA424313 AW972853 AI732692 AA425887 AA426456	Hs.98402 Hs.112237 Hs.165066 Hs.98502	ESTs ESTs Moderately similar to ALUZ_HUMAN ALU SUBFAMILY SB SECUENCE hypothetical protein FLJ 14303 ESTs

	121917 RC_AA428218 AA40639		ESTs
	121918 RC_AA428242 BE27468		chromosome 2 open reading frame 3
	121919 RC_AA428281 AA42828		EST
5	121941 RC_AA428865 AA42886		ESTs
3	121942 RC_AA428994 AW45270 121970 RC AA429666 AA42968		ESTs EST
	121970 RC_AA429666 AA42966 121993 RC_AA430181 AW29788		ESTs
	134660 RC_AA430184_s U73524	Hs.87465	ATP/GTP-binding protein
	126753 RC_AA431288_s AA30647		CD3D antigen, delta polypeptide (TTT3 complex)
10	122022 RC_AA431293 AA43129		ESTs, Moderately similar to T42650 hypothetical protein DKFZp434D0215.1 [H.saciens]
	122050 RC_AA431478 AI453076	Hs.166109	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2
	122051 RC_AA431492 AA43149		EST
	122055 RC_AA431732 AA43173		EST
	122105 RC_AA432278 AW24168		ESTs
15	122125 RC_AA434411 AK00049		hypothetical protein
	135235 RC_AA435512_i AW29824	4 Hs.293507	ESTs cylochrome P450, subfamily XIX (aromatization of androgens)
	122162 · RC_AA435698 AA62823 129406 RC_AA435711 AB01825		KIAA0712 gene product
	318801 RC_AA435815_s U40763	Hs.77965	peptidyl-prolyl isomerase G (cyclophilin G)
20	122186 RC_AA435842 AA39881		ESTs
20	122235 RC AA436475 AA43647		membrane-associated nucleic acid binding protein
	129131 RC_AA436489 AB02643		dual specificity phosphalase 10
	134664 RC_AA442060 AA25610	Hs.87507	ESTs
	122310 RC_AA442079 AW19280		ESTs, Weakly similar to S65824 reverse transcriptase homolog [H.sapiens]
25	122334 RC_AA443151 BE46589		ESTs, Weakly similar to LB4D_HUMAN NADP-DEPENDENT LEUKOTRIENE B4 12-
	122382 RC_AA446133 AA44644		ESTs
	122425 RC_AA447145 AB00785	Hs.100955	KIAA0399 protein
	122431 RC_AA447398 AA44739 122450 RC_AA447643 AA44764	3 Hs.99104 3 Hs.112095	ESTs hypothetical protein DKFZp434F1819
30	302653 RC_AA447742_s AJ40446		dynein, axonemal, heavy polypeptide 9
50	122477 RC_AA448226 AA44822	Hs.324123	ESTs
	122500 RC_AA448825 AA44882		ESTs
	122522 RC_AA449444 AA29960		ESTs
	122536 RC_AA450087 AF08087	Hs.99236	regulator of G-protein signalling 20
35	122538 RC_AA450211 AA45021		ESTs
	122540 RC_AA450244 AA47674		ESTs, Weakly similar to A43932 mucin 2 precursor, Intestinal [H.sapiens]
	122560 RC_AA452123 AW39234		centrosomal P4.1-associated protein; uncharacterized bone marrow protein BM032
	421919 RC_AA452155 AJ22490		zinc finger protein 198 gb:zx29c03.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:787876 3',
40	122562 RC_AA452156 AA45215	•	gb:xxzecus.sn soares_total_tetus_wbznro_ew notitu saprens curva ciune imacerozoro o ,
40	mRNA 122585 RC_AA453036 Al681654	Hs.170737	hypothetical protein FLJ23251
	122608 RC_AA453526 AA45352		ESTs
	122635 RC_AA454085 AA45408		gb:zx33a08.s1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:788246 31
	similar to		•
45	122636 RC_AA454103 AW65170		hypothetical protein FLJ14007
	122653 RC_AA454642 AW00916		ESTs
	122660 RC_AA454935 Al816827		nuclear respiratory factor 1
	122703 RC_AA456323 AA45632		ESTS
50	122724 RC_AA457395 AA45739 122749 RC_AA458850 AA45885		ESTs ESTs, Weakly similar to B34087 hypothetical protein [H.sapiens]
50	122772 RC_AA459662 AW1174		ESTs
	131098 RC_AA459668 U66669	Hs.236642	3-hydroxyisobutyryl-Coenzyme A hydrolase
	129045 RC_AA459679_s Al082883		hypothetical protein FLJ13409; KIAA1711 protein
	122777 RC_AA459702 AK00102	Hs.214397	hypothetical protein FLJ10160 similar to Insulin related protein 2
55	135362 RC_AA460017_f AA97812	Hs.99513	ESTs, Weakly similar to T17454 diaphanous-related formin - mouse [M.musculus]
	122798 RC_AA460324 AW36628		splicing factor (CC1.3)
	122837 RC_AA461509 AA46150		ESTs, Weakly similar to putative p150 [H.sapiens]
	122860 RC_AA464414_1 AA46441	١ .	gb:zx/8g01.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:809904 3',
60	mRNA sequence. 122861 RC AA464428 AA33572	1 Hs.119394	ESTs
00	122861 RC_AA464428 AA33572 122910 RC_AA470084 AA47008		ESTs
	132899 RC_AA476606_s AA47660		SMAD in the antisense orientation
	122967 RC_AA478521 AA80618		glucose regulated protein, 58kD
	129560 RC_AA478523 AA31784		hypothetical protein MGC2752
65	123009 RC_AA479949 AA53524	Hs.78305	RAB2, member RAS oncogene family
	128917 RC_AA481252 Al365215		oncogene TC21
	123081 RC_AA485351 Al815486		Homo sapiens cDNA FLJ20738 fis, clone HEP08257
	123133 RC_AA487264 AA48726		Homo sapiens mRNA; cDNA DKFZp667N064 (from clone DKFZp667N064)
70	123184 RC_AA489072 BE24776		KIAA0870 protein
70	129671 RC_AA489630 NM_014		KIAA0665 gene product ESTs, Weakly similar to MAPB_HUMAN MICROTUBULE-ASSOCIATED PROTEIN 1B
	123233 RC_AA490225 AW9741 [H.sapiens]	o na.100/01	COLO, FECURIO DI MATE DI DOMANI MICA OTOSSE TIGOSONI IL DENOTRA ID
	123234 RC_AA490227 NM_0019	38 Hs.16697	down-regulator of transcription 1, TBP-binding (negative cofactor 2)
	123236 RC_AA490255 AW9685		CDC2-related protein kinase 7
75	123255 RC_AA490890 AA83033	5 Hs.105273	ESTs
	129503 RC_AA490916_s AW7683	9 Hs.112157	ESTs

	131043 RC_AA490925 123259 RC_AA490955 [H.sapiens]	AF084535 AI744152	Hs.22464 Hs.283374	epilepsy, progressive myoclonus type 2, Lafora disease (laforin) ESTs, Wealdy similar fo CA15_HUMAN COLLAGEN ALPHA 1(V) CHAIN PRECURSOR
5	123284 RC_AA495812 123286 RC_AA495824 123315 RC_AA496369	AA488988 AA495824 AA496369	Hs.293796 Hs.188822	ESTs ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.saplens] gb:zx/37d10.s1 Scares ovary tumor NbHOT Homo saplens cDNA clone IMAGE:755827 3' similar
10	to contains 129179 RC_AA504125_s 131612 RC_AA521473 123421 RC_AA598440 123449 RC_AA598899_j 129021 RC_AA599244	AU076668 AA598440 AL049325 AL044675	Hs.109154 Hs.334884 Hs.291154 Hs.112493 Hs.173081	ESTs SEC10 (S. carevisiae)-like 1 EST, Weakly similar to 158022 hypothetical protein [H.sapiens] Homo sapiens mRNA; dNNA DKF2p6940036 (from done DKF2p6640036) KANASS0 protein
15	132830 RC_AA599694_s 123497 RC_AA60037 123604 RC_AA609135 129539 RC_AA609582 123712 RC_AA609884 123731 RC_AA609839	AA765256 AA609135 T47614 AA609684 AA609839	Hs.57730 Hs.135191 Hs.293076 Hs.323022 Hs.112748	KIAMO133 gene product ESTA, Weakly shirin or humamed protein product (\$1.sapiens) EST4 EST4, Healthy shirilar to p80 katanin (\$1.sapiens) Henco spiens GNN+FLZ1543 (\$6, done COL0517) Electrophysiologisms GNN+FLZ1543 (\$6, done COL0517) Electrophysiologisms (\$7.sapiens electrophysiologisms a97218) Homo sapiens cDNA done IMAGE:551481 3'
20	similar to 130725 RC_AA609862 123800 RC_AA620423 123841 RC_AA620747	T98807 AA620423 AA620747	Hs.80248 Hs.112862 Hs.112896	PNA-binding protein gene with multiple splicing EST ESTs
25	123929 RC_AG21364 123978 RC_C20653 133184 RC_D20085 132835 RC_D20749 132406 RC_D51285_s	AA621364 T89632 AA001021 Z83844 AL133731	Hs.112981 Hs.170278 Hs.6685 Hs.5790 Hs.4774	ESTS ESTS ESTS Hyroid hormone receptor interactor 8 Hyroid hormone receptor interactor 8 Hyroid hormone address Hyroid hormone process Hy
30	128695 RC_D59972_I 124028 RC_F04112_f sequence.	NM_003478 F04112 AA902384	Hs.101299 Hs.73853	cullin 5 gbHSC2JH062 normalized infant brain cDNA Homo sapiens cDNA clone c-2 h06 3, mRNA bone morphogenetic protein 2
35	124057 RC_F13604 134899 RC_H01662 130973 RC_H05135_i 124106 RC_H12245	Al609045 Al638418 H12245	Hs.78580 Hs.101770	cone moprosgeneus protein X hyporhelical protein (NFZp43AD1428 DEADH (Asp-Stu-Ala-AspHis) box potypeptide 1 gloym17a12x1 Scares infant brain 1NIB Homo sapiens cDNA clone 3; mRNA seguence EST
33	124138 RC_H22842 124165 RC_H30894 131229 RC_H43442_s 124178 RC_H45996	H22842 H30039 NM_015340 BE463721	Hs.107674 Hs.2450 Hs.97101	ESTs leucyl-IRNA synihetase, milochondrial gutative G protein-coupled receptor
40	129948 RC_H69281_I 134374 RC_H69485_f 124254 RC_H69899 similar to	Al537162 N22687 H69899	Hs.263988 Hs.8236	ESTs ESTs gbyu/70c12.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:239158 3'
45	129056 RC_H70627_s 100919 RC_H73050_s 130724 RC_H73280 100716 RC_H77531_s 124274 RC_H80552 129078 RC_H80737_s	AI769958 X54534 AK001507 X89887 H80552 AI351010	Hs.108336 Hs.278994 Hs.306084 Hs.172350 Hs.102249 Hs.102267	ESTS, Weakly similar to ALUE_HUMAN IIII ALU CLASS E WARNING ENTRY III [H-sopiero] Rhemas blood group, CEG antigens Homo sepiero done FLB9914 PRO1821 mRNA, complete cds HRIR (Ristone call cycle regulation defective, S. cerevisian) homotog A EST [Noscome]
50	124828 RC_H93412 124315 RC_H94892_s 100747 RC_H95643_s 124324 RC_H98552 452933 RC_H97146	AW952124 NM_005402 X04588 H96552 AW391423	Hs.13094 Hs.288757 Hs.85844 Hs.159472 Hs.288555	presentina associated monitori-like proble varial simina leukemia viral oncogene homolog A (ras related) neurologich (tyndine kinase, receptor, type 1 Homo sepiera GNA: FLUZZ26 fis, clone IRC01703 Homo sepiera GNA: FLUZZ26 fis, clone IRC018686
55	132231 RC_H99131_s 129170 RC_H99462_s 133143 RC_H99837_s 132963 RC_N22140 135297 RC_N22197	AA662910 AW250380 AA094538 AA099693 AL118782	Hs.42635 Hs.109059 Hs.272806 Hs.34851 Hs.300206	hypothecisal prolein INFZpASI4CA35 mischodridal Folkoorel prolein L12 patative transcription regulation nudear prolein; VIAA1689 prolein epsilon-tultulin Sec23-alteroating prolein p125
60	134347 RC_N23756_s 130365 RC_N24134 421642 RC_N24195 439311 RC_N26739 124383 RC_N27098	AF164142 W56119 AF172066 BE270868 N27098	Hs.82042 Hs.155103 Hs.106346 Hs.151945 Hs.102463	solute carrier family 23 (nucleobase transporters), member 1 eukaryotic translation initiation factor 1A, Y chromosome relinoic acid repressible protein mitochondrial ribosomal protein L43 EST
65	124385 RC_N27096 124387 RC_N27637 129341 RC_N33090 129081 RC_N35967 102827 RC_N38959_1 124433 RC_N39069	N27637 AI193519 AI364933 BE244588 AA280319	Hs.109019 Hs.226396 Hs.168913 Hs.6456 Hs.288840	Exis ECIsts (Exists the Control of t
70	124441 RC_N46441 132338 RC_N48270_f 131403 RC_N48365_s 124466 RC_N51316	AW450481 AA353868 Al473114 R10084	Hs.161333 Hs.182982 Hs.26455 Hs.113319	ESTs godjin-67 ESTs kinesin heavy châin member 2
75	132210 RC_N51499_s 124483 RC_N53976 124484 RC_N54157 124485 RC_N54300	NM_007203 AI821780 H66118 AE040933	Hs.42322 Hs.179864 Hs.285520 Hs.15420	A kinase (PRKA) anohor protein 2 ESTs ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens] KIAA1500 protein

	124494 RC_N54831	N54831	Hs.271381	ESTs, Weakly similar to (38022 hypothetical protein [H.sapiens]
	129200 RC_N59849	N59849	Hs.13565	Sam68-like phosphotyrosine protein, T-STAR
	124527 RC_N62132	N79264	Hs.269104	ESTs
	124532 RC_N62375	N62375	Hs.102731	EST
5	133213 RC_N63138	AA903424	Hs.6786	ESTs
	124539 RC_N63172	D54120	Hs.146409	cell division cycle 42 (GTP-binding protein, 25kD)
	133651 RC_N63772	Al301740	Hs.173381	dihydropyrimidinase-like 2
	129196 RC_N63787	BE296313 N68168	Hs.265592	ESTs, Wealthy similar to 138022 hypothetical protein [H.sapiens] gb:za11c01.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 3', mRNA sequence
10	124575 RC_N68168 124576 RC_N68201	N68201	Hs.269124	gb.2a (CDT.ST Solates letal liver speech five ESTs, Weakly similar to (38022 hypothetical protein [H.sapiens]
10	124577 RC_N68300	N68300	110.200124	gb:za12g07.s1 Soares fetal liver spicen 1NFLS Homo sapiens cDNA clone IMAGE:292380 3',
	mRNA	1400300		guaranzgor an course scall inter epiceri in a comente expense estre in internal and
	124578 RC N68321	N68321	Hs.231500	EST
	124593 RC_N69575	N69575	Hs.102788	EST _S
15	128501 RC_N75007	AL133572	Hs.199009	protein containing CXXC domain 2
	105691 RC_N75542	AI680737	Hs.289068	Homo sapiens cDNA FLJ11918 fls, clone HEMBB1000272
	128473 RC_N90066	T78277	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-
	128639 RC_N91246 124652 RC_N92751	AW582962 W19407	Hs.102897 Hs.3862	CGI-47 protein regulator of nonsense transcriots 2: DKFZP434D222 protein
20	133137 RC_N93214_s	AB002316	Hs.65746	KIAA0318 protein
20	124671 RC_N99148	AK001357	Hs.102951	Homo sapiens cDNA FLJ10495 fis, clone NT2RP2000297, moderately similar to ZINC FINGER
	PROTEIN	1		, , , , , , , , , , , , , , , , , , , ,
	133054 RC_R07876	AA464836	Hs.291079	ESTs, Weakly similar to T27173 hypothetical protein Y54G11A.9 - Caenorhabditis elegans
	[C.elegans]			
25	130410 RC_R10865_f	J00077	Hs.155421	alpha-fetoprolein
	124720 RC_R11056	R05283		gb:ye91c08.s1 Soares fetal liver spieen 1NFLS Homo saplens cDNA clone IMAGE:125102 31
	similar to	T07799	Hs.185685	ESTs
	124722 RC_R11488 129961 RC_R22947	T97733 R23053	ris. 100000	gb:yh31a05.r1 Soares placenta Nb2HP Homo sapiens cDNA clone 5' similar to contains L1
30		RC_R23930_s	AL137586	Hs,52763 anaphase-promoting comptex subunit 7
	132965 RC_R26589_f	A1248173	Hs.191460	hypothetical protein MGC12936
	133740 RC_R37588_s	AW162919	Hs.170160	RAB2, member RAS oncogene family-like
	133074 RC_R37613	AL134275	Hs.6434	hypothetical protein DKFZp761F2014
2.5	124757 RC_R38398	H11368	Hs.141055	Homo sapiens clone 23758 mRNA sequence
35	124762 RC_R39179_f	AA553722	Hs.92096	ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]
	124773 RC_R40923 135266 RC_R41179	R45154 R41179	Hs.106604 Hs.97393	ESTs KIAA0328 protein
	131375 RC_R41294_s	AW293165	Hs.143134	ESTs
	133753 RC_R42307_f	NM_004427	Hs.165263	early development regulator 2 (homolog of polyhomeotic 2)
40	128540 RC_R43189_f	AW297929	Hs.328317	EST
	124785 RC_R43306	W38537	Hs.280740	hypothetical protein MGC3040
	124792 RC_R44357	R44357	Hs.48712	hypothetical protein FLJ20736
	124793 RC_R44519	R44519		gb:yg24h04.s1 Soares Infant brain 1NiB Homo sapiens cDNA done IMAGE:33350 31, mRNA
45	sequence. 124799 RC_R45088	R45088		gb:vg38g04.s1 Source infant brain 1NIB Homo sapiens cDNA clone IMAGE:34896 31, mRNA
73	sequence.	1145000		guilgogotta i dezen intan bean inter rente appara april acino intradicione e i intra
	124812 RC_R47948_i	R47948	Hs.188732	ESTs
	124821 RC_R51524	H87832	Hs.7388	kelch (Drosophila)-like 3
	127274 RC_R54950	AW966158	Hs.58582	Homo saplens cDNA FLJ12789 fis, clone NT2RP2001947
50	124835 RC_R55241	R55241	Hs.101214	EST
	124845 RC_R59585	R59535	Hs.101255	ESTS
	124847 RC_R60044	W07701 BE561430	Hs.304177 Hs.239388	Homo sapiens clone FLB8503 PRO2286 mRNA, complete cds Human DNA sequence from clone RP1-304B14 on chromosome 6. Contains a gene for a novel
	440630 RC_R60872	o for a neval no	ris.233300 stoin with two io	oforms. Contains ESTs, STSs, GSSs and a CpG island
55	124861 RC_R66690	R67567	Hs.107110	ESTS
	130141 RC_R67266_s	NM_004455	Hs.150956	exostoses (multiple)-like 1
	124879 RC_R73588	R73588	Hs.101533	ESTs
	124892 RC_R79403	AI970003	Hs.23756	hypothetical protein similar to swine acylneuraminate lyase
60	124906 RC_R87647	H75964	Hs.107815	ESTs
00	124922 RC_R93622 124940 RC_R99599_s	R93622 AF068846	Hs.12163 Hs.103804	eukaryotic translation initiation factor 2, subunit 2 (beta, 38kD.) heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
	124941 RC_R99612	AI766661	Hs.27774	ESTs, Highly similar to AF161349 1 HSPC086 [H.sapiens]
	124943 RC_T02888	AW963279	Hs.123373	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
	WARNING ENTRY [H.sap			
65	124947 RC_T03170	T03170	Hs.100165	ESTs
	124954 RC_T10465	AW964237	Hs.6728	KIAA1548 protein
	132924 RC_T15418_f	U55184	Hs.154145	hypothetical protein FLJ11585
	133113 RC_T15597_f	BE383768 R43504	Hs.65238 Hs.6181	95 kDa retinoblastoma protein binding protein; KIAA0661 gene product ESTs
70	132975 RC_T15652_i 133235 RC_T16898_s	AW960782	Hs.6856	ash2 (absent, small, or homeotic, Drosophila, homolog)-like
, 0	131082 RC_T26644_i	Al091121	Hs.246218	Homo sapiens cDNA: FLJ21781 fis, clone HEP00223
	124980 RC_T40841	T40841	Hs.98681	ESTs
	124984 RC_T47566_i	BE313210	Hs.223241	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
75	124991 RC_T50116	T50116	00 OFFIF -	gb:yb77c10.s1 Stratagene ovary (937217) Homo sapiens cDNA clone IMAGE:772023' similar
75	to similar to SP:VE22_LAN	MBD P03756 EA NM_004477	VZZ GENE, mR	NA sequence. FSHD region gene 1
	129475 RC_T50145_s	MINE COMMITT	110-200112	i oriz region gane i

	125000 RC_T58615	T58615	Hs.110640	ESTs
	132932 RC_T59940_f	AW118826	Hs.6093	Homo sapiens cDNA; FLJ22783 fis, clone KAIA1993
	129534 RC_T63595	AK002126	Hs.11260	hypothetical protein FLJ11264
	125008 RC_T64891	T91251		gb:yd60a10.s1 Soares fetal liver spicen 1NFLS Homo sapiens cDNA clone 3, mRNA sequence
5	125009 RC_T64924	T64924 T79136	Hs.303046 Hs.127243	ESTs Homo sapiens mRNA for KIAA1724 protein, partial cds
	132940 RC_T64933_r 125017 RC_T68875	T68875	HS. 12/243	gb:yc30f05.s1 Stratagene liver (937224) Homo sapiens cDNA clone IMAGE:82209 3', mRNA
	sequence.	100075		ga.youtoca i dediagono moi (our zer) i omo supreta soria sono mi occazzas e i mossi
	125018 RC_T69027	T69027	Hs.57475	sex comb on midleg homolog 1
10	125020 RC_T69924	T69981		gb:yc19d03.r1 Stratagene lung (937210) Homo sapiens cDNA clone 5', mRNA sequence
	129891 RC_T70353	A1084813	Hs.13197	ESTs
	134204 RC_T79780_s	AI873257 AW970209	Hs.7994 Hs.111805	hypothetical protein FLJ20551 ESTs
	125050 RC_T79951 125052 RC_T80174_s	T85104	Hs,222779	ESTs, Moderately similar to similar to NEDD-4 [H.sapiens]
15	125054 RC_T80622	T80622	Hs.268601	ESTs, Weakly similar to envelope [H.sapiens]
	125063 RC_T85352	T85352		gb:yd82d01.s1 Soares fetal liver spieen 1NFLS Homo saplens cDNA clone IMAGE:114721 3'
	similar to contains Alu repe	titive element;	ontains L1 repe	etitive element ;, mRNA sequence.
	125064 RC_T85373	T85373		gb:yd82f07.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:114757 3'
20	similar to contains Alu repa	titive element; T86284	contains MER3 i	repetitive element;, mRNA sequence. gb;yd77b07.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone 3' similar to contains
20	125066 RC_T86284 Alu repetitive element;, mF			guyurrours addres retainver special intrice round supremo contr. doine a similar to contains
	112264 RC_T89579_s	AL045364	Hs.79353	transcription factor Dp-1
	125080 RC_T90360	T90360	Hs,268620	ESTs, Highly similar to ALU6_HUMAN ALU SUBFAMILY SP SEQUENCE CONTAMINATION
	WARNING ENTRY [H.sap			
25	125097 RC_T94328_i	AW576389	Hs.335774	EST, Moderately similar to S65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]
	125104 RC_T95590	T95590	DNA V DNA	gb:ye40a03.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone 3' similar to sequence
	gb[M10817]IGURRAA Igua 135107 RC_T97257_f	T97257	Hs.337531	ESTs, Moderately similar to i38022 hypothetical protein [H.sapiens]
	129550 RC_T97599_i	AA845462	Hs.124024	dellex (Drosophila) homolog 1
30	125118 RC_T97620	R10606		gb:yf35f11.s1 Soares fetal liver spleen 1NFLS Homo saplens cDNA clone IMAGE:128877 3'
	similar to contains Alu rece	titive element;,	mRNA sequen	08.
	125120 RC_T97775 134160 RC_T98152 125136 RC_W31479	T97775	Hs.100717	EST
	134160 RG_198152	T98152 AW962364	Hs.79432 Hs.129051	fibrilin 2 (congenital contractural arachnodactyly) ESTs
35	125144 RC_W37999	AB037742	Hs.24336	KIAA1321 protein
33	125150 RC_W38240	W38240		Empirically selected from AFFX single probeset
	104180 RC_W40150	AA247778	Hs.119155	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 814975
	131987 RC_W45435	AW453069	Hs.3657	activity-dependent neuroprotective protein
40	125178 RC_W58202	W93127	Hs.31845	ESTs
40	125180 RC_W58344 125182 RC_W58650	W58469 AA451755	Hs.103120 Hs.263560	ESTs ESTs
	130588 RC_W68736	ALG30996	Hs.16411	hypothetical prolein LOC57187
	125197 RC_W69106	AF086270	Hs.278554	heterochromatin-like protein 1
	133497 RC_W69111	BE617303	Hs.74266	hypothetical protein MGC4251
45	100562 RC_W69385_s	NM_006185	Hs.301512	nuclear mitotic apparatus protein 1
	125639 RC_W69399_s 129232 RC_W69459	Z97630 R98881	Hs.226117 Hs.109655	H1 histone family, member 0 sex comb on midleg (Orosophila)-like 1
	101495 RC_W72424	W72424	Hs. 112405	S100 calcium-binding protein A9 (calgranulin B)
	125209 RC_W72724	W72724	Hs.103174	ESTs, Weakly similar to TSP2_HUMAN THROMBOSPONDIN 2 PRECURSOR [H.sapiens]
50	125212 RC_W72834	AA746225	Hs.103173	ESTs
	129132 RC_W73955	BE383436	Hs.108847	hypothetical protein MGC2749
	125223 RC_W74701	Al916269	Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU SUBFAMILY SC SEQUENCE CONTAMINATION
	WARNING ENTRY [H.sap 125225 RC_W76540	W74169	Hs.16492	DKFZP564G2022 protein
55	125228 RC_W79397	AA033982	Hs.110059	ESTs, Weakly similar to 138022 hypothetical protein [H.sapiens]
	132393 RC_W65888	AL135094	Hs.47334	hypothetical protein FLJ14495
	125238 RC_W86038	N99713	Hs.109514	ESTs
	125247 RC_W86881	AA694191	Hs.163914	ESTs
60	129296 RC_W87804 125263 RC_W88942	AI051967 AA098878	Hs.110122	ESTs gb:zn45g10.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 5', mRNA sequence
00	125266 RC_W90022	W90022	Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKOCYTE CELL-DERIVED CHEMOTAXIN 2
	PRECURSOR [H.sapiens]			
	131321 RC_W92272	U91543	Hs.25601	chromodomain helicase DNA binding protein 3
	131601 RC_W92764_s	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced protein 6
65	131677 RC_W93040	H05317 BE149656	Hs.283549 Hs.306621	ESTs Homo saplens cDNA FLJ11963 fis, done HEMBB1001051
	120837 RC_W93092 125277 RC_W93227	W93227	Hs.103245	EST
	125278 RC_W93523	AI218439	Hs.129998	enhancer of polycomb 1
	125280 RC_W93659	Al123705	Hs.106932	ESTs
70	131856 RC_W94003_s	W93949	Hs.33245	ESTs
	131844 RC_W94401_s	AI419294	Hs.324342	ESTs
	125284 RC_W94688 313447 RC_W94787_s	NM_002666 AW016321	Hs.103253 Hs.82306	perilipin destrin (actin depolymerizing factor)
	130799 RC_Z38294_s	AB028945	Hs.12696	cortactin SH3 domain-binding protein
75	125289 RC_Z38311	T34530	Hs.4210	Homo sapiens cDNA FLJ13069 fis, clone NT2RP3001752
	128874 RC_Z38465_s	H06245	Hs.106801	ESTs, Weakly similar to PC4259 fertitin associated protein [H.sapiens]

	130966 RC_		AW971018	Hs.21659	ESTs
	128875 RC_			Hs.106808	kelch (Drosophila)-like 1
	133200 RC_			Hs.183639	hypothetical protein FLJ10210
-	130158 RC_			Hs.151301	Ca2+-dependent activator protein for secretion
5	125295 RC_	Z39113	AB022317	Hs.25887	sema domain, immunoglobulin domain (lg), transmembrane domain (TM) and short cytoplasmic
	domain, (sem	aphonn) 4F			II THE PROPERTY OF THE
	125298 RC_			Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone HEP01068
	125300 RC_			Hs.101376	EST Homo saplens cDNA FLJ12908 fis, clone NT2RP2004399
10	323122 RC_			Hs.264915 Hs.22142	cytochrome b5 reductase b5R.2
10	311463 RC_ 130882 RC_	25882J 240466 f		Hs.20887	hypothetical protein FLJ10392
	128888 RC_	740100_I		Hs.241558	ariadne (Drosophila) homolog 2
	125310 RC_			Hs.124953	ESTs 2
	125315 RC_	741697		Hs.106296	ESTs
15	125317 RC_			Hs.112461	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
	135096 RC	Z99394 s		Hs.132390	zinc finger protein 36 (KOX 18)
	104786 RC_			Hs.10031	KIAA0955 protein
	132837 D58		AA370362	Hs.57958	EGF-TM7-latrophilin-related protein
	120456 RC_			Hs.88414	BTB and CNC homology 1, basic leucine zipper transcription factor 2
20	132459 RC_			Hs.48998	fibronectin leucine rich transmembrane protein 2
	101545 M31			Hs.154210	endothelial differentiation, sphingolipid G-protein-coupled receptor, 1
	133505 C01			Hs.324504	Homo sapiens mRNA; cDNA DKFZp586J0720 (from clone DKFZp586J0720)
	132360 RC_			Hs.46440	solute carrier family 21 (organic anion transporter), member 3
25	132738 RC_			Hs.264636	hypothetical protein FLJ20731
25	119586 RC_		AF088033	Hs.159225	ESTs
	129914 RC_			Hs.13321	rearranged L-myc fusion sequence
	130839 AF0		AB011169	Hs.20141 Hs.57435	similar to S. cerevisiae SSM4 solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2
	132813 L37: 134342 M99		BE313625 NM_000275	Hs.82027	oculoculaneous albinism II (pink-eye dilution (murine) homolog)
30	131878 RC_	A 4420072	AA083764	Hs.6101	hypothetical protein MGC3178
50	105426 RC_	AA261207	W20027	Hs.23439	ESTs
	132968 RC_		AF234532	Hs.61638	myosin X
	132173 RC_		X89426	Hs.41716	endothelial cell-specific molecule 1
	113932 RC		AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692 protein
35	114452 RC_		Al369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HEMBB1001294, highly similar to GTP-BINDING
	PROTEIN TO				
	115243 RC_	AA278766	AA806600	Hs.116665	KIAA1842 protein
	134403 RC_	H93708_s	AA334551	Hs.82767	sperm specific antigen 2
	129647 RC_	N49394	AB018259	Hs.118140	KIAA0716 gene product
40	111428 RC_		AL031428	Hs. 174174	KIAA0601 protein
	115967 RC_		Al745379	Hs.42911	ESTs
	120726 RC_		AA293655	Hs.97293	ESTs
	114995 RC_		AA769266	Hs.193657	ESTs Machado-Joseph disease (spinocerebellar ataxia 3, olivopontocerebellar ataxia 3, autosomal
45		_AA233334_s	U64820	Hs.66521	Machago-Joseph disease (spinocarebalia) ataxia 3, unvopultiocarebaliai ataxia 3, autosotriai
43	dominant, ata 311463 RC		R55344	Hs.22142	cytochrome b5 reductase b5R.2
	120302 RC_		AA837098	Hs.269933	ESTs
	133071 RC		BE384932	Hs.64313	ESTs, Weakly similar to AF257182 1 G-protein-coupled receptor 48 [H.sapiens]
	121032 RC_	AA398504	AA393037	Hs.161798	ESTs
50	129829 U41		AF010258	Hs.127428	homeo box A9
50	120245 RC		AW959615	Hs.111045	ESTs
	120985 RC		Al219896	Hs.97592	ESTs .
	114184 RC_	Z39095	R56434	Hs.21062	ESTs
	447503 RC	_AA284744_f	AA115496	Hs.336898	Homo sapiens, Similar to RIKEN cDNA 1810038N03 gene, clone MGC:9890, mRNA, complete
55	cds				
	132837 RC		AA370362	Hs.57958	EGF-TM7-latrophilin-related protein
	121034 RC_		AL389951	Hs.271623	nucleoporin 50kD
	119718 RC		W69216	Hs.92848	ESTS
co	120455 RC		AA251720	Hs.104347	ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! [H.saplens]
60	125280 RC		Al123705	Hs.106932 Hs.41127	hypothelical protein FLJ13220
	132155 RC.		AK001607 AW978721	Hs.266076	ESTs, Weakly similar to A46010 X-linked retinopathy protein [H.sapiens]
	120609 RC 121278 RC	_AA2039UZ	AA037121	Hs.98518	Homo sapiens cDNA FLJ11490 fls, ctone HEMBA1001918
	109023 RC	AA467302	AA157293	Hs.72168	ESTs
65	129815 RC	D80208 £	BE565817	Hs.26498	hypothetical protein FLJ21657
05	108061 RC		AA043979	Hs.62651	EST
	113287 RC		T66847	Hs.194040	ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]
	114082 RC		AK001612	Hs.26962	Homo sapiens cDNA FLJ10750 fis, clone NT2RP3001929
	116334 RC	AA491457	AL038450	Hs.48948	ESTs
70	131486 RC	Z40071_s	F06972	Hs.27372	BMX non-receptor tyrosine kinase
	107860 RC		AA024961	Hs.50730	ESTs
	131263 RC		AU077002	Hs.24950	regulator of G-protein signalling 5
	132207 RC	_AA443294	BE206939	Hs.42287	E2F transcription factor 6
~~	129183 RC	_AA155743	BE561824	Hs.273369	uncharacterized hematopoietic stem/progenitor cells protein MDS027
75	408431 RC	_T23708	AI338631	Hs.43266	Homo sapiens cDNA: FLJ22536 fis, clone HRC13155
	120575 RC	_AA280934	AW978022	Hs.238911	hypothetical protein DKFZp762E1511; KIAA1816 protein

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myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to, 3
        132121 RC_AA443284_s NM_004529
                                            Hs.404
        117657 RC N39074
                               N39074
                                             He 44933
                                                          FSTs
        134922 RC W04507 s
                               AI718295
                                             Hs 91161
                                                          prefoldin 4
        118523 RC_R41828_s
                                                          myosin VA (heavy polypeptide 12, myoxin)
                               Y07759
                                             Hs.170157
                                AA649530
                                                          gb:ns44f05.s1 NCI_CGAP_Alv1 Homo saplens cDNA clone, mRNA sequence
        116845 RC_H64973
        115291 RC AA279943
                               BE545072
                                             Hs.122579
                                                          hypothetical protein FLJ10461
        120326 RC AA196300
                               AA196300
                                             Hs.21145
                                                          hypothetical protein RG083M05.2
                                                          protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform (calcineurin A beta)
        130174 M29550
                               M29551
                                             Hs.151531
        129131 RC_AA436489
                               AB026436
                                             Hs.177534
                                                          dual specificity phosphatase 10
10
        129868 RC AA287032
                               AW/172431
                                             Hs.13012
                                                          ESTs
        118661 RC N70777
                                AI 137554
                                             He 49927
                                                          protein kinase NYD-SP15
        129829 RC AA496921
                               AF010258
                                             Hs.127428
                                                          homeo hox A9
       115985 RC_AA447709 AA44770
134637 RC_AA369856_s U87309
                                                          ESTs. Weakly similar to T08599 probable transcription factor CA150 (H. sapiens)
                               AA447709
                                             Hs.268115
                                                          vacuolar protein sorting 41 (yeast homolog)
                                             Hs.180941
15
        132714 RC_AA252598
                               W/30388
                                             He 55336
                                                          Homo sapiens, cione MGC:17421, mRNA, complete cds
        129771 RC H73237
                                AL 096748
                                             Hs.102708
                                                          DKFZP434A043 protein
        123360 RC AA504784
                               AA532718
                                             Hs.178604
                                                          ESTs
                               AI936442
                                                          hypothetical protein FLJ10808
        132902 RC_AA490969
                                             Hs.59838
                                A A001356
        113716 RC_T97750
                                             He 18159
                                                          FSTs
20
        113825 RC W48860
                                AW014486
                                             Hs.22509
                                                          ESTs
                                                          hypothetical protein FLJ10849
        130367 RC_Z38501
                                AL135301
                                             Hs.8768
        120541 RC_AA278298
                               M/07318
                                             He 240
                                                          M-phase phosphoprotein 1
        116727 RC F13684
                               R76472
                                             He RERAR
                                                          ESTs
                                             Hs.48494
        118219 RC N62231
                               AA862391
                                                          ESTs. Moderately similar to A46010 X-linked retinopathy protein [H.saplens]
25
        119767 RC W72562
                                W72562
                                             Hs 58119
                                                          ESTs
                               AI365215
        128917 RC AA481252
                                             Hs 206097
                                                          oncogene TC21
        451553 RC_AA020928
                                AA018454
                                             Hs.269211
                                                          ESTs
        132716 RC_AA251288
                               BE379595
                                             He 283738
                                                          casein kinase 1, aloha 1
        118525 RC_N67861
                                N67861
                                             Hs 49390
                                                          FSTs
30
        114618 RC AA084162
                               AW979261
                                             Hs 291993
                                                          ESTs
                                AA947552
                                                          ESTs
        119743 RC_W70242
                                             Hs.58086
        108154 RC_AA425151_s NM_005754
                                             Hs.220689
                                                          Ras-GTPase-activating protein SH3-domain-binding protein
        122798 RC_AA460324 AW366286
                                             Hs 145696
                                                          solicing factor (CC1.3)
                                                          MAD (mothers against decapentaplegic, Drosophila) homolog 4
        133746 U44378
                                AW410035
                                             Hs.75862
35
        119822 RC_W74471
122186 RC_AA435842
                                AF086409
                                             Hs.301327
                                                          ESTs
                               AA398811
                                             Hs.104673
                                                          ESTs
                               AA236512
        114941 RC AA243017
                                             Hs 87331
                                                          FSTs
        118053 RC_N53367
                                N53391
                                             Hs.47629
                                                          ESTs
        123234 RC AA490227
                               NM 001938
                                                           down-regulator of transcription 1, TBP-binding (negative cofactor 2)
                                             Hs.16697
40
                                M63154
                                             He 110014
                                                          gastric intrinsic factor (vitamin B synthesis)
        129280 M63154
        118995 RC N94591
                                N94591
                                             He 323056
                                                          FSTs.
        116750 RC H05960
                                AA760689
                                             Hs.92418
                                                          ESTs
        129026 M98833
                                Al 120297
                                             Hs.108043
                                                           Friend laukemia virus integration 1
                                                          nudix (nucleoside diphosphate linked moiety X)-type motif 5
                                             Hs.301957
        105127 RC_AA158132
                               AA045648
45
        114513 RC AA044825
                                AA044873
                                             He 103448
                                                          FSTs.
        411856 RC T35697
                                H67899
                                             Hs.4190
                                                           Homo sapiens cDNA: FLJ23269 fls, clone COL09533
                                AL157433
                                             Hs.37706
                                                          hypothetical protein DKFZp434E2220
        132036 W01568
        130091 RC_W88999
                                W88999
                                                          gb:zh70h03.s1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone 3', mRNA
        sequence
        414108 U09564
50
                                Al267592
                                             Hs.75761
                                                           SFRS protein kinase 1
                                             Hs.58648
        119881 RC_W81456
                                W81486
                                                          ESTs
        117770 RC_N47953
                                                          ESTs. Weakly similar to 138022 hypothetical protein [H.sapiens]
                                AW957372
                                             Hs.46791
        119850 RC W80447
                                Al247568
                                             Hs.58452
                                                          ESTs, Highly similar to AF161437 1 HSPC319 [H.sapiens]
        115439 RC_AA284561
                                AI567972
                                             Hs.193090
55
        123107 RC_AA486071
                                AA225048
                                             Hs.104207
                                                          FSTs
                                                           major histocompatibility complex, class II, DQ beta 1
        406698 M24364
                                X03068
                                             Hs.73931
         121231 RC AA400780
                                AA814948
                                             Hs.96343
                                                          ESTs, Weakly similar to ALUC_HUMAN !!!! ALU CLASS C WARNING ENTRY !!! [H.sapiens]
         132074 AB002366
                                AA478486
                                             Hs.3852
                                                          KIAA0368 nmtein
                                AB000115
                                             Hs.75470
                                                           hypothetical protein, expressed in osteoblast
        413670 AB000115
60
        125277 RC_W93227
                                W93227
                                             Hs.103245
                                                          EST
        114056 RC AA186324
                              AA188175
                                             He 82506
                                                           KIAA1254 protein
         121153 RC_AA399640
                                AA399640
                                             Hs 97694
                                                          FSTs
        121609 RC_AA416867
                                A A 416863
                                             Hs.98185
                                                           EST
        120661 RC_AA287556
                                AA287556
                                             Hs.263412
                                                           ESTs. Weakly similar to ALUB HUMAN !!!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]
65
                                AA349647
        120850 RC_AA349647
                                             Hs.96927
                                                           Homo saplens cDNA FLJ12573 fis, clone NT2RM4000979
         124947 RC_T03170
                                T03170
                                             Hs 100165
                                                           gb:zp39e03.s1 Stratagene muscle 937209 Homo sapiens cDNA clone 3' similar to contains Alu
                                AA178953
        130529 RC_AA280886
        repetitive element; mRNA sequence
        117683 RC N40180
                                N40180
                                                           gb:yy44d02.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA clone
70
        IMAGE:276387 3' similar to contains L1.11 L1 repetitive element; mRNA sequence.
                                                           gb:EST10426 Adipose tissue, white I Homo sapiens cDNA 3' end, mRNA sequence.
         120745 RC AA302809 AA302809
        120936 RC_AA385934
                                AA385934
                                              Hs.97184
                                                           EST, Highly similar to (define not available 7499603) [C.elegans]
        112597 RC_R78376
                                R78376
                                              Hs.29733
                                                          EST
         120183 RC Z40174
                                AW082866
                                             Hs 65882
                                                           FSTs
75
         120644 RC_AA287038
                                Al869129
                                              Hs.96616
                                                          ESTs
```

	119023 RC_N98488	N98488		gb:zb82h01.s1 Soares_senescent_fibroblasts_NbHSF Homo sapiens cDNA clone
	IMAGE:310129 3', mRNA			
	107582 RC_AA002147	AA002147	Hs.59952	EST
5	118249 RC_N62580 115022 RC AA252029	N62580 AA252029	Hs.322925 Hs.87935	EST, Weakly similar to putative p150 [H.saplens] ESTs
,	117710 RC_N45198	N45198	Hs.47248	ESTs, Highly similar to similar to Cdc14B1 phosphatase [H.sapiens]
	115341 RC_AA281452	AA281452	Hs.88840	EST, Weakly similar to granule cell marker protein [M.musculus]
	118896 RC_N90680	N46213	Hs.54642	methionine adenosyltransferase II, beta
10	121121 RC_AA399371	AA399371 N63520	Hs.189095	similar to SALL1 (sal (Drosophila)-like qb:yy62f01.s1 Soares_multiple_solerosis_2NbHMSP Homo sapiens cDNA clone IMAGE:278137
10	118329 RC_N63520 3', mRNA sequence.	N03320		gu.yyozu i.si adales_iidiipie_suleiosis_zitoi iiilar Tiolilo sapialis coltit violie iiilitec
	119496 RC W35416	W35416	Hs.156861	ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]
	118111 RC_N55493	N55493		gb:yv50c02.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:246146 3',
15	mRNA sequence. 119062 RC R16698	AW444881	Hs.77829	ESTs
15	116710 RC F10577_f	F10577	Hs.306068	v-crk avian sarcoma virus CT10 oncogene homolog
	119261 RC_T15956	T15956	Hs.65289	EST
	122723 RC_AA457380	AA457380		gb:aa86b10.s1 Stratagene fetal retina 937202 Homo sapiens cDNA clone IMAGE:638171 31
20	similar to contains L1.b3 L 117732 RC_N46452	1 repetitive eler N46452	nent;, mRNA si	equence. gb:yy76h09.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA done
40	IMAGE:279521 3' similar b	o contains L1.t2	L1 repetitive el	
	104787 RC_AA027317	AA027317		gb:ze97d11.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:366933 3
	similar to contains Alu repe		mRNA sequen	
2.5	100071 A28102 115819 RC_AA426573	A28102 AA486620	Hs.41135	Human GABAa receptor alpha-3 subunit endomucin-2
23	130882 RC_Z40166_f	AA497044	Hs.20887	hypothetical protein FLJ10392
	125225 RC_W76540	W74169	Hs.16492	DKFZP564G2022 protein
	108339 RC_AA070801	AW151340	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION
30	WARNING ENTRY [H.sap 100338 D63483	nensj D86864	Hs.57735	acelyl LDL receptor; SREC
50	121638 RC_AA417027	AA379203	Hs.306654	Homo sapiens cDNA FLJ13574 fis, clone PLACE1008625
	103875 RC_AA418387	T26379	Hs.48802	Homo sapiens clone 23632 mRNA sequence
	118716 RC_N73460	Al658908	Hs.118722	fucosyltransferase 8 (alpha (1,6) fucosyltransferase)
35	119763 RC_W72450 121917 RC_AA428218	R54146 AA406397	Hs.10450 Hs.98038	Homo sapiens cDNA: FLJ22063 fis, clone HEP10326 ESTs
55	132806 M91488	AI699432	Hs.278619	hypothetical protein FLJ10099
	130949 Y10659	AV656840	Hs.285115	interleukin 13 receptor, alpha 1
	108806 RC_AA129933 133276 RC_AA490478	AF070578 AW978439	Hs.71168 Hs.69504	Homo sapiens clone 24674 mRNA sequence ESTs
40	134760 RC_H16758	NM_000121	Hs.89548	erythropoletin receptor
	132887 AA121287	AF226667	Hs.58553	CTP synthase II
	132051 AA091284	AA393968	Hs.180145	HSPC030 protein
	114208 RC_Z39301 104094 AA418187	AL049466 AA418187	Hs.7859 Hs.330515	ESTs ESTs
45	128718 AA426361	NM_002959	Hs.281706	sortiin 1
	302032 RC_N20407	NM_001992	Hs.128087	coagulation factor il (thrombin) receptor
	115501 RC_AA291553	AA291553 AU076536	Hs.190086 Hs.50984	ESTs sarcoma amplified sequence
	101997 U01160 103708 AA037206	AA430591	Hs.72071	hypothetical protein FLJ/20038
50	101899 S59184	859184	Hs.79350	RYK receptor-like tyrosine kinase
	115839 RC_AA429038	BE300266	Hs.28935	transducin-like enhancer of split 1, homolog of Drosophila E(sp1)
	409459 D50678 103563 Z22534	D86407 L02911	Hs.54481 Hs.150402	low density lipoprotein receptor-related protein 8, apolipoprotein e receptor Activin A receptor, type I (ACVR1) (ALK-2)
	123233 RC_AA490225	AW974175	Hs.188751	ESTs, Weakly similar to MAPB_HUMAN MICROTUBULE-ASSOCIATED PROTEIN 1B
55	[H.saplens]			
	121305 RC_AA402468	AA402468	Hs.291557 Hs.54900	ESTs
	114798 RC_AA159181 133145 RC_AA196549	AA159181 H94227	Hs.6592	serologically defined colon cancer antigen 1 Homo sapiens, done IMAGE:2961368, mRNA, partial cds
	131567 RC_AA291015_s		Hs.28853	CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1
60	112300 RC_R54554	H24334	Hs.26125	ESTs
	129507 RC_AA192099	AJ236885 AA398505	Hs.112180 Hs.97360	zinc finger profein 148 (pHZ-52) ESTs
	121033 RC_AA398505 121151 RC_AA399636	AA399636	Hs.143629	ESTs
	121402 RC_AA406063	AA406063	Hs.98003	ESTs
65	123203 RC_AA489671	AA352335	Hs.65641	hypothetical protein FLJ20073
	132271 RC_AA236466	AE030034 AF086270	Hs.115175 Hs.278554	sterile-alpha motif and leucine zipper containing kinase AZK heterochromatin-like protein 1
	125197 RC_W69106 114935 RC_AA242809	H23329	Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION
	WARNING ENTRY [H.sag	olens]		
70	125279 RC_W93640	AW401809	Hs.4779	KIAA1150 protein
	108778 RC_AA128548 108087 RC_AA045709	AF133123 AA045708	Hs.40545	general transcription factor IIIC, polypeptide 3 (102kD) ESTs
	132466 RC_N66810_s	A1597655	Hs.49265	ESTs
	133328 R36553	AW452738	Hs.265327	hypothetical protein DKFZp7611141
75	124057 RC_F13604	AA902384 AW864086	Hs.73853 Hs.138617	bone morphogenetic protein 2 thyroid hormone receptor interactor 12
	124800 RC_R45115	VANODANGO	110,10001/	myrora normono receptor instructor in

	121029 RC_AA398482	AA398482	Hs.97641	EST
	120663 RC_AA287627	AA827798	Hs.105089	ESTs
	102133 U15173	AU076845 AI423132	Hs.155596 Hs.146343	BCL2/adenovirus E1B 19kD-interacting protein 2 ESTs
5	108246 RC_AA062855 125226 RC_W78134	AA782536	Hs.122647	N-myristoyltransferase 2
,	120260 RC_AA171739	AK000061	Hs.101590	hypothetical protein
	124906 RC_R87647	H75964	Hs.107815	ESTs
	109406 RC_AA226877	AA199883	Hs.67624	ESTs
10	109271 RC_AA195668	AW137422	Hs.86022	ESTs
10	125052 RC_T80174_s	T85104 AW608930	Hs.222779 Hs.52184	ESTs, Moderately similar to similar to NEDD-4 [H.saplens] hypothetical protein FLJ20618
	109101 RC_AA167708 115241 RC_AA278723	AA648278	Hs.193859	ESTs
	117163 RC_H97909	N36861	Hs.42344	EST8
	113530 RC_T90313	T90313	Hs.16732	ESTs
15	120375 RC_AA227260	AF028706	Hs.111227	Zic family member 3 (odd-paired Drosophila homolog, heterotaxy 1)
	129435 AA314256	AF151852	Hs.111449	CGI-94 protein
	114864 RC_AA235256 103988 AA314389	AA135332 AA314389	Hs.71608 Hs.42500	ESTs ADP-ribosylation factor-like 5
	131006 RC_AA242763	AF064104	Hs.22116	CDC14 (cell division cycle 14, S. cerevisiae) homolog B
20	106781 RC_AA478474	AA330310	Hs.24181	ESTs
	106141 RC_AA424558	AF031463	Hs.9302	phosducin-like
	116213 RC_AA476738	AA292105	Hs.326740	hypothetical protein MGC10947
	135266 AB002326	R41179	Hs.97393	KIAA0328 protein
25	135058 RC_AA430152 119908 RC_W85844	Al379720 AA524470	Hs.93814 Hs.58753	hypothetical protein ESTs
23	103695 AA018758	AW207152	Hs.186600	ESTs
	103978 AA307443	NM_016940	Hs.34136	chromosome 21 open reading frame 6
	109485 RC_AA233472	BE619092	Hs.28465	Homo sapiens cDNA: FLJ21869 fis, clone HEP02442
	129574 AA458603	AA026815	Hs.11463	UMP-CMP kinase
30	115347 RC_AA261528	AA356792	Hs.334824 Hs.96752	hypothetical protein FLJ14825 ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION
	120765 RC_AA338735 WARNING ENTRY [H.sar	AW961026	ns.90/52	ES15, Heavy silling to Accomplished Social Affiliation Concentration of the
	121059 RC_AA398628	AA393283		gb:zt74e03.r1 Soares_testis_NHT Homo sapiens cDNA clone 5', mRNA sequence
	131887 AA046548	W17064	Hs.332848	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e,
35	member 1			
	112064 RC_R43812	AL049390	Hs.22689	Homo sapiens mRNA; cDNA DKFZp586O1318 (from clone DKFZp586O1318)
	115606 RC_AA400465	Al025829 NM_004349	Hs.86320 Hs.31551	ESTs core-binding factor, runt domain, alpha subunit 2; translocated to, 1; cyclin D-related
	131750 RC_H94855_s 102123 U14518	NM_001809	Hs.1594	centromere protein A (17kD)
40	129847 RC_W46767	N64025	Hs.296178	hypothetical protein FLJ22637
	133809 RC_AA235275	AV649326	Hs.76359	catalase
	132210 RC_N51499_s	NM_007203	Hs.42322	A kinase (PRKA) anchor protein 2
	122356 RC_AA443794	AA443794 N20912	Hs.98390 Hs.42369	ESTs FSTs
45	114958 RC_AA243708 103951 AA287840	N20912 AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (from clone DKFZp761J1112)
45	134703 RC_AA280704	AF117065	Hs.88764	male-specific lethal-3 (Drosophila)-like 1
	128727 AA287864	Al223335	Hs.50651	Janus kinase 1 (a protein tyrosine kinase)
	105743 RC_AA293300_	s BE246502	Hs.9598	sema domain, immunoglobulin domain (lg), transmembrane domain (TM) and short cytoplasmic
50	domain, (semaphorin) 4B	11000000		gb:zm97e10.s1 Strategene colon HT29 (937221) Homo sapiens cDNA clone 3', mRNA
50	103744 AA076003 sequence	AA079267		go.ziig/e io.si olialoguiu color 11125 (55/221) 10110 Salponi Genti Gone o 11111011
	114348 N80402	AL050321	Hs.301532	CRP2 binding protein
	114009 RC_W90087	AI248544	Hs.103000	KIAA0831 protein
	134704 RC_AA280849	AA837124	Hs.88780	ESTs
55	128629 AA399187	AL096748	Hs.102708 Hs.104520	DKFZP434A043 protein Homo sapiens cDNA FLJ13694 fis, clone PLACE2000115
	104410 H65925 110200 RC_H21075	Al807519 H21075	Hs.31802	ESTs, Highly similar to A59266 unconventional myosin-15 [H.sapiens]
	124483 RC N53976	Al821780	Hs.179864	ESTs
	101391 M14648	NM_002210	Hs.295726	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51)
60	109657 RC_F04826	R60900	Hs.26814	ESTs
	117140 RC_H96813	H96813	Hs.42241	ESTs
	132937 RC_AA233706_	AW952912 AW967473	Hs.300383 Hs.239114	hypothetical protein MGC3032 mannosidase, alpha, class 1A, member 2
	129799 R36410 105077 RC_AA142919	W55946	Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HEMEB1002492
65	100850 RC_N58561_s	AA836472	Hs.297939	cathepsin B
	131043 RC_AA490925	AF084535	Hs.22464	epilepsy, progressive myoclonus type 2, Lafora disease (laforin)
	118417 RC_N66048_f	AF080229		gb:Human endogenous retrovirus K clone 10.1 polymerase mRNA, partial cds
	129254 RC_AA243695	AA252468	Hs.1098 Hs.65732	DKFZp434J1813 protein ESTs
70	119149 RC_R58910 133996 AA091367	BE304701 AA380267	Hs.78277	DKFZP434F2021 protein
70	133990 AAU91307 110223 RC_H23747	H19836	Hs.31697	ESTs
	117626 RC_N36090	AK001757	Hs.281348	hypothetical protein FLJ10895
	135286 RC_AA424469_	s AW023482	Hs.97849	ESTs
75	122967 RC_AA478521	AA806187	Hs.289101	glucose regulated protein, 58kD ubiquitination factor E4B (homologous to yeast UFD2)
75	131236 AA282640	AF043117 H12912	Hs.24594 Hs.274691	adenylate kinase 3
	128568 AA463380	1112312	113.214051	OCCUPANO MINOCO

	112888 RC T03872	AW195317	Hs.107716	hypothetical protein FLJ22344
	115192 RC_AA261920	AA741024	Hs.88378	ESTs
	118688 RC_N71484	AK000708	Hs.169764	hypothetical protein FLJ20701
-	122264 RC_AA436837	AA436837		gb:zv57g07.s1 Soares_testis_NHT Horno sapiens cDNA clone 3', mRNA sequence
5_	128981 AA135452 131042 RC_R42457	AA927177 AI826288	Hs.86041 Hs.171637	CGG triplet repeat binding protein 1 hypothetical protein MGC2628
	103704 AA028171	AA028171	Hs.151258	hypothetical protein FLJ21062
	121341 AA233107	AF035528	Hs.153863	MAD (mothers against decapentaplegic, Drosophila) homolog 6
	106593 RC AA456826	AW296451	Hs.24605	ESTs
10	115195 RC_AA262156	AW968619	Hs.155849	ESTs
	115425 RC_AA284071	AA811895 AF086041	Hs.180680 Hs.42975	ESTs, Weakly similar to 154374 gene NF2 protein [H.sapiens] ESTs
	117258 RC_N21299 120209 RC Z40892	F02951	HSAZ273	gb:HSC1HB032 normalized infant brain cDNA Homo sapiens cDNA clone c-1hb08 3', mRNA
	sequence	, 0220		
15	134082 L16991	L16991	Hs.79006	deoxythymidylate kinase (thymidylate kinase)
	104774 RC_AA026066	AW959755	Hs.288896	Homo saptens cDNA FLJ12977 fis, clone NT2RP2006261
	115625 RC_AA401630 104469 N28707	AA059459 N28707	Hs.62592 Hs.154304	ESTs Homo sapiens chromosome 19, BAC 282485 (CIT-B-344H19)
	107409 N28707 107401 W20054	N91453	Hs.102987	ESTs
20	111686 RC_R21510	R22039	Hs.23217	ESTS
	115300 RC_AA280026	AA280095	Hs.88689	ESTs
	115378 RC_AA282292	AA282292	Hs.279841	hypothetical protein FLJ10335
	132224 RC_H97819 113791 M95767	N41549 Al269096	Hs.285410 Hs.135578	ESTs chitobiase, di-N-acetyl-
25	129144 AA004987	AL137275	Hs.20137	hypothetical protein DKFZp434P0116
	104448 L44574	NM_007331	Hs.110457	Wolf-Hirschhom syndrome candidate 1
	132084 RC_T26981_s	NM_002267	Hs.3886	karyopherin alpha 3 (importin alpha 4)
	111831 RC_R36083	R36095	Hs.268695	ESTs
30	114765 RC_AA252163	AA463550	Hs.337532 Hs.40096	ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.saplens] ESTs
30	115029 RC_AA252219 100457 H81492	AL137939 BE246400	Hs.285176	acelyl-Coenzyme A transporter
	104536 R24011	R24024	Hs.158101	Homo sapiens cDNA FLJ14673 fis, done NT2RP2003714, moderately similar to ZINC FINGER
	PROTEIN 91			
25	116167 RC_AA461562	AI091731	Hs.87293	hypothetical protein FLJ20045
35	103889 AA236771 131978 RC_H48459_s	R85350 AA355925	Hs.101368 Hs.36232	ESTs KIA40186 gene product
	118843 RC_N80181	N80181	Hs.221498	ESTS
	120837 RC W93092	BE149656	Hs.306621	Homo sapiens cDNA FLJ11963 fls, done HEMBB1001051
	133647 D21852	NM_015361	Hs.268053	KIAA0029 protein
40	129521 U41815	AF071076	Hs.112255	nucleoporin 98kD qb:zm63c07.s1 Stratagene ovarian cancer (937219) Homo sapiens cDNA done 3', mRNA
	103746 AA081876 sequence	AA075000		gozmosov/.st Stratagene ovarian cancer (95/2 ta) notice sapietas contra come 5, minera
	132019 RC_AA134965_I	H56995	Hs.37372	Homo saplens DNA binding peptide mRNA, partial cds
	132310 RC_AA284107	AA173223	Hs.289044	Homo sapiens dDNA FLJ12048 fis, clone HEMBB1001990
45	117367 RC_N24954	AI041793	Hs.42502	ESTs
	103743 AA075998 gb:M15887 ACYL-COA-BI	AA075998		gb:zm89b09.r1 Stratagene ovarian cancer (937219) Homo saplens cDNA clone 5' similar to
	103761 AA085138	AA765163	an (nomen),,	gbmz79b10.s1 NCL_CGAP_GCB1 Homo sapiens dDNA clone 3' similar to gb:M34539 FK506-
	BINDING PROTEIN (HUM		aquence	
50	130237 L39060	AA913909	Hs.153088	TATA box binding protein (TBP)-associated factor, RNA polymerase I, A, 48kD
	128752 RC_N72879	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA, partial cds
	135162 AA045930 131386 AA096412	AJ187925 BE219898	Hs.95667 Hs.173135	F-box protein 30 dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2
	129021 RC AA599244	AL044675	Hs.173081	KIAA0530 protein
55	424274 AA293634	W73933	Hs.283738	casein kinase 1, alpha 1
	129913 H06583	NM_001310	Hs.13313	cAMP responsive element binding protein-like 2
	131888 U79298	AW294659	Hs.34054	Homo sapiens cDNA: FLJ22488 fis, clone HRC10948, highly similar to HSU79298 Human clone
	23803 mRNA 118612 RC_N69466	AB037788	Hs.224961	cleavage and polyadenylation specific factor 2, 100kD subunit
60	322026 AA203138	AW024973	Hs.283675	NPD009 protein
00	110892 RC_N38882	AL035301	Hs.97375	H.sapiens gene from PAC 106H8
	111429 RC_R01245	AI038052	Hs.19162	ESTs, Weakly similar to 154374 gene NF2 protein [H.sapiens]
	113334 RC_T76962	AW974666	Hs.293024	ESTs
65	104091 AA417310 105246 RC_AA226879	BE465093 AA226879	Hs.106101	hypothetical protein FLJ22557 gb:zr19c09.s1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone
05	IMAGE:663856 3' similar t		repetitive eleme	nt. mRNA sequence.
	113300 RC_T67448	T67448	Hs.13101	ESTs
	117147 RC_H97225_s	AW901347	Hs.38592	hypothetical protein FLJ23342
70	121349 RC_AA405205	AA405205	Hs.97960	ESTs, Weakly similar to T51146 ring-box protein 1 [H.sapiens] peroxiredoxin 3
70	100294 D49396 133999 M28213	AA331881 AA535244	Hs.75454 Hs.78305	RAB2, member RAS oncogene family
	133259 AA278548	BE379646	Hs.6904	Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 2004403
	129423 AA371418	AA204686	Hs.234149	hypothetical protein FLJ20647
	131098 RC_AA459668	U66669	Hs.236642	3-hydroxyisobutyryl-Coenzyme A hydrolase
75	135272 AA399391 129155 AA046865	AI828337 AI952677	Hs.97591 Hs.108972	ESTs Homo sapiens mRNA; cDNA DKFZp434P228 (from clone DKFZp434P228)

	311291 AA056319	AA782601	Hs.319817	ESTs
	120750 RC_AA310499	AI191410	Hs.96693	ESTs, Moderately similar to 2109260A B cell growth factor [H.sapiens]
	101002 J04058	AV655843	Hs.169919	electron-transfer-flavoprotein, alpha polypeptide (glutaric aciduria II)
	133012 AA099241	AA847843	Hs.62711	Homo sapiens, clone IMAGE:3351295, mRNA
5	103879 AA228148_s	BE543269	Hs.50252	mitochondrial ribosomal protein L32
	131281 RC_AA443212	AA251716	Hs.25227	ESTs
	115109 RC_AA256383	AJ249977	Hs.88049	protein kinase, AMP-activated, gamma 3 non-catalytic subunit
	118502 RC_N67317	AL157488	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (from clone DKFZp564B182)
10	134100 L07540	AA460085	Hs.171075	replication factor C (activator 1) 5 (36.5kD)
10	131869 AA484944	AW968547 AA810854	Hs.33540 Hs.89081	ESTs, Weakly similar to dJ309K20.4 [H.sapiens] ESTs
	115396 RC_AA282985 103860 AA203742	AW976877	Hs.38057	ESTs
	135089 N75611_s	AI918035	Hs.301198	roundabout (axon quidance receptor, Drosophila) homolog 1
	129938 U79300	AW003668	Hs.135587	Human clone 23629 mRNA sequence
15	107508 W90095	N74925	Hs.38761	Homo sapiens cDNA: FLJ21564 ffs, clone COL06452
	103685 AA005190	AA158008	Hs.292444	ESTs
	125170 AA203147	AL020996	Hs.8518	selenoprotein N
	129179 RC_AA504125	s AW969025	Hs.109154	ESTs
20	116262 AA477046	A1936442	Hs.59838 Hs.78305	hypothetical protein FLJ10808 RAB2, member RAS oncogene family
20	123009 RC_AA479949 131004 D29833	AA535244 D29833	Hs.2207	salivary proline-rich protein
	103317 X83441	X83441	Hs.166091	ligase IV, DNA, ATP-dependent
	132814 RC_C15251_f	D60730	Hs.57471	ESTs
	103992 U77718	BE018142	Hs.300954	Huntingtin interacting protein K
25	109258 X59710	AL044818	Hs.84928	nuclear transcription factor Y, beta
	110754 RC_N20814	AW302200	Hs.6336	KIAA0672 gene product
	132727 AA136382_s	N27495	Hs.5565	hypothetical protein FLJ22626
	100341 D63506	AF032922	Hs.8813	syntaxin binding protein 3
30	134664 AA256106 103826 AA165564	AA256106 AW162998	Hs.87507 Hs.24684	ESTs KIAA1376 protein
30	111678 RC_R20628	R38487	Hs.169927	ESTs
	101341 L76159	NM_004477	Hs.203772	FSHD region gene 1
	115455 RC_AA285068		Hs.120551	toll-like receptor 10
	111192 RC_AA477748	AW021968	Hs.109438	Homo sapiens clone 24775 mRNA sequence
35	129385 RC_AA235604	AA172106	Hs.110950	Rag C protein
	125050 RC_T79951	AW970209	Hs.111805	ESTs
	122105 RC_AA432278		Hs.98699 Hs.97842	ESTs EST
	121324 RC_AA404229 120938 RC_AA386260	AA404229 AA386260	Hs.104632	EST
40	115001 RC_AA350260		110.104032	gb:zs10a06.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:684754 3', mRNA
40	seguence.	704201070		
	124799 RC_R45088	R45088		gb:yg38g04.s1 Soares infant brain 1NIB Homo saplens cDNA clone IMAGE:34896 3', mRNA
	sequence.			
45	122724 RC_AA457395	AA457395	Hs.99457	ESTs
45	117791 RC_N48325 121895 RC_AA427396	N48325 AA427396	Hs.93956	gb:zw33a02.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone IMAGE:771050 3'
	similar to contains Alu re		contains MED 15	
	108244 RC_AA062839		CONTRACTO MALLY 12	gb:zm05c09.s1 Stratagene corneal stroma (937222) Homo sapiens cDNA clone IMAGE:513232
	3', mRNA sequence.			, , ,
50	117852 RC_N49408	AW877787	Hs.136102	KIAA0853 protein
	109298 RC_AA205432	R77854	Hs.250693	Krueppet-related zinc finger protein
	122432 RC_AA447400	AA447400	Hs.187684	ESTs, Weakly similar to B34087 hypothetical protein [H.sapiens]
	124627 RC_N74625	N74625	DELET DECETTI	gb:za55c03.s1 Soares fetal liver spicen 1NFLS Homo sapiens cDNA clone IMAGE:296452 3'
55	similar to gb:M14338 VI 115141 RC_AA258071		Hs.64001	NS PRECURSOR (HUMAN); contains OFR.b3 OFR repetitive element; mRNA sequence. Homo saplens clone 25218 mRNA sequence
33	128636 U49065	U49065	Hs.102865	interleukin 1 receptor-like 2
	115373 RC_AA282197		Hs.181022	CGI-07 protein
	114651 RC_AA101400	AA101400	Hs.189960	ESTs
	132796 RC_AA180487	NM_006283	Hs.173159	transforming, acidic colled-coil containing protein 1
60	103749 RC_N35583	AL135301	Hs.8768	hypothetical protein FLJ10849
	107328 T83444	AW959891	Hs.76591	KIAA0887 protein
	115349 RC_AA281563 111490 RC_R06862	AF121176 R06862	Hs.12797	DEAD/H (Asp-Glu-Ala-Asp/His) box potypeptide 16 gb:yf11e09.s1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE:126568 3°
	similar to contains L1 re		mPNA somion	
65	103763 AA085354	AA085291	, mi des ocquen	gb::zn01g06.s1 Stratagene colon HT29 (937221) Homo sapiens cDNA clone 3' similar to
0.0	contains Alu repetitive e		ecuence	, , ,
	118791 RC_N75520	N75520	Hs.261003	ESTs, Moderately similar to B34087 hypothetical protein [H.saplens]
	116644 RC_F03032	F03032	Hs.290278	ESTs, Weakly similar to B34087 hypothetical protein (H.sapiens)
	116823 RC_H56485	AW204742	Hs.143542	ESTS, Highly similar to CSA_HUMAN COCKAYNE SYNDROME WD-REPEAT PROTEIN CSA
70	[H.sapiens]	********		abiza00c04 of Circles are paymonthalium NT2DAN/ 02723/ Homo egginne aCNI/ along
	108940 RC_AA148603 IMAGE:5671983', mRN			gb:zo09e04.s1 Stratagene neuroepithelium NT2RAMI 937234 Homo sapiens cDNA clone
	112218 RC_R50057	A sequence. R50057	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (from clone DKFZp586M1418)
	116557 RC_D20572_i	D20572	Hs.90171	EST
75	133649 U25849	U25849	Hs.75393	acid phosphatase 1, soluble
	131745 RC_C20746	A1828559	Hs.31447	ESTs, Moderately similar to A46010 X-linked retinopathy protein [H.sapiens]

		RC_H43879	H43879		gb:yo69h09.s1 Sources breast 3NbHBst Homo sapiens cDNA clone IMAGE:183233 3', mRNA
	sequence			II. omnon	FOT
		RC_AA251548	AA251548 H29882	Hs.87886 Hs.162614	EST ESTs
5		RC_AA598500			
)		RC_AA347919 AA018298	AA347919 AA018298	Hs.96889 Hs.103332	EST ESTs
			AF025771	Hs.50123	zinc finger protein 189
		RC_AA412491 RC_N67946	N67946	Hs.117569	ESTs
		RC_AA058946	AB020700	Hs.3830	KIAA0693 protein
10			AA194568	Hs.85938	EST EST
10		RC AA252794	AA252794	Hs.88009	ESTs
	420208		BE276055	Hs.95972	silver (mouse homolog) ike
			R66740	Hs.110613	KIAA0220 protein
	128546		NM 003478	Hs.101299	culin 5
15		RC_R40697	R40697	Hs.78666	C9orf10 protein
10		RC_R73588	R73588	Hs.101533	ESTs
		AA410345	AF255910	Hs.54650	junctional adhesion molecule 2
		AA018418	AW137912	Hs.227583	Homo sapiens chromosome X map Xp11,23 L-type calcium channel alpha-1 subunit
	(CACNA	1F) gene, complet	e cds: HSP27 p	seudogene, cor	mplete sequence; and JM1 protein, JM2 protein, and Hb2E genes, complete cds
20		AA089688	BE244667	Hs.296155	CGI-100 protein
	125266	W90022	W90022	Hs.186809	ESTs, Highly similar to LCT2 HUMAN LEUKOCYTE CELL-DERIVED CHEMOTAXIN 2
		RSOR [H.sapiens]			
	135235	AA435512	AW298244	Hs.293507	ESTs
	134497	RC_AA404494	BE258532	Hs.251871	CTP synthase
25	426754	RC_AA278529_i	NM_014264	Hs.172052	serine/threonine kinase 18
	412177	RC_AA342828_s		Hs.73734	glycoprotein V (platelet)
		RC_AA044644	AW247017	Hs.36978	melanoma antigen, family A, 3
		RC_AA044644	T07568	Hs.137158	ESTs
		RC_AA196729_I		Hs.190213	ESTs
30		RC_AA196729_i		Hs.334825	Homo sapiens cDNA FLJ14752 fis, clone NT2RP3003071
		RC_AA025858	AW247017	Hs.36978	melanoma antigen, family A, 3
		RC_AA025858	N75346	Hs.82906	CDC20 (cell division cycle 20, S. cerevisiae, homolog)
		RC_AA233519	Al949109	Hs.246885	hypothetical protein FLJ20783
35		RC_N52271	D31139	Hs.154103	LIM protein (similar to rat protein kinase C-binding enigma)
22		RC_N88399	NM_003528	Hs.2178 Hs.16621	H2B histone family, member Q
		RC_AA098874 RC_AA279667_s	AB037850	Hs.297939	DKFZP4341116 protein cathepsin B
		RC_H22556	W27893	Hs.150580	putative translation initiation factor
		RC_N45979_s	BE296690	Hs.288173	Homo sapiens cDNA: FLJ21747 fis, clone COLF5160, highly similar to AF182198 Homo sapiens
40		in 2 long isoform (I		118.200173	Troito sapietis cores. I Caz 1747 ilis, cione coca 3100, tilginy sittilica ilo Ai 102 100 110110 sapietis
70		RC_AA431288_s		Hs.95327	CD3D antigen, delta polypeptide (TiT3 complex)
		RC AA809862	BE280456	Hs.80248	RNA-binding protein gene with multiple splicing
		RC_N35583	AW994032	Hs.8768	hypothetical protein FLJ10849
	124541		AF112222	Hs.44499	pinin, desmosome associated protein
45		AA203147	AL020996	Hs.8518	selencorotein N
		RC_W93092	AW175787	Hs.334841	selenium binding protein 1
		RC_W93092	AW516428	Hs.78687	neutral sphingomyelinase (N-SMase) activation associated factor
		RC_N58561_s	L04268	Hs.297939	cathepsin B
		RC_W93092	AW516428	Hs.78687	neutral sphingomyelinase (N-SMase) activation associated factor
50		RC_W69385_s	BE543412	Hs.250505	retinoic acid receptor, alpha
	332489	RC_R22947	R23053	NA	Hu01 Chip Redos
		RC_N38959_f	AL042444	Hs.62402	p21/Cdc42/Rac1-activated kinase 1 (yeast Ste20-related)
		RC_N38959_f	A1678638	Hs.6456	chaperonin containing TCP1, subunit 2 (beta)
		RC_H73050_s	AA744902	Hs.107767	hypothetical protein PRO1489
55	100920	RC_H73050_s	X54534	Hs.278994	Rhesus blood group, CcEe antigens

TABLE 1A

Table 1A shows the accession numbers for those plays lacking unigeneID's for Tables 1. The plays in Table 7 lacking unigeneID's are represented within Tables 1-AR. For each probaset we have itself the gene cluster number from which the dignounceotides were designed. Gene clusters were compiled using sequences derined from enterthin ESTs and mRNNs. These sequences were cubstered based to sequence similarly using Clustering and Alignment Tools (DoubleTwist, Cakland California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	CAT number: Gen	us Eos probeset Identifier number a clusier number Benk accession numbers
15	Pkey CAT Number	Accession
20	108469 116761_1 124106 125446_1 108501 1368412 108562 36375_1	ALOTISEST AA 12854T AA 12852F AAOTISESS AAOTISESS HI 12245 AAOG4758 H 14576 AAOSISES AAJOOTISE A POECOSS AAOTISES AAOTISES AAOTISESS AAOSISSAT AA 128309 AAOTISESS AAOSISEZTA
	125008 1802095_1 125020 116017_1 125066 1814993_1 116661 1532859_1	T91251 T64891 T66965 T64991 T66965 T69981 T69324 AUG/PAF6 T86924 T81933 Ref6104 F04247
25	125104 413347_1 124575 1666649_1 125263 1547_2 116845 393481_1	T95599 AA703278 H82794 NS6169 N916198 N90450 AA088378 W89842 AA686500 A4665318 H84673
30	118417 37186_1	AFRIGUZZA AFRIBUZZA FARBUZZA AFRIBUZZA AFRIBUZ
35	118584 532052_1 103743 112194_1 103744 114161_1 103746 113452_1	AAA4836A AM83192 AM83565 BEZ18384 BE46978 N88983 AA975338 BE141159 N76377 AA073686 AA073696 AA070696 AA070696 AA070694 AA070842 AA070783 AA078941 AA07367A AA07600 AA07367A AA07600
40	103761 114208_1 103763 48290_6 120209 1531817_1 120284 158963_1 112540 1605263_1	A-AT-6163 AVX26222 A-A126126 A-A085138 A-A076088 A-A085221 A-A085354 F02951 240822 F0471 A-A173626 AV162606 AV162607 A-A173626 AV162607 H000279 H00078
45	111904 1719336_1 121059 273450_1 121094 275729_1 14106 1182096_1 130091 239613	241572 R98330 A4836235 A439663 A4436255 A398900 AM050228 RE073899 238412 W88899
50	122264 296527_1 108280 110682_1 129961 1706092_1 130529 158447_1 108309 111495_1	AA43633T AA442594 AA06069 AA06500 RC2035 R79884 R78271 AA176623 AA162740 AA06899 BAA068971 AA06892 AA069608
55	107832 genbank_AA0 123731 genbank_AA0 116571 genbank_D46 132225 genbank_AA 125017 genbank_T68	224473 AA021473 60839 AA069839 6562 DI46662 AA128800 AA128800 AA1288075
60	125063 genbank_T85 125064 genbank_T85 100964 entrez_J0021 125118 149288_1 102269 entrez_U3024	3373 T85373 12 J00212 R10606 197620 AA576309
65	125150 NOT_FOUNE 116801 genbank_H4: 118111 genbank_N5: 118129 genbank_N5: 118329 genbank_N6:	<u>7_entrez_V85240</u> W38240 H3879 H43879 H493 N55493
70	118475 genbank_N6i 111490 genbank_R0i 111514 genbank_R0i 104534 R22303_at 120340 genbank_AA:	6845 N66845 6862 R66862 R07998 R07998

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                                         AA227469
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        120745 genbank_AA302809
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                                         AA302809
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                                         AA348913
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                                         T97307
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                                         AA251376
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                                         AA457380
        124028 genbank_F04112
                                         F04112
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        108403 genbank AA075374
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108427 genbank_AA076382
108439 genbank_AA078986
131353 231290_1
                                         AA464414
                                         AA076382
                                         AA078986
                                         AW411259 H23555 AW015049 Al684275 AW015886 AW068953 AW014085 Al027260 R52686 AA916278 Al129462
20
        AA969360
                                         N34869 AI948416 AA534205 AA702483 AA705292
                                         AA084415
         108533 genbank_AA084415
         117031 genbank_H88353
                                         H88353
         124254 genbank_H69899
                                         H69899
25
                                                    M21305
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         101458 entrez_M22092
                                                    M22092
         124577 genbank_N68300
                                         N68300
         108940 genbank_AA148603
                                          AA148603
                                          AA148650
         108941 ganbank_AA148650
30
        124627 genbank_N74625
124720 144582 1
                                          N74625
                                          R05283 R11056
         124793 ganbank_R44519
                                          R44519
         124799 genbank_R45088
                                          R45088
         117683 ganbank_N40180
                                          N40180
         117732 ganbank_N46452
35
                                          N46452
         124991 genbank_T50116
                                          T50116
        119023 genbank_N98488 N984
119239 95573_2 T114
119558 NOT_FOUND_entrez_W38194
                                          N98488
                                          T11483 T11472
40
         119654 genbank_W57759
                                          W57759
         105246 genbank AA226879
                                          AA226879
         121350 genbank_AA405237
                                          AA405237
                                          AA412497
         121558 genbank_AA412497
         105985 genbank_AA406610
                                          AA406610
         100071 entrez_A28102A28102
                                          AA101056
         114648 genbank_AA101056
                                          AA427396
         121895 genbank_AA427396
         100327 entrez D55640D55640
         123315 714071_1 AA496369 AA496646
```

TABLE 2:

	Pkev:		Unique Eas prob	oset identifier n	umber			
5	Accession:		Accession number used for previous patent filings					
	ExAcon:				enbank accession number			
	Unigenel		Unigene number					
	Unigene	Title:	Unigene gene titl	е				
10	Pkey	Accessio	n ExAcen	UnigenelD	UnigeneTitle			
	100420		D86983	Hs.118893	Melanoma associated gene			
		100484	NM_005402	Hs.288757	v-ral simian leukemia viral oncogene hom			
15		100991 101168	J03836 NM 005308	Hs.82085 Hs.211569	serine (or cysteine) proteinase inhibito G protein-coupled receptor kinase 5			
13		101261	D30857	Hs.82353	protein C receptor, endothelial (EPCR)			
	101447		M21305	110.0000	gb:Human alpha satellite and satellite 3			
	101543		M31166	Hs.2050	pentaxin-related gene, rapidly induced b			
	101560	101560	AW958272	Hs.347326	intercellular adhesion molecule 2			
20	101714		M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,			
	101838		BE243845	Hs.75511	connective tissue growth factor			
	102012	102012	BE259035 NM 000107	Hs.118400 Hs.77602	singed (Drosophila)-like (sea urchin fas damage-specific DNA binding protein 2 (4			
	102283		AW161552	Hs.83381	quanine nucleotide binding protein 11			
25		102584	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr			
	102759	102759	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)			
	102804		NM_002318	Hs.83354	lysyl oxidase-like 2			
		102898	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,			
30	103036 103095	103036 103095	M13509 NM_005424	Hs.83169 Hs.78824	matrix metalloproteinase 1 (interstitial tyrosine kinase with immunoglobulin and			
30	103095	103166	AA159248	Hs.180909	peroxiredoxin 1			
	103280	103260	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula			
	103850	103850	AA187101	Hs.213194	hypothetical protein MGC10895			
	104592	104592	AW630488	Hs.25338	protease, serine, 23			
35	104786	104786	AA027167	Hs.10031	KIAA0955 protein			
	104865	104865	T79340	Hs.22575 Hs.345588	B-cell CLL/lymphoma 6, member B (zinc fi desmoplakin (DPI, DPII)			
	104952 105178	104952 105178	AW076098 AA313825	Hs.21941	AD036 protein			
	105330		AW338625	Hs.22120	ESTs			
40		105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds			
	105977	105977	AK001972	Hs.30822	hypothetical protein FLJ11110			
	106031	106031	X64116	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H nuclear factor I/B			
	106155 106423	106155	AA425414 AB020722	Hs.33287 Hs.16714	Rho quanine exchange factor (GEF) 15			
45		107174	BE122762	Hs.25338	ESTs			
	107295		AA186629	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp			
	108756	108756	AA127221	Hs.117037	ESTs			
	108888		AA135606	Hs.189384	gb:zi10a05.s1 Soares_pregnant_uterus_NbH			
50	109166	109166	AA219691 F06838	Hs.73625 Hs.14763	RAB6 interacting, kinesin-like (rabkines ESTs			
30	109768 110906	109768 110906	AA035211	Hs.17404	ESTS			
	111006		BE387014	Hs.166146	Homer, neuronal immediate early gene, 3			
	111133	111133	AW580939	Hs.97199	complement component C1q receptor			
	113073	113073	N39342	Hs.103042	microtubule-associated protein 1B			
55	113923		AW953484	Hs.3849	hypothetical protein FLJ22041 similar to			
	115061 115145	115061	Al751438 AA740907	Hs.41271 Hs.88297	Homo sapiens mRNA full length insert cDN ESTs			
		115947	R47479	Hs.94761	KIAA1691 protein			
	116339		AK000290	Hs.44033	dinentidyl pentidase 8			
60	116589	116589	Al557212	Hs.17132	ESTs, Moderately similar to 154374 gene			
	117023		AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f			
	117563		AF055634	Hs.44553	unc5 (C.elegans homolog) c			
		118475	N66845 BE245360	Hs.279477	gb:za46c11.s1 Soares fetal liver spicen			
65		119073 119174	R71234	NS.2/34//	gbn/64c08,s1 Soares placenta Nb2HP Homo			
05		119416	T97186		gb;ve50h09.s1 Soares fetal liver spleen			
		121335	AA404418		gb:zw37e02,s1 Soares_total_fetus_Nb2HF8_			
		123160	AA488687	Hs.284235	ESTs, Weakly similar to 138022 hypotheti			
70	123523	123523	AA608588		gb:ae54e06,s1 Stratagene lung carcinoma			
70		123964	C13961	Hs.288757	gb:C13961 Clontech human aorta polyA+mR v-ral simian leukemia viral oncogene hom			
		124315 124669	NM_005402 Al571594	Hs.102943	hypothetical protein MGC12916			
		124875	AI887664	Hs.285814	sprouty (Drosophila) homolog 4			
	125103	125103	AA570056	Hs.122730	ESTs, Moderately similar to KIAA1215 pro			
75	125565	125565	R20840		gb;yg05c08,r1 Soares infant brain 1NIB H			

	126511 126511	T92143	Hs.57958	EGF-TM7-latrophilin-related protein
	126649 126649	AA001860	Hs.279531 Hs.279531	ESTs ESTs
	449602 449602	AA001860		
5	127402 127402	AA358869	Hs.227949	SEC13 (S. cerevisiae)-like 1 FSTs
3	128992 128992	H04150	Hs.107708	
	129188 129188	NM_001078	Hs.109225 Hs.110802	vascular cell adhesion molecule 1 von Willebrand factor
	129371 129371	X06828 M86933	Hs.110002	amelogenin (Y chromosome)
	129765 129765 129884 129884	AF055581	Hs.13131	lysosomal
10				
10	130639 130639 130828 130828	Al557212 AW631469	Hs.17132 Hs.203213	ESTs, Moderately similar to 154374 gene ESTs
			Hs.2271	endolhelin 1
	131080 131080	NM_001955 Al824144	Hs.23912	ESTs ·
	131182 131182	AA040311	Hs.28959	ESTs
15	131573 131573 131756 131756	AA443966	Hs.31595	ESTs
13	131756 131756 131881 131881	AW361018	Hs.3383	upstream regulatory element binding prot
	132083 132083	BE386490	Hs.279663	Pin
	132358 132358	NM_003542	Hs.46423	H4 histone family, member G
	132456 132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2
20	132676 132676	N92589	Hs.261038	ESTs, Weakly similar to I38022 hypotheti
20	132718 132718	NM 004600	Hs.554	Sjogren syndrome antigen A2 (60kD, nbon
	132760 132760	AA125985	Hs.56145	thymosin, beta, identified in neuroblast
	132968 132968	AF234532	Hs.61638	myosin X
	133061 133061	Al186431	Hs.296638	prostate differentiation factor
25	133161 133161	AW021103	Hs.6631	hypothetical protein FLJ20373
23	133260 133260	AA403045	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R
	133491 133491	BE619053	Hs.170001	eukarvolic translation initiation factor
	133550 133550	Al129903	Hs.74669	vesicle-associated membrane protein 5 (m
	133614 133614	NM_003003	Hs.75232	SEC14 (S. cerevisiae)-like 1
30	133691 133691	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perlecan
30		AU076964	Hs.7753	calumenin
	133913 133913 133985 133985	L34657	Hs.78146	platelet/endothelial cell adhesion molec
	134088 134088	Al379954	Hs.79025	KIAA0096 protein
	134299 134299	AW580939	Hs.97199	complement component C1q receptor
35	116470 116470	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
55	134989 134989	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi
	135073 135073	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
	100114 100114	X02308	Hs.82962	flymidylate synthetase
	100143 100143	AU076465	Hs.278441	KIAA0015 gene product
40	100208 100208	NM_002933	Hs.78224	ribonuclease, RNase A family, 1 (pancrea
40	100405 100405	AW291587	Hs.82733	nidogen 2
	100455 100455	AW888941	Hs.75789	N-myc downstream regulated
	100618 100618	AI752163	Hs.114599	collagen, type VIII, alpha 1
	100658 100658	U56725	Hs.180414	heat shock 70kD protein 2
45	100718 100718	BE295928	Hs.75424	Inhibitor of DNA binding 1, dominant neg
-10	100828 100828	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch
	100991 100991	J03836	Hs.82085	serine (or cysteine) proteinase inhibito
	101110 101110	Al439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r
	101156 101156	AA340987	Hs.75693	prolylcarboxypeptidase (angiotensinase C
50	101184 101184	NM_001674	Hs.460	activating transcription factor 3
50	101317 101317	L42176	Hs.8302	four and a half LIM domains 2
	101345 101345	NM_005795	Hs.152175	calcitonin receptor-like
	101475 101475	BE410405	Hs.76288	calpain 2, (m/ll) large subunit
	101496 101496	X12784	Hs.119129	collagen, type IV, alpha 1
55	101543 101543	M31166	Hs.2050	pentaxin-related gene, rapidly induced b
55	101560 101560	AW958272	Hs.347326	intercellular adhesion molecule 2
	101592 101592	AF064853	Hs.91299	guanine nucleotide binding protein (G pr
	101634 101634	AV650262	Hs.75765	GRO2 oncogene
	101682 101682	AF043045	Hs.81008	filamin B, beta (actin-binding protein-2
60	101720 101720	M69043	Hs.81328	nuclear factor of kappa light polypeptid
00	101744 101744	Al879352	Hs.118625	hexokinase 1
	101837 101837	M92843	Hs.343586	zinc finger protein homologous to Zfp-36
	101840 101840	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito
	101864 101864	BE392588	Hs.75777	transaelin
65	101966 101966	X96438	Hs.76095	immediate early response 3
05	102013 102013	BE616287	Hs.178452	catenin (cadherin-associated protein), a
	102059 102059	AI752666	Hs.76669	nicotinamide N-methyltransferase
	102283 102283	AW161552	Hs.83381	guanine nudeotide binding protein 11
	102378 102378	AU076887	Hs.28491	spermidine/spermine N1-acetyltransferase
70	102460 102460	U48959	Hs.211582	myosin, light polypeptide kinase
, ,	102499 102499	BE243877	Hs.76941	ATPase, Na+/K+ transporting, beta 3 poly
	102560 102560	R97457	Hs.63984	cadherin 13, H-cadherin (heart)
	102589 102589	AU076728	Hs.8867	cysteine-rich, angiogenic inducer, 61
	102645 102645	AL119566	Hs.6721	lysosomal
75	102693 102693	AA532780	Hs.183684	eukaryotic translation initiation factor
, ,	102759 102759	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)
	1021-1-			, process (green-y

	102882 102882	Al767736	Hs.290070	gelsolin (amyloidosis, Finnish type)
	102915 102915	X07820.	Hs.2258 Hs.76053	matrix metalloproteinase 10 (stromelysin
	102960 102960 103020 103020	Al904738 X53416	Hs.195464	DEADIH (Asp-Glu-Ala-Asp/His) box polypep filamin A, alpha (actin-binding protein-
5	103036 103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial
-	103080 103080	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos
	103138 103138	X65965		gb:H.sapiens SOD-2 gene for manganese su
	103195 103195	AA351647 X91247	Hs.2642 Hs.13046	eukaryotic translation elongation factor thioredoxin reductase 1
10	103371 103371 103471 103471	Y00815	Hs.75216	projein tyrosine phosphatase, receptor t
10	104447 104447	AW204145	Hs.156044	ESTs
	104783 104783	AA533513	Hs.93659	protein disulfide isomerase related prot
	104865 104865	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi
15	104894 104894 105113 105113	AF065214 AB037816	Hs.18858 Hs.8982	phospholipase A2, group IVC (cytosolic, Homo sapiens, clone IMAGE:3506202, mRNA,
13	105196 105196	W84893	Hs.9305	angiotensin receptor-like 1
	105263 105263	AW388633	Hs.6682	solute carrier family 7, (cationic amino
	105330 105330	AW338625	Hs.22120	ESTs
20	105492 105492	Al805717	Hs.289112	CGI-43 protein
20	105594 105594	AB024334 AW504170	Hs.25001 Hs.274344	tyrosine 3-monooxygenase/tryptophan 5-mo hypothetical protein MGC12942
	105732 105732 105882 105882	W46802	Hs.81988	disabled (Drosophila) homolog 2 (milogen
	106031 106031	X64116	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H
	106222 106222	AA356392	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA,
25	106263 106263	W21493	Hs.28329	hypothetical protein FLJ14005
	106366 106366 106634 106634	AA186715 W25491	Hs.336429 Hs.288909	RIKEN cDNA 9130422N19 gene hypothetical protein FLJ22471
	106793 106793	H94997	Hs.16450	FSTs
	106842 106842	AF124251	Hs.26054	novel SH2-containing protein 3
30	106890 106890	AA489245	Hs.88500	mitogen-activated protein kinase 8 inter
	106974 106974	Al817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL
	107061 107061 107216 107216	BE147611 D51069	Hs.6354 Hs.211579	stromal cell derived factor receptor 1 melanoma cell adhesion molecule
	107444 107444	W28391	Hs.343258	proliferation-associated 2G4, 38kD
35	108507 108507	AI554545	Hs.68301	ESTs
	108931 108931	AA147186		gb:zo38d01.s1 Stratagene endothelial cel
	109195 109195	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon ESTs
	109456 109456 110411 110411	AW956580 AW001579	Hs.42699 Hs.9645	Homo saplens mRNA for KIAA1741 protein,
40	110906 110906	AA035211	Hs.17404	ESTs
	111091 111091	AA300067	Hs.33032	hypothetical protein DKFZp434N185
	111378 111378	AW160993	Hs.326292	hypothetical gene DKFZp434A1114
	111769 111769	AW629414	Hs.24230 Hs.6650	ESTs vacuolar protein sorting 45B (yeast homo
45	112951 112951 113195 113195	AA307634 H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
73	113542 113542	H43374	Hs.7890	Homo saplens mRNA for KIAA1671 protein,
	113847 113847	NM_005032	Hs.4114	plastin 3 (T isoform)
	113947 113947	W84768		gb:zh53d03.s1 Soares_fetal_liver_spleen_
50	115061 115061	AI751438 NM_005985	Hs.41271 Hs.48029	Homo sapiens mRNA full length insert cDN snail 1 (drosophila homolog), zinc finge
30	115870 115870 116228 116228	AI767947	Hs.50841	ESTs
	116314 116314	Al799104	Hs.178705	Homo sapiens cDNA FLJ11333 fis, done PL
	117023 117023	AW070211	Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
~ ~	117156 117156	W73853		ESTs
55	117280 117280 119866 119866	M18217 AA496205	Hs.172129 Hs.193700	Homo sapiens cDNA: FLJ21409 fis, clone C Homo sapiens mRNA; cDNA DKFZp586I0324 (f
	121314 121314	W07343	Hs.182538	phospholipid scramblase 4
	121822 121822	AI743860		metallothionein 1E (functional)
	122331 122331	AL133437	Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H
60	123160 123160	AA488687	Hs.284235	ESTs, Weakly similar to 138022 hypotheti ESTs. Weakly similar to S64054 hypotheti
	124059 124059 124358 124358	BE387335 AW070211	Hs.283713 Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
	124726 124726	NM_003654	Hs.104576	carbohydrate (keratan sulfate Gal-6) sul
	125167 125167	AL137540	Hs.102541	netrin 4
65	125307 125307	AW580945	Hs.330466	ESTs
	107985 107985	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr Homo sapiens mRNA; cDNA DKFZp564F053 (fr
	125598 125598 413731 413731	T40064 BE243845	Hs.71968 Hs.75511	connective tissue growth factor
	116024 116024	AA088767	Hs.83883	transmembrane, prostate androgen induced
70	418000 418000	AA932794	Hs.83147	guanine nucleotide binding protein-like
	126399 126399	AA088767	Hs.83883	transmembrane, prostate androgen induced
	127566 127566	AI051390 X02761	Hs.116731	ESTs fibronectin 1
	128453 128453 128515 128515	BE395085	Hs.287820 Hs.10066	type I transmembrane protein Fn14
75	128623 128623	BE076608	Hs.105509	CTL2 gene
	128669 128669	W28493	Hs.180414	heat shock 70kD protein 8

	128914 128914	AW867491	Hs.107125	plasmalemma vesicle associated protein
	129188 129188	NM_001078	Hs.109225	vascular cell adhesion molecule 1
	129265 129265	AA530892	Hs.171695	dual specificity phosphatase 1
	129468 129468	AW410538	Hs.111779	secreted protein, acidic, cysteine-rich
5	101838 101838	BE243845	Hs.75511	connective tissue growth factor
	129619 129619	AA209534	Hs.284243	tetraspan NET-6 protein
	129762 129762	AA453694	Hs.12372	tripartite motif protein TRIM2
	130018 130018	AA353093		metaliothlonein 1L
	130178 130178	U20982	Hs.1516	insulin-like growth factor-binding prote
10	130431 130431	AW505214	Hs.155560	calnexin
	130553 130553	AF062649	Hs.252587	pituitary tumor-transforming 1
	130639 130639	Al557212	Hs.17132	ESTs, Moderately similar to 154374 gene
	130686 130686	EE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV
1.5	130818 130818	AW190920	Hs.19928	hypothetical protein SP329
15	130899 130899	AI077288	Hs.296323	serum/glucocorticold regulated kinase
	131080 131080	NM_001955	Hs.2271	endothelin 1
	131091 131091	AJ271216	Hs.22880	dipeptidylpeptidase III ESTs
	131182 131182 131319 131319	Al824144 NM_003155	Hs.23912 Hs.25590	stanniocalcin 1
20	131319 131319 131328 131328	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
20	131328 131328	AW939251	Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131555 131555	T47364	Hs.278613	interferon, alpha-inducible protein 27
	131573 131573	AA040311	Hs.28959	ESTs
	131756 131756	AA443966	Hs.31595	ESTs
25	131909 131909	NM_016558	Hs.274411	SCAN domain-containing 1
	132046 132046	Al359214	Hs.179260	chromosome 14 open reading frame 4
	132151 132151	BE379499	Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H
	132187 132187	AA235709	Hs.4193	DKFZP586O1624 protein
	132314 132314	AF112222	Hs.323806	pinin, desmosome associated protein
30	132398 132398	AA876616	Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p
	132490 132490	NM_001290	Hs.4980	LIM domain binding 2
	132546 132546	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)
	132716 132716	BE379595	Hs.283738	casein kinase 1, alpha 1
	132883 132883	AA373314	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f hypothetical protein FLJ13213
35	132989 132989	AA480074	Hs.331328	hypothetical protein FLJ13213
	133071 133071	BE384932	Hs.64313	ESTs, Weakly similar to AF257182 1 G-pro
	133099 133099	W16518	Hs.279518	amyloid beta (A4) precursor-like protein
	133149 133149	AA370045	Hs.6607	AXIN1 up-regulated
40	133200 133200	AB037715	Hs.183639	hypothetical protein FLJ10210 Homo sapiens cONA: FLJ23197 fis, clone R
40	133260 133260	AA403045	Hs.6906	L-3-hydroxyacyl-Coenzyme A dehydrogenase
	133349 133349	AW631255 NM_000499	Hs.8110 Hs.72912	cylochrome P450, subfamily I (aromatic c
	133398 133398 133454 133454	BE547647	Hs.177781	hypothetical protein MGC5618
	133491 133491	BE619053	Hs.170001	eukaryotic translation initiation factor
45	133517 133517	NM_000165	Hs.74471	gap junction protein, alpha 1, 43kD (con
75	133538 133538	NM_003257	Hs.74614	tight junction protein 1 (zona occludens
	133584 133584	D90209	Hs.181243	activating transcription factor 4 (tax-r
	133617 133617	BE244334	Hs.75249	ADP-ribosylation factor-like 6 Interacti
	133671 133671	AW503116	Hs.301819	zinc finger protein 146
50	133681 133681	Al352558		tyrosine 3-monooxygenase/tryptophan 5-mo
	133730 133730	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3
	133802 133802	AW239400	Hs.76297	G protein-coupled receptor kinase 6
	133838 133838	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg
	133889 133889	U48959	Hs.211582	myosin, light polypeptide kinase
55	133975 133975	C18356	Hs.295944	tissue factor pathway inhibitor 2
	134039 134039	NM_002290	Hs.78672	laminin, alpha 4
	134081 134081	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t
	134203 134203	AA161219	Hs.799	diphtheria toxin receptor (heparin-bindi
60	134299 134299	AW580939 R70429	Hs.97199 Hs.81988	complement component C1q receptor disabled (Drosophila) homolog 2 (mitogen
00	134339 134339 134381 134381	Al557280	Hs.184270	capping protein (actin filament) muscle
	134381 134381 134416 134416	X68264	Hs.211579	melanoma cell adhesion molecule
	134558 134558	NM_001773	Hs.85289	CD34 antigen
	134983 134983	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p
65	135052 135052	AL136653	Hs.93675	decidual protein induced by progesterone
05	135069 135069	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr
	135073 135073	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
	135196 135196	C03577	Hs.9615	myosin regulatory light chain 2, smooth
	134404 134404	AB000450	Hs.82771	vaccinia related kinase 2
70	100082 100082	AA130080	Hs.4295	proteasome (prosome, macropain) 26S subu
. 0	130150 130150	BE094848	Hs.15113	homogentisale 1,2-dioxygenase (homogenti
	130839 130839	AB011169	Hs.20141	similar to S. cerevisiae SSM4
	100113 100113	NM_001269	Hs.84746	chromosome condensation 1
	100129 100129	AA469369	Hs.5831	tissue inhibitor of metalloproteinase 1
75	100169 100169	AL037228	Hs.82043	D123 gene product
	100190 100190	M91401	Hs.178658	RAD23 (S. cerevisiae) homolog B

	100211 100211	D26528	Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
	130283 130283	NM_012288	Hs.153954	TRAM-like prolein
	100248 100248	NM_015156	Hs.78398 Hs.278468	KIAA0071 protein postmeiotic segregation increased 2-like
5	100262 100262 100281 100281	D38500 AF091035	Hs.184627	KIAA0118 protein
,	100327 100327	D55640	110.104027	gb:Human monocyte PABL (pseudoautoson
	134495 134495	D63477	Hs.84087	KIAA0143 protein
	135152 135152	M96954	Hs.182741	TIA1 cytotoxic granule-associated RNA-bi
	100372 100372	NM_014791	Hs.184339	KIAA0175 gene product
10	100394 100394	D84284	Hs.66052	CD38 antigen (p45)
	100418 100418 134347 134347	D86978	Hs.84790 Hs.82042	KIAA0225 protein solute carrier family 23 (nucleobase tra
	100438 100438	AF164142 AA013051	Hs.91417	topoisomerase (DNA) Il binding protein
	100481 100481	X70377	Hs.121489	cystatin D
15	100591 100591	NM_004091	Hs.231444	Homo sapiens, Similar to hypothetical pr
	100662 100662	A\368680	Hs.816	SRY (sex determining region Y)-box 2
	100905 100905	L12260	Hs.172816	neuregulin 1
	100950 100950 135407 135407	AF128542 J04029	Hs.166846 Hs.99936	polymerase (DNA directed), epsilon keratin 10 (epidermolytic hyperkeratosis
20	131877 131877	J04029 J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)
20	134786 134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous
	134078 134078	L08895	Hs.78995	MADS box transcription enhancer factor 2
	134849 134849	BE409525	Hs.902	neurofibromin 2 (bilateral acoustic neur
0.5	101152 101152	AI984625	Hs.9884	spindle pole body protein
25	131687 131687	BE297635	Hs.3069	heat shock 70kD protein 9B (mortalin-2)
	421155 421155 133975 133975	H87879 C18356	Hs.102267 Hs.295944	lysyl oxidase tissue factor pathway inhibitor 2
	130155 130155	AA101043	Hs.151254	kallikrein 7 (chymotryptic, stratum com
	132813 132813	BE313625	Hs.57435	solute carrier family 11 (proton-coupled
30	101300 101300	BE535511		transmembrane trafficking protein
	130344 130344	AW250122	Hs.154879	DiGeorge syndrome critical region gene D
	101381 101381	AW675039	Hs.1227	aminolevulinate, delta-, dehydratase
	133780 133780	AA557660	Hs.76152	decorin gb:Human alpha satellite and satellite 3
35	101447 101447 101470 101470	M21305 NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)
55	101478 101478	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa
	133519 133519	AW583062	Hs.74502	chymotrypsinogen B1
	134116 134116	R84694	Hs.79194	cAMP responsive element binding protein
40	130174 130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat
40	132983 132983	M30269	11- 0050	nidogen (enactin) pentaxin-related gene, rapidly induced b
	101543 101543 101620 101620	M31166 S55271	Hs.2050 Hs.247930	Epsilon , IgE
	133595 133595	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond
	101700 101700	D90337	Hs.247916	natriuretic peptide precursor C
45	134246 134246	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6 h
	133948 133948	X59960	Hs.77813	sphingomyelin phosphodlesterase 1, acid
	133948 133948	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid sphingomyelin phosphodiesterase 1, acid
	133948 133948 101812 101812	X59960 BE439894	Hs.77813 Hs.78991	DNA segment, numerous copies, expressed
50	133396 133396	M96326	Hs.72885	azurocidin 1 (cationic antimicrobial pro
50	129026 129026	AL120297	Hs.108043	Friend leukemia virus integration 1
	134831 134831	AA853479	Hs.89890	pyruvate carboxylase
	134395 134395	AA456539	Hs.8262	lysosomal
	101977 101977	AF112213	Hs.184062	putative Rab5-interacting protein
55	101998 101998	U01212	Hs.248153 Hs.75307	olfactory marker protein t-complex-associated-testls-expressed 1-
	102007 102007 416658 416658	U02556 U03272	Hs.79432	fibrillin 2 (congenital contractural ara
	135389 135389	U05237	Hs.99872	fetal Alzheimer antigen
	130145 130145	U34820	Hs.151051	mitogen-activated protein kinase 10
60	420269 420269	U72937	Hs.96264	alpha thalassemia/mental retardation syn
	102123 102123	NM_001809	Hs.1594	centromere protein A (17kD)
	102133 102133	AU076845 AA450274	Hs.155596 Hs.1592	BCL2/adenovirus E1B 19kD-interacting pro
	102162 102162 427653 427653	AA450274 AA159001	Hs.180069	CDC16 (cell division cycle 16, S. cerevi nuclear respiratory factor 1
65	427653 427653 102200 102200	AA232362	Hs.157205	branched chain aminotransferase 1, cytos
05	102214 102214	U23752	Hs.32964	SRY (sex determining region Y)-box 11
	131319 131319	NM_003155	Hs.25590	stanniocalcin 1
	132316 132316	U28831	Hs.44566	KIAA1641 protein
70	134365 134365	AA568906	Hs.82240	syntaxin 3A
70	102298 102298 302344 302344	AA382169 BE303044	Hs.54483 Hs.192023	N-myc (and STAT) interactor eukaryotic translation initiation factor
	302344 302344 102367 102367	U39656	Hs.192023 Hs.118825	mitogen-activated protein kinase kinase
	102394 102394	NM 003816	Hs.2442	a disintegrin and metalloproteinase doma
	129521 129521	AF071076	Hs.112255	nucleoporin 98kD
75	102251 102251	NM_004398	Hs.41706	DEAD/H (Asp-Glu-Ala-Asp/His) box polyper
	133746 133746	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr

	132828 132828	AB014615	Hs.57710	fibroblast growth factor 8 (androgen-ind
	132828 132828	AB014615	Hs.57710	fibroblast growth factor 8 (androgen-ind
	130441 130441	U63630	Hs.155637	protein kinase, DNA-activated, catalytic
_	129350 129350	U50535	Hs.110630	Human BRCA2 region, mRNA sequence CG006
5	130457 130457	AB014595	Hs.155976	culin 4B
	102560 102560	R97457	Hs.63984	cadherin 13, H-cadherin (heart)
	134305 134305	U61397	Hs.81424	ubiquitin-like 1 (sentrin)
	132736 132736	AW081883	Hs.211578	Homo sapiens cDNA: FLJ23037 fis, clone L
	102663 102663	NM_002270	Hs.168075	karyopherin (importin) beta 2
10	102735 102735	AF111106	Hs.3382	protein phosphatase 4, regulatory subuni
	101175 101175	U82671	Hs.36980	melanoma antigen, family A, 2
	132164 132164	Al752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
	102826 102826	NM_007274	Hs.8679	cytosolic acyl coenzyme A thioester hydr
1.5	102846 102846	BE264974	Hs.6566	thyroid hormone receptor interactor 13
15	134161 134161	AA634543	Hs.79440	IGF-II mRNA-binding protein 3
	302363 302363	AW163799	Hs.198365	2,3-bisphosphoglycerate mutase apolipoprotein A-I
	125701 125701 134656 134656	T72104 AI750878	Hs.93194 Hs.87409	thrombospondin 1
	102968 102968	AU076611	Hs.154672	methylene tetrahydrofolate dehydrogenase
20	134037 134037	A1808780	Hs.227730	integrin, alpha 6
20	103023 103023	AW500470	Hs.117950	multifunctional polypeptide similar to S
	130282 130282	BE245380	Hs.153952	5' nucleotidase (CD73)
	128568 128568	H12912	Hs.274691	adenylate kinase 3
	103093 103093	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine
25	129063 129063	X63094	Hs.283822	Rhesus blood group, D antigen
	133227 133227	AW977263	Hs.68257	general transcription factor IIF, polype
	103184 103184	U43143	Hs.74049	fms-related tyrosine kinase 4
	103208 103208	AW411340	Hs.31314	retinoblastoma-binding protein 7
	131486 131486	F06972	Hs.27372	BMX non-receptor tyrosine kinase
30	103334 103334	NM_001260	Hs.25283	cyclin-dependent kinase 8
	135094 135094	NM_003304	Hs.250687	transient receptor potential channel 1
	103352 103352	H09366	Hs.78853	uracil-DNA glycosylase
	132173 132173	X89426	Hs.41716	endothelial cell-specific molecule 1
	131584 131584	AA598509	Hs.29117	purine-rich element binding protein A
35	103378 103378	AL119690	Hs.153618	HCGVIII-1 protein
	103410 103410	AA158294	Hs.295362	DR1-associated protein 1 (negative cofac
	103438 103438	AW175781	Hs.152720	M-phase phosphoprotein 6
	103452 103452	NW_006936	Hs.85119	SMT3 (suppressor of mil two 3, yeast) ho
40	135185 135185	AW404908	Hs.96038	Ric (Drosophila)-like, expressed in many
40	134682 134662	NM_007048	Hs.284283	butyrophilin, subfamily 3, member A1
	103500 103500	AW408009	Hs.22580 Hs.3886	alkylglycerone phosphate synthase karyopherin alpha 3 (importin alpha 4)
	132084 132084	NM_002267 Z11695	Hs.324473	mitogen-activated protein kinase 1
	133152 133152 103612 103612	BE336654	Hs.70937	H3 histone family, member A
45	103692 103692	AW137912	Hs.227583	Homo sapiens chromosome X map Xp11.23 L-
43	129796 129796	BE218319	Hs.5807	GTPase Rab14
	132883 132683	BE264633	Hs.143638	WD repeat domain 4
	103723 103723	BE274312	Hs.214783	Homo sapiens cDNA FLJ14041 fis, clone HE
	133260 133260	AA403045	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R
50	103766 103766	Al920783	Hs.191435	ESTs
	132051 132051	AA393968	Hs.180145	HSPC030 protein
	135289 135289	AW372569	Hs.9788	hypothetical protein MGC10924 similar to
	103794 103794	AF244135	Hs.30670	hepatocellular carcinoma-associated anti
	134319 134319	BE304999	Hs.285754	fumarate hydratase
55	119159 119159	AF142419	Hs.15020	homolog of mouse quaking QKI (KH domain
	103850 103850	AA187101	Hs.213194	hypothetical protein MGC10895
	322026 322026	AW024973	Hs.283675	NPD009 protein
	103861 103861	AA206236	Hs.4944	hypothetical protein FLJ12783
	447735 447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L
60	131236 131236	AF043117	Hs.24594	ubiquitination factor E4B (homologous to
	129013 129013	AA371156	Hs.107942	DKFZP564M112 prolein
	103988 103988	AA314389 AF155568	Hs.342849 Hs.348043	ADP-ribosylation factor-like 5 NS1-associated protein 1
	425284 425284 133281 133281	AK001601	Hs.69594	high-mobility group 20A
65	133281 133281 108154 108154	NM_005754	Hs.220689	Ras-GTPase-activating protein SH3-domain
03		W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
	135073 135073 129593 129593	Al338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f
	132064 132064	AA121098	Hs.3838	serum-inducible kinase
	131427 131427	AF151879	Hs.26706	CGI-121 protein
70	104282 104282	C14448	Hs.332338	EST
70	130443 130443	D25216	Hs.155650	KIAA0014 gene product
	132837 132837	AA370362	Hs.57958	EGF-TM7-latrophilin-related protein
	104334 104334	D82614	Hs.78771	phosphoglycerate kinase 1
	134731 134731	D89377	Hs.89404	msh (Drosophila) homeo box homolog 2
75	131670 131670	H03514	Hs.15589	ESTs
	104402 104402	H56731	Hs.132956	ESTs

	129077 129077	N74724	Hs.108479	ESTs
	134927 134927	L36531	Hs.91296	integrin, alpha 8
	134498 134498	AW246273	Hs.84131	threonyl-tRNA synthetase
	104488 104488	N56191	Hs.106511	protocadherin 17
5	129214 129214	AL044335	Hs.109526	zinc finger protein 198
	104530 104530	AK001676	Hs.12457	hypothetical protein FLJ10814
	104544 104544	Al091173	Hs.222362	ESTs, Weakly similar to p40 [H.sapiens]
	104567 104567	AA040620	Hs.5672	hypothetical protein AF140225
	129575 129575	F08282	Hs.278428	progestin induced protein
10	104599 104599	AW815036	Hs.151251	ESTs
	104667 104667	Al239923	Hs.63931	ESTs
	104764 104764	Al039243	Hs.278585	ESTs
	104787 104787	AA027317		gb:ze97d11.s1 Soares_fetal_heart_NbHH19W
1.5	104804 104804	A1858702	Hs.31803	ESTs, Weakly similar to N-WASP [H.sapien
15	130828 130828	AW631469	Hs.203213 Hs.114218	ESTs frizzled (Drosophila) homolog 6
	104943 104943 105024 105024	AF072873	Hs.9879	
	105024 105024 105038 105038	AA126311 AW503733	Hs.9414	ESTs KIAA1488 protein
	105096 105096	AL042506	Hs.21599	Kruppel-like factor 7 (ubiquitous)
20	105169 105169	BE245294	Hs.180789	S164 protein
20	130401 130401	BE396283	Hs.173987	eukaryotic translation initiation factor
	130114 130114	AA233393	Hs.14992	hypothetical protein FLJ11151
	105337 105337	Al468789	Hs.347187	myotubularin related protein 1
	105376 105376	AW994032	Hs.8768	hypothetical protein FLJ10849
25	131962 131962	AK000046	Hs.343877	hypothetical protein FLJ20039
23	128658 128658	BE397354	Hs.324830	diptheria toxin resistance protein requi
	105508 105508	AA173942	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f
	135172 135172	AB028956	Hs.12144	KIAA1033 protein
	132542 132542	AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434l0812 (f
30	105659 105659	AA283044	Hs.25625	hypothetical protein FLJ11323
	105674 105674	A1609530	Hs.279789	histone deacetylase 3
	105722 105722	Al922821	Hs.32433	ESTs
	115951 115951	BE546245	Hs.301048	sec13-like protein
	105985 105985	AA406610		gb:zv15b10.s1 Soares_NhHMPu_S1 Homo sapi
35	131216 131216	AI815486	Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE
	113689 113689	AB037850	Hs.16621	DKFZP434I116 protein
	130839 130839	AB011169	Hs.20141	similar to S. cerevisiae SSM4
	130777 130777	AW135049	Hs.26285	Homo sapiens cDNA FLJ10643 fis, clone NT
40	106196 106196	AA525993	Hs.173699	ESTs, Weakly similar to ALU1_HUMAN ALU S
40	133200 133200	AB037715	Hs.183639 Hs.28020	hypothetical prolein FLJ10210 KIAA0766 gene product
	108328 106328 106423 106423	AL079559 AB020722	Hs.18714	Rho guanine exchange factor (GEF) 15
	439608 439608	AW864696	Hs.301732	hypothetical protein MGC5306
	106503 106503	AB033042	Hs.29679	cofactor required for Sp1 transcriptiona
45	106543 106543	AA876939	Hs.69265	neuropilin 1
75	106589 106589	AK000933	Hs.28661	Homo saplens cDNA FLJ10071 fis, clone HE
	106596 106596	AA452379		ESTs, Moderately similar to ALU7_HUMAN A
	106636 106836	AW958037	Hs.286	ribosomal protein L4
	131353 131353	AW754182		gb:RC2-CT0321-131199-011-c01 CT0321 Homo
50	131710 131710	NM_015368	Hs.30985	pannexin 1
	131775 131775	AB014548	Hs.31921	KIAA0648 protein
	106773 106773	AA478109	Hs.188833	ESTs
	106817 106817	D61216	Hs.18672	ESTs
	106848 106848	AA449014	Hs.121025	chromosome 11 open reading frame 5
55	418699 418699	BE539639	Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S
	130638 130638	AW021276	Hs.17121 Hs.23044	ESTs RAD51 (S. cerevisiae) homolog (E coli Re
	107059 107059 107115 107115	BE614410 BE379623	Hs.27693	peptidylprolyl isomerase (cyclophilin)-l
	107156 107156	AA137043	Hs.9663	programmed cell death 6-interacting prot
60	130621 130621	AW513087	Hs.16803	LUC7 (S. cerevisiae)-like
00	132626 132626	AW504732	Hs.21275	hypothetical protein FLJ11011
	131610 131610	AA357879	Hs.29423	scavenger receptor with C-type lectin
	107295 107295	AA186629	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp
	107315 107315	AA316241	Hs.90691	nucleophosmin/nucleoplasmin 3
65	107328 107328	AW959891	Hs.76591	KIAA0887 protein
	134715 134715	U48263	Hs.89040	prepronociceptin
	129938 129938	AW003668	Hs.135587	Human clone 23629 mRNA sequence
	130074 130074	AL038596	Hs.250745	polymerase (RNA) III (DNA directed) (62k
	132036 132036	AL157433	Hs.37706	hypothetical protein DKFZp434E2220
70	113857 113857	AW243158	Hs.5297	DKFZP564A2416 protein
	130419 130419	AF037448	Hs.155489	NS1-associated protein 1
	132616 132616	BE262677	Hs.283558	hypothetical protein PRO1855
	132358 132358	NM_003542	Hs.46423 Hs.97496	H4 histone family, member G
75	125827 125827 107609 107809	NM_003403 R75654	Hs.97496 Hs.164797	YY1 transcription factor hypothetical protein FLJ13693
13	107609 107809 107714 107714	AA015761	Hs.60642	ESTs
	10//14 10//14	, 51010101		

	107832 107832	AA021473		qb:ze66c11.s1 Soares retina N2b4HR Homo
	124337 124337	N23541	Hs.281561	Homo sapiens cDNA: FLJ23582 fis, clone L
	129577 129577	N75346	Hs.306121	CDC20 (cell division cycle 20, S. cerevi
	132000 132000	AW247017	Hs.36978	melanoma antigen, family A, 3
5	107935 107935	AA029428	Hs.61555	ESTs
,		AA992841	Hs.27263	KIAA1458 protein
	131461 131461	AA040740	Hs.62007	ESTs
	108029 108029			Homo sapiens, clone IMAGE:4154008, mRNA,
	108084 108084	AA058944	Hs.116602	
* 0	108168 108168	AI453137	Hs.63176	ESTs
10	108189 108189	AW376061	Hs.63335	ESTs, Moderately similar to A46010 X-lin
	108203 108203	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C
	108217 108217	AA058686	Hs.62588	ESTs
	108277 108277	AA064859		gb:zm50f03.s1 Stratagene fibroblast (937
	108309 108309	AA069818		gb:zm67e03.r1 Stratagene neuroepithelium
15	108340 108340	AA069820	Hs.180909	peroxiredoxin 1
	108427 108427	AA076382		gb:zm91g08.s1 Stratagene ovarian cancer
	108439 108439	AA078986		gb:zm92h01.s1 Stratagene ovarian cancer
	108469 108469	AA079487		gb:zm97f08.s1 Stratagene colon HT29 (937
	108501 108501	AA083256		gb:zn08g12.s1 Stratagene hNT neuron (937
20	108562 108562	AA100796		gb:zm26c06.s1 Stratagene pancreas (93720
	130890 130890	AI907537	Hs.76698	stress-associated endoplasmic reticulum
	130385 130385	AW067800	Hs.155223	stanniocalcin 2
	108807 108807	Al652236	Hs.49376	hypothetical protein FLJ20644
	108833 108833	AF188527	Hs.61661	ESTs, Weakly similar to AF174605 1 F-box
25	108846 108846	AL117452	Hs.44155	DKFZP586G1517 protein
23	131474 131474	L46353	Hs.2726	high-mobility group (nonhistone chromoso
	108941 108941	AA148650	11011111110	gb:zo09e06.s1 Stratagene neuroepithelium
	108996 108996	AW995610	Hs.332436	EST
	131183 131183	Al611807	Hs.285107	hypothetical protein FLJ13397
30	109022 109022	AA157291	Hs.21479	ubinuclein 1
30	109068 109068	AA164293	Hs.72545	ESTs
	129021 129021	AL044675	Hs.173081	KIAA0530 protein
	109146 109146	AA176589	Hs.142078	EST
	131080 131080	NM_001955	Hs.2271	endothelin 1
35	109222 109222	AA192833	Hs.333512	similar to rat myomegalin
33	109222 109222	AA192033 AA878923	Hs.289069	hypothetical protein FLJ21016
			Hs.71913	ESTs
	109516 109516	Al471639		ESTs
	109556 109556	Al925294	Hs.87385	ESTS
	109578 109578	F02208	Hs.27214	
40	109625 109625	H29490	Hs.22697	ESTs
	109648 109648	H17800	Hs.7154	ESTs
	109699 109699	H18013	Hs.167483	ESTs
	109933 109933	R52417	Hs.20945	Homo sapiens clone 24993 mRNA sequence
	110039 110039	H11938	Hs.21907	histone acelyltransferase

TABLE 2A

Table 2A shows the accession numbers for those pixeys leading unigenetD's for Table 2. The pixeys in Table 7 lecking unigenetD's are represented within Tables 1-6A. For each probaset we have Island the gene cluster number from which the disponuteboffices were designed. Gene clusters were compiled using executiones derived from Genetian-ESTs and mRNNs. These sequences were clustered based to sequence safeting line (Dustaring and Alignment Tools (DoubleTwist, Cakiand California). The Genbank accession numbers for sequences comprising each cluster are Islaed in the "Accession" column.

10	Pkey: GAT numl Accession	per: Gene clus	os probeest klanifier number ober number accassion numbeis
15	Pkey	CAT Number	Accession
20	108469 108501 108562	116761_1 1368412 36375_1	AA079487 AA128547 AA128291 AA079587 AA079600 AA083256 AA100756 AR020589 AA074629 AA075946 AA100849 AA085347 AA126309 AA075311 AA075323 AA085274
20	101300	4669_1	BESS51 1 MXXXXXX AVXXXX AVXXXXX AVXXXXXX AVXXXXXX AVXXXXXX AVXXXXXXXX
25			ALDBSSGA ALASSEAS ALTZDYS ARZSEON ACESTEON ADSERVAT ALBSGASS ALBSGASS ALBSGASS ALASSESS ALTRIGOS HYDDOD ABDUTAS ALASSESS ALTRIGOS HYDDOD ABDUTAS ALASSESS ALBSGASS ALBSGAS ALBSG
30	117156	145392_1 1704098 1	W73863, AA028112 W77887 AW869237 AH46524 A1746182 A175442 A1338392 A1253102 A1079403 A1370541 A1697341 H97558 AW86021 A1827669 W7571 A1657402 A186074 7363990 O K7547 A76 W92522 A1691028 A1913512 A144448 W73819 AA004358 N28900 W96221 A1868132 H96465 AA148793 A20040 P20393
35	132983	11922_1	M30269 NM_00260 X82254 NR76760 AWS5703 D78945 M27445 AA650439 AL045616 AV660256 AV650347 AA333056 E326257 T00969 AA33094 AW56987 729695 KAW17570 M AA33262 KW173957 A1816389 W17308 W17302 H15591 AA37124 AA370412 W94668 BE384365 T28498 R80714 R16959 H21723 AW835154 D65097 D55381 W21222 A439056 XW379755 AW067895
	133681	13893_1	A1352558 Z82248 X78138 NM_003405 AU077248 AA223125 S80794 D78577 AI124697 AW403970 BE614089 BE296713 BE621334 L20422 X80536 D54224 D54950 X57345 N29226 AA127798 AA340253 F08031 AA192540 H67636 AA321827
40			AMB6028 AA084198 BESSBOR AMMISTA AASSTA COSSEG WARGES WITFOR AA050009 HIGHST HERST ENDED TO TOO THE THITTOR AA030077 HAS STS THE 2004 FITFORD AMPROSEA AN A18368 AA032074 AA032078 HIGH SIGN SACE AND THE AT A1836 AA03207 HIGH SIGN SIGN SIGN SIGN SIGN SIGN SIGN SIGN
45			ANGSS019 ANGZ213 ANGS1996 HOSGGC ANTIGODO A SINGSOTO ANTI-STIGO WIGSELA AAGGGGT NIHAGUZ ALGOGGGE ANGGGGA ANGGGGA AAGGGGA NIHAGUZ ALGOGGGE ANGGGGA AAGGGGA AAGGGGA AAGGGGA AAGGGGA ANGGGA ANGGA ANGGGA
50			A2269696 A4720884 A1872093 NV1500/C AL128288 AA216627 A4888086 C71937 A1595337 H25337 A159749 AA615146 A15952CA A147378 A159732 AVASS528 AVASS528 A1786547 BA5828 A1088547 B1543 N86107 WA459 AA669555 N26207 AL279762 W46559 AA77557 B12204 A1695547 B16828 A108559 N1500 A412597 D26230 M56537 A108597 AWA50256 A108597 H56946 AVASS527 B16827 L06839 AA21670 A42503 DW1473 W4155 A422044 A018597 AWA50256 A108597 H56946 AVASS527 B16827 L06839 AA21670 A450530 W4747 W4155 A422044 AWA5035 A346041 D6528000 AA66912 T2001 A4691576 M6913 AA774559 AWA50250 A456915 W4743 W47455 A422044
55	121335	279548_1	ANASISDA (NIVOSA/27 ANATHUS ANAESSIS ANESISSA ANESISSA SA BUTTI (2 AB 11116 BE-64-550 BE-55076 I H75021 T15-05 H21979 AA211466 H13301 AA5ISSBA SABSIDIS ANESISSA (ANESISSA SA BUTTI (2 AB 1116 BE-64-550 BE-55076 I H75021 T15-05 H21979 AA21346 H13301 AA5ISSBA SABSIDIS ANESISSA (ANESISSA SA BUTTI (3 AB 1116 BE-64-550 BE-550 BE-55
60	121336 130018 121822	2/9548_1 18986_1 244391_1	AA35093 AW657317 AW727480 AB500755 AW28110 AW135512 X72761 T68573 A1738806 W16945 AW627759 E524697 AB56228 HE56397 F63052 A257031 AW655302 ALD42109 NS3052 Al611424 AL079362 AB69203 AB520610 E5236912 E550920 E547505 Al811611 Al611407 Al811452 W56437 A2524566 AL6353340 AW185056 A1500665 AB7652 AWA5715 A A452616 AW3607152 AM156224 AM607157 AW457776 AV23355
65	108309	111495_1	AAG99462 AI281973 AM22414 ABB4994 M583355 AM01550 AA389757 AI809976 AA442357 AA359393 AA43706 AA370301 AA42923 AW272056 AB66062 AI832944 AI038530 AA425107 AI014996 AI148349 AW237721 AW779755 AW137877 AI125263 AA400404 R28554 AA089816 AA0896971 AA089623 AA085608
70	107832 123523 123964 118475 104787 106596	genbank_AA02 genbank_AA60 genbank_C139 genbank_N668 genbank_AA02 304084_1	1473 AA021473 8588 AA608588 61 C13961
75	113947	genbank_W847 genbank_AA08	*68W84768

	108427 108439	genbank_AA076382 genbank_AA078986	AA076382 AA078986
	131353	231290 1 AW411259 H2355	55 AW015049 Al684275 AW015886 AW068953 AW014085 Al027260 R52686 AA918278 Al129462
		AA969360 N3486	9 AI948416 AA534205 AA702483 AA705292
5	101447	entrez M21305 M21305	
-	108931	genbank AA147186	AA147186
	108941	genbank AA148650	AA148650
	103138	entrez X65965 X65965	
	119174	genbank R71234 R71234	
10	119416	genbank_T97186 T97186	
	105985	genbank AA406610	AA406610
	100327	entrez D55640 D55640	•
	100027	0110.00 000010	

TABLE 3:

5 Pkey: Unique Ecs probeset identifier number Accession: ExAcces: Unique Ecs probeset identifier number Section: Unique Ecs probeset identifier number Section: Unique Ecs probeset identifier number Unique eque title Unique eque title

	Unigene Title: Unigene gene title					
10						
10	Pkey	Accessi	on	ExAccn	UniGene	UnigeneTitle
	100405	D86425		AW291587	Hs.82733	nidogen 2
	100420			D86983	Hs.118893	Melanoma associated gene
15	100481	HG1098-	HT1098	X70377	Hs.121489	cystatin D
	100484	HG1103-	HT1103	NM_005402	Hs.288757	y-ral simian leukemia viral oncogene hom
	100718	HG3342-	HT3519	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg
	100991	J03764		J03836	Hs.82085	serine (or cysteine) proteinase inhibito
		L06797		BE245301		chemokine (C-X-C motif), receptor 4 (fus
20		L15388		NM_005306		G protein-coupled receptor kinase 5
	101194			L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun
		L35545		D30857	Hs.82353	protein C receptor, endothelial (EPCR) calcitonin receptor-like
		L76380 M21305		NM_005798 M21305	HS.1521/5	ob:Human alpha satellite and satellite 3
25		M24736		AA296520	Hs.89546	selectin E (endothelial adhesion molecul
23	101543			M31166	Hs.2050	pentaxin-related gene, rapidly induced b
		M31551		Y00630	Hs.75716	serine (or cysteine) proteinase inhibito
		M32334			Hs.347326	intercellular adhesion molecule 2
		M61916		NM_00229	Hs.82124	laminin, beta 1
30		M68874		M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,
	101741				Hs.326198	transcription factor 4
		M92934		BE243845		connective tissue growth factor
		M94856			Hs.153179	fatty acid binding protein 5 (psoriasis- singed (Drosophlia)-like (sea urchin fas
35		U03057 U03877		AA301867	Hs.118400	EGF-containing fibulin-like extracellula
33		U18300		NM_00010		damage-specific DNA binding protein 2 (4
		U27109			1Hs.268107	multimerin
		U31384		AW161552		guanine nucleotide binding protein 11
	102303	U33053		U33053	Hs.2499	protein kinase C-like 1
40		U59423		U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr
		U70322			0Hs.168075	karyopherin (importin) beta 2
		U81607		NM_00510		A kinase (PRKA) anchor protein (gravin)
		U83463		AF000652 NM_00231		syndecan binding protein (syntentn) lysyl oxidase-like 2
45	102804	U89942 X04729		J03836	Hs.82085	serine (or cysteine) proteinase Inhibito
73		X06256			5Hs.149609	integrin, alpha 5 (fibronectin receptor,
	102915			X07820	Hs.2258	matrix metalloprotelnase 10 (stromelysin
		X54925		M13509	Hs.83169	matrix metalloproteinase 1 (Interstitial
	103037	X54936		BE018302	Hs.2894	placental growth factor, vascular endoth
50		X60957		NM_00542		tyrosine kinase with immunoglobulin and
		X67235			Hs.118651	hematopoietically expressed homeobox
		X67951			Hs.180909	peroxiredoxin 1 transmembrane protein (63kD), endoplasmi
		X69910		NM_00682 U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula
55	103260	X79981 Z18951		A1878826	Hs.74034	caveolin 1, caveolae protein, 22kD
55		AA1871	01	AA187101		hypothetical protein MGC10895
		N24990		Z44203	Hs.26418	ESTs
		R81003		AW630488		protease, serine, 23
		AA0253		AID39243	Hs.278585	ESTs
60	104786	AA0271	68	AA027167		KIAA0955 protein
	104850	AA0404	65	AL133035	Hs.8728 Hs.22575	hypothetical protein DKFZp434G171 B-cell CLL/lymphoma 6, member B (zinc fi
	104865	AA0451	36	T79340 AF065214		phospholipase A2, group IVC (cytosolic,
	104899	AA0540 AA0710	100		Hs.345588	desmoplakin (DPI, DPII)
65	104932	AA0859	18	Y12059	Hs.278675	bromodomain-containing 4
00		AA1874			Hs.21941	AD036 protein
		AA2279		AW388633	Hs.6682	solute carrier family 7, (cationic amino
	105330	AA2347	43		Hs.22120	ESTs
		AA2365		AW994032	Hs.8768	hypothetical protein FLJ10849
70	105729	AA2926	94	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds
		AA3982			Hs.194477	E3 ubiquitin ligase SMURF2 hypothetical protein FLJ11110
		AA4063		AR001972 AB033888	Hs.30822 Hs.8619	SRY (sex determining region Y)-box 18
	100008	AA4114 AA4122	NEC NEC	X64116	Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H
75		AA4239		H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, done H
,,,	10012					,

	106155 AA425309	AA425414 Hs.33287	nuclear factor I/B
	106302 AA435896	AA398859 Hs.18397	hypothetical protein FLJ23221
	106423 AA448238	AB020722 Hs.16714	Rho guanine exchange factor (GEF) 15
	106793 AA478778	H94997 Hs.16450	ESTs
5	107174 AA621714	BE122762 Hs.25338	ESTs
-	107216 D51069	D51069 Hs.211579	melanoma cell adhesion molecule
	107295 T34527	AA186629 Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:potyp
	107385 U97519	NM_005397 Hs. 16426	podocalyxin-like
	108756 AA127221	AA127221 Hs.117037	ESTs
10	108846 AA132983	AL117452 Hs.44155	DKFZP586G1517 protein
	108888 AA135606	AA135606 Hs.189384	gb:zl10a05.s1 Soares_pregnant_uterus_NbH
	109001 AA156125	Al056548 Hs.72116	hypothetical protein FLJ20992 similar to
	109166 AA179845	AA219691 Hs,73625	RAB6 interacting, kinesin-like (rabkines
	109456 AA232645	AW956580 Hs.42699	ESTs
15	109768 F10399	F06838 Hs.14763	ESTs
	110107 H16772	AW151660 Hs.31444	ESTs
	110906 N39584	AA035211 Hs.17404	ESTs
	110984 N52006	AW613287 Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp
	111006 N53375	BE387014 Hs.166146	Homer, neuronal immediate early gene, 3
20	111018 N54067	Al287912 Hs.3628	mitogen-activated protein kinase kinase
	111133 N64436	AW580939 Hs.97199	complement component C1q receptor
	111760 R26892	BE551929 Hs.268754	Homo sapiens cDNA FLJ11949 fis, clone HE
	113073 T33637	N39342 Hs.103042	microtubule-associated protein 1B
25	113195 T57112	H83265 Hs.8881	ESTs, Weakly similar to S41044 chromosom
23	113923 W80763	AW953484 Hs.3849	hypothetical protein FLJ22041 similar to
	114521 AA046808	AW139036 Hs.108957	40S ribosomal protein S27 isoform Homo sapiens mRNA full length insert cDN
	115061 AA253217	AI751438 Hs.41271 AI683069 Hs.175319	ESTs
	115096 AA255991	AI683069 Hs.175319 AA740907 Hs.88297	ESTs
30	115145 AA258138 115819 AA426573	AA486620 Hs.41135	endomucin-2
50	115947 AA443793	R47479 Hs.94761	KIAA1691 protein
	116314 AA490588	Al799104 Hs.178705	Homo sapiens cDNA FLJ11333 fis, clone PL
	116339 AA496257	AK000290 Hs.44033	dipeptidyi peptidase 8
	116430 AA609717	AK001531 Hs.66048	hypothetical protein FLJ10669
35	116589 D59570	Al557212 Hs.17132	ESTs, Moderately similar to 154374 gene
55	116733 F13787	AL157424 Hs.61289	synaptolanin 2
	117023 H88157	AW070211 Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
	117186 H98988	H98988 Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S
	117563 N34287	AF055634 Hs.44553	unc5 (C.elegans homolog) c
40	117997 N52090	N52090 Hs.47420	EST
	118475 N66845	N66845	qb:za46c11.s1 Soares fetal liver spleen
	118581 N68905	N68905	gb:za69b09.s1 Soares_fetal_lung_NbHL19W
	119073 R32894	BE245360 Hs.279477	ESTs
	119155 R61715	R61715 Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A
45	119174 R71234	R71234	gb:yi54c08.s1 Soares placenta Nb2HP Homo
	119221 R98105	C14322 Hs.250700	tryplase bela 1
	119416 T97186	T97186	gb:ye50h09.s1 Soares fetal liver spieen
	119866 W80814	AA496205 Hs.193700	Homo sapiens mRNA; cDNA DKFZp58610324 (f
50	121335 AA404418	AA404418	gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_ hypothetical protein FLJ22252 similar to
30	121381 AA405747 123160 AA488687	AW088642 Hs.97984 AA488687 Hs.284235	ESTs, Weakly similar to 138022 hypotheti
	123160 AA488687 123473 AA599143	AA599143	gb:ae52d04.s1 Stratagene lung carcinoma
	123523 AA608588	AA608588	gb:ae54e06.s1 Stratagene lung carcinoma
	123533 AA608751	AA608751	gb:ae56h07.s1 Stratagene lung carcinoma
55	123964 C13961	C13961	gb:C13961 Clontech human acrta polyA+mR
55	124006 D60302	AI147155 Hs.270016	ESTs
	124315 H94892	NM_005402Hs.288757	v-ral simian leukemia viral oncogene hom
	124659 N93521	AI680737 Hs.289068	Homo sapiens cDNA FLJ11918 fis, clone HE
	124669 N95477	Al571594 Hs.102943	hypothetical protein MGC12916
60	124847 R60044	W07701 Hs.304177	Homo sapiens done FLB8503 PRO2286 mRNA,
	124875 R70506	Al887664 Hs.285814	sprouty (Drosophila) homolog 4
	125091 T91518	T91518	gb:ye20f05.s1 Stratagene lung (937210) H
	125103 T95333	AA570056 Hs.122730	ESTs, Moderately similar to KIAA1215 pro
	125355 R45630	R60547 Hs.170098	KJAA0372 gene product
65	125565 R20839	R20840	gb:yg05c08.r1 Soares infant brain 1NIB H
	125590 R23858	R23858 Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,
	126511 Al024874	T92143 Hs.57958	EGF-TM7-latrophilin-related protein
	126563 W26247	AA516391 Hs.181368	U5 snRNP-specific protein (220 kD), orth
70	126649 AA856990	AA001860 Hs.279531	ESTs gb:UI-H-Bl3-ala-a-12-0-UI.s1 NCI_CGAP_Su
70	126872 AA136653 127402 AA358869	AW450979 AA358869 Hs.227949	SEC13 (S. cerevisiae)-like 1
		AA382523 Hs.105689	MSTP031 protein
		Al369384 Hs.292441	ESTs
	127759 Al369384 128062 AA379500	AA379621 Hs.105547	neural proliferation, differentiation an
75	128992 R49693	H04150 Hs.107708	ESTs
13	129046 AA195678	AB029290 Hs.108258	actin binding protein; macrophin (microf

129169 MO2027 NML, 00107978-16, 100225 Nat. 110002 Nat. 110002 Nml (100025) Nml (10		129188	M30257	NM 00107	BMe 100226	vascular cell adhesion molecule 1
128971 M10321 200828		129314				
129469						
29 12976 M69833 M69833 M1238 anakagamin (Y shomasome) through the company of the	_			AW410538	Hs.111779	secreted protein, acidic, cysteine-rich
13989 AA36270 A695581 ht s.13131 bycoomail of microbrondial protein L12 13969 G8971 A557722 ht s.17152 A55772 ht s.17152 h	5					amelogenin (Y chromosome)
19968 AAA43278 AAA5900						
13659 D58711 A557212 Hs 17132 ESTs, Moderably similar is 154374 gene 13502 A4053400				AF055581	Hs.13131	
10 10967 1784452						mitochondnal nibosomal protein L12
19868 AAST5902	10					
139877 AA370029 D81868						
1 31147 U85193						
15 1511/162 AA2561655 AB264144 https://doi.org/10.1001/163.1001/1						
131466 X831907	1.5					
131673 AAA046893 AAA04030 AAA40396 Ha.3069 ESTs ESTs ESTs ESTs ESTs AAA04699 AAA040396 Ha.3069 ESTs ESTs ESTs ESTs ESTs ESTs ESTs ESTs	15					
131647 AA/10480						
31756 D-45394						
131691 AA010163						
13/881 AA/10183	20	131859	M90657			transmembrane 4 superfamily member 1
12043 1/07887 BES8499 he.279853 Print proceedings-rysins, 2-cocyclaterals 5-dio processing services and processing service						upstream regulatory element binding prot
12169 U84573						
25 13293 MS0486 MM,003542Hs.48423 Hs historic family, number G 12445 A413296 MS048138 Hs.20115 MS04813						
12413 AA132989 ANSS 1333 H 2,20115 ANSS 1335 H 2,20115 ANSS 14,20115 ANSS	25					procollagen-lysine, 2-oxoglutarate 5-dio
124:69 AA114250 AB011034 In-46924 124:79 AA233125 126:79 AA233125 126:79 AA233125 126:79 AA233125 126:79 AA233125 127:79 AA233	23					
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1,3876 A,263035						
13887 AB002301 Hs.4985						
132736 J8801019 AW861835 H3.211978 Homos spelme cDNA-F. PLZ0537 fin, done L throw spelme cDNA-F. PLZ0537 fin, done N cDNA-F. PLZ0537 fi	30	132687	AB002301	AB002301	Hs.54985	KIAA0303 protein
1,37700 1961989						Sjogren syndrome antigen A2 (60kD, ribon
3383 AAS98702 BE263222 Ind. 6/101 Important protein MGC31773 Imp						
350 132969 N77-151 AF23452 Ha-5/832 migrals X 2004 AAA65153 AF1246 Ha-27955 cone HCX310 PROX310PT COST0PT COST						
13989 AA058133 AA112746 Ita.279605 Cohon H02310 PROCNICIPOT	35			AE203252		
133061 A8000984	22					
133147 1012763 AA02833 ha.68						
1 33161 AA253193 AW021103 Ha6831 hypothesial proline FLX3073 Aw32304 AA03545 Ha6805 Ha7182 hypothesial proline FLX3073 Aw32304 AA03545 Ha6805 Ha7182 hypothesial proline FLX3073 Ha7183 Aw3230 AA03545 Ha6805 Ha7182 hypothesial proline FLX3073 Ha7183						
13320 AA033172 AA03031 He8908 He.1905 Hom segiment CINN-F. IL2/3197 Ils, done R 150 13349 IL0036 BES1950 He.17001 BES17, Worldy similar to 85289 pricine 2 Section 15349 IL0036 BES1950 He.17001 He.17001 BES17, Worldy similar to 85289 pricine 2 Section 15349 Ilong 15349 I						
13383 AA/78713 A86928 Ha.71982 EST3, Weeldy similar to \$82598 profiner equippol translation inflation factor of the company of	40					hypothetical protein FLJ10210
133461 L/0396 BE519033 Ha.170001 133507 W50477 M.00105HE;Ar471 45 13550 W50476 A129930 ha.170691 135507 W50476 A129930 ha.170697 135507 W50476 W50476 A129930 ha.170697 135507 W50476						Homo sapiens cDNA: FLJ23197 fis, clone R
13517 X25947					Hs.71962	
45 13560 W80466 A129903 har74669 13367 W804539 AND						
13807 M34399 B2273749 F3205 F3	15					gap junction protein, alpha 1, 43kU (con
13814 D67029 MM_0030018+72222 MV 150027+18-7282	7.5				ris./4008	
13827 (19857) MM_002047Hr.57280 glycyl-RR4 symhetase (1985) MS (19				NM 00300	3Hs.75232	
138891 M82289 M82289 hs 21147573 higher matthis proteoplycan 2 perfection mythology of the protein mythology of the p				NM_00204	7Hs.75280	
139191 VMA/1/2					Hs.211573	heparan sulfate proteoglycan 2 (perlecan
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55 34088 D43338 Al37984 Ha.78025 314161 U9786 ASA4454 Ha.7846 3429 A4407569 AV908039 Ha.7193 Corplement Component C1q receptor 3429 A4407569 Ha.7193 AV90803 Ha.7293 Ha.7193 Ha.71				L34657		
134161 U97-188	55					
134299 AA467588 AV989039 h b 37199 Complement component Crit groeptor	55					
134418 M26982						complement component C1g receptor
60 13468 X14787 A756878 Ha57409 timorhozoporish 1 13468 X14787 A8756878 Ha57409 timorhozoporish 1 13468 X14787 A8756878 Ha57409 timorhozoporish 1 13468 A452200 Visios Ha57409 timorhozoporish 1 13469 Visios Ha57409 Visios Ha				X68264		
0.00000000000000000000000000000000000		134453	X70683	Al272141	Hs.83484	SRY (sex determining region Y)-box 4
180961 C15324	60					thrombospondin 1
18973 AA452000 V65996 Its-94/030 Horiz spiers mFNIX-CONA DRZ-2696E 1824 (f etc.) V6596 V65						
33349 D83174						
65 100114 000598 X022308 Hs.82982 thymrifyleide synthetise 1 100130 101429 Mx.000394Hs.10724 prefipielar imyreli protein 22 100143 011430 Hx.007485 hs.278441 hs.394 100186 014674 K7344 Hs.394 100280 10474 K7344 Hs.394 100280 1028175 Att.10715 Hs.13857 Hx.00740 10282 1028175 Att.10715 Hs.13857 Hx.00450 1028175 Att.10715 Hs.13857 Hx.00450 1028185 103858 Hs.13853 Hx.00450 1028185 K73858 Hs.13853 Hx.00450 1028185 Hs.13853 Hs.13853 Hx.00450 10282 Hs.13853 Hs.13853 Hx.00450 10282 Hs.13853 Hs.13853 Hx.00450 10282 Hs.13853 Hs.13853 Hx.00450 10282 Hx.00450 Hx.0045						
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100168 D14674				AU076465	Hs.278441	
70 000224 (28478 A.1.21516 Is.139817 thyroid flormone receptor interactor 12 indicages 2 100420 (268425 AV2918F8 Ha.8273 indicages 12 indicages 2 indicages 12 indicages						
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		HG2855-HT2995		Hs.180414	heat shock 70kD protein 2
	100676	HG3044-HT3742		Hs.287820	fibronectin 1
	100718		T81309	Hs.75424	inhibitor of DNA binding 1, dominant neg
5	100752			Hs.303649	insulin-like growth factor 2 (somatomedi small inducible cytokine A2 (monocyte ch
	100850		AA836472	Hs.297939	cathepsin B
	100991	J03764	J03836	Hs.82085	serine (or cysteine) proteinase inhibito
	101097	L06797	BE245301	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus
10	101110	L08246 L12711	Al439011 L12711	Hs.86386 Hs.89643	myeloid cell leukemia sequence 1 (BCL2-r
10	101156	L13977	AA340987	Hs.75693	transketolase (Wemicke-Korsakoff syndro protylcarboxypeptidase (angiotensinase C
	101168	L15388		3Hs.211569	G protein-coupled receptor kinase 5
	101184		NM_001674		activating transcription factor 3
1.5	101192		BE247295		solute carrier family 20 (phosphale tran
15	101317	L42176	L42176 NM_006732	Hs.8302	four and a half LIM domains 2 FBJ murine osteosarcoma viral oncogene h
	101345			5Hs.152175	calcitonin receptor-like
	101400	M15990	M15990	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene
20		M23254	BE410405	Hs.76288	calpain 2, (m/ll) large subunit
20	101485		AA296520	Hs.89546	selectin E (endothelial adhesion molecul
	101496 101505	M26576 M27396	X12784 AA307680	Hs.119129 Hs.75692	collagen, type IV, alpha 1 asparagine synthelase
	101543	M31166	M31166	Hs.2050	pentaxin-related gene, rapidly induced b
	101557	M31994		Hs.76392	aldehyde dehydrogenase 1 family, member
25	101560	M32334	AW958272		Intercellular adhesion molecule 2
	101587	M35878 M36429	AI752416 AF064853	Hs.77326 Hs.91299	Insulin-like growth factor binding prote
	101633	M57730	NM 004428		guanine nucleotide binding protein (G pr ephrin-A1
	101634	M57731	AV650262		GRO2 oncogene
30	101667	M60858	NM_005381		nucleolin
	101682	M62994	AF043045		filamin B, beta (actin-binding protein-2
	101714	M68874 M69043	M68874 M69043	Hs.211587 Hs.81328	phospholipase A2, group IVA (cylosolic, nuclear factor of kappa light polypeptid
	101741	M74719	NM_003199		transcription factor 4
35	101744	M75126	Al879352	Hs.118625	hexokinase 1
	101793	M84349	W01076	Hs.278573	CD59 antigen p18-20 (antigen identified
	101837	M92843 M92934	M92843 BE243845	Hs.343586	zinc finger protein homologous to Zfp-36
	101838 101840	M93056	AA236291	Hs.75511 Hs.183583	connective tissue growth factor serine (or cysteine) proteinase inhibito
40	101857	M94856	BE550723	Hs.153179	fatty acid binding protein 5 (psoriasis-
	101864		BE392588	Hs.75777	transgelin
	101931 101966	S76965 S81914	NM_006823 X96438	Hs.75209 Hs.76095	protein kinase (cAMP-dependent, catalyti immediate early response 3
	102012	U03057		Hs.118400	singed (Drosophila)-like (sea urchin fas
45	102013	U03100	BE616287	Hs.178452	catenin (cadherin-associated protein), a
	102024	U03877		Hs.76224	EGF-containing fibulin-like extracellula
	102059	U08021		Hs.76669	nicotinamide N-methyltransferase
	102121	U14391 U31384	NM_004998 AW161552		myosin IE quanine nucleotide binding protein 11
50	102300	U32944		Hs.5120	dynein, cytoplasmic, light polypeptide
	102378	U40369		Hs.28491	spermidine/spermine N1-acetyltransferase
	102395	U41767		Hs.92208	a disintegrin and metalloproteinase doma
	102460 102491	U48959 U51010	U48959 U51010	Hs.211582	myosin, light polypeptide kinase gb:Human nicotinamide N-methyltransferas
55	102499	U51478		Hs.76941	ATPase, Na+/K+ transporting, beta 3 poly
	102523	U53445	U53445	Hs.15432	downregulated in ovarian cancer 1
	102560	U59289	R97457	Hs.63984	cadherin 13, H-cadherin (heart)
		U59423	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr
60	102589 102600	U62015 U63825	AU076728 AI964144	Hs.8867 Hs.66713	cysteine-rich, angiogenic inducer, 61 hepatitis delta antigen-interacting prot
00				Hs.6721	lysosomal
	102687	U73379	NM_007019	Hs.93002	ubiquitin carrier protein E2-C
	102693		AA532780		eukaryotic translation initiation factor
65	102709		AA122237		microsomal glutathione S-transferase 2
03	102759 102804		NM_005100 NM_002318		A kinase (PRKA) anchor protein (gravin) lysyl oxidase-iike 2
	102882		A1767736	Hs.290070	gelsolin (amyloidosis, Finnish type)
	102907	X06985	BE409861	Hs.202833	heme oxygenase (decycling) 1
70			X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
70	102927 102960	X12876 X15729	BE512730 AI904738	Hs.65114 Hs.76053	keratin 18 DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
	103011	X52541		Hs.326035	early growth response 1
	103020	X53416	X53416	Hs.195464	filamin A, alpha (actin-binding protein-
75	103029		AW800726		GRO1 oncogene (melanoma growth stimulati
75	103036	X54925 X57206	M13509 Y18024	Hs.83169 Hs.78877	matrix metalloproteinase 1 (interstitial inositol 1,4,5-trisphosphate 3-kinase B
	103000	Au 200	10024	110.10011	почно тутичнарницанняю очинава в

	103080 X59798	AU077231 Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos
	103095 X60957	NM_005424Hs.78824	tyrosine kinase with immunoglobulin and
	103138 X65965	X65965	gb:H.sapiens SOD-2 gene for manganese su
-	103176 X69111	AL021154 Hs.76884	inhibitor of DNA binding 3, dominant neg
5	103195 X70940	AA351647 Hs.2642	eukaryotic translation elongation factor
	103347 X87838	AU077309 Hs.171271	catenin (cadherin-associated protein), b
	103371 X91247	X91247 Hs.13046	thioredoxin reductase 1
	103432 X97748	X97748	gb:H.sapiens PTX3 gene promotor region.
	103471 Y00815	Y00815 Hs.75216	protein tyrosine phosphatase, receptor t
10			
10	103967 AA303711	AL120051 Hs.144700	ephrin-B1
	104447 L44538	AW204145 Hs.158044	ESTs
	104764 AA025351	AI039243 Hs.278585	ESTs
	104783 AA027050	AA533513 Hs.93659	protein disulfide Isomerase related prot
	104798 AA029462	AW952619 Hs.17235	Homo sapiens clone TCCCIA00176 mRNA sequ
1.5	104790 MMUZ940Z		notific sapiens clotte i Occido i 70 timina sequ
15	104865 AA045136	T79340 Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi
	104877 AA047437	Al138635 Hs.22968	Homo saplens clone IMAGE:451939, mRNA se
	104894 AA054087	AF065214 Hs.18858	phospholipase A2, group IVC (cytosolic,
	104952 AA071089	AW076098 Hs.345588	desmoplakin (DPI, DPII)
	105113 AA156450	AB037816 Hs.8982	Homo sapiens, clone IMAGE:3506202, mRNA,
20			
20	105178 AA187490	AA313825 Hs.21941	AD036 protein
	105196 AA195031	W84893 Hs.9305	angiotensIn receptor-like 1
	105215 AA205724	AA205759 Hs.10119	hypothetical protein FLJ14957
	105263 AA227926	AW388633 Hs.6682	solute carrier family 7, (cationic amino
	105271 AA227986	AA807881 Hs.25329	ESTs
25		AW338625 Hs.22120	ESTs
23	105330 AA234743		
	105461 AA253216	BE539071 Hs.69388	hypothetical protein FLJ20505
	105492 AA256210	Al805717 Hs.289112	CGI-43 protein
	105493 AA256268	AL047586 Hs.10283	RNA binding motif protein 8B
	105594 AA279397	AB024334 Hs.25001	tyrosine 3-monoxygenase/tryptophan 5-mo
20			
30	105727 AA292379	AL135159 Hs.20340	KIAA1002 protein
	105732 AA292717	AW504170 Hs.274344	hypothetical protein MGC12942
	105787 AA346551	AW370946 Hs.23457	ESTs
	105882 AA400292	W46802 Hs.81988	disabled (Drosophila) homolog 2 (mitogen
	105936 AA404338	Al678765 Hs.21812	ESTs
35	106031 AA412284	X64116 Hs.171844	Homo sapiens cDNA: FLJ22296 fis, clone H
22			
	108124 AA423987	H93366 Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H
	106222 AA428594	AA356392 Hs.21321	Homo sapiens clone FLE9213 PRO2474 mRNA
	106241 AA430108	BE019681 Hs.6019	Homo saplens cDNA: FLJ21288 fis, clone C
	106283 AA431462	W21493 Hs.28329	hypothetical protein FLJ14005
40	106264 AA431470	AL046859 Hs.3407	protein kinase (cAMP-dependent, catalyti
40		ALU40035 NS.3407	DUCEN COLO 400 400 400 400 400 400 400 400 400 40
	106366 AA443756	AA186715 Hs.336429	RIKEN cDNA 9130422N19 gene
	108454 AA449479	NM_014038Hs.5216	HSPC028 protein
	106634 AA459916	W25491 Hs.288909	hypothetical protein FLJ22471
	106724 AA465226	N48670 Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H
45	106793 AA478778	H94997 Hs.16450	ESTs
45			Homo sapiens clone 25012 mRNA sequence
	106799 AA479037		
	106842 AA482597	AF124251 Hs.26054	novel SH2-containing protein 3
	106868 AA487561	BE185536 Hs.301183	molecule possessing ankyrin repeats indu
	108890 AA489245	AA489245 Hs.88500	mitogen-activated protein kinase 8 inter
50	106961 AA504110	AW243614 Hs.18063	Homo saplens cDNA FLJ10768 fis, clone NT
50	106974 AA520989	AI817130 Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL
	107030 AA599434	AL117424 Hs.25035	chloride Intracellular channel 4
	107061 AA608649	BE147611 Hs.6354	stromal cell derived factor receptor 1
	107086 AA609519	NM_012331Hs.26458	methionine sulfoxide reductase A
55	107216 D51069	D51069 Hs.211579	melanoma cell adhesion molecule
00	107385 U97519	NM 005397Hs.16426	podocalyxin-like
	107444 W28391	W28391 Hs.343258	proliferation-associated 2G4, 38kD
	107985 AA035638	T40064 Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fi
	108507 AA083514	Al554545 Hs.68301	ESTs
60	108695 AA121315	AB029000 Hs.70823	KIAA1077 protein
00	108931 AA147186	AA147186	gb:zo38d01.s1 Stratagene endothelial cel
	109001 AA156125	AI056548 Hs.72116	hypothetical prolein FLJ20992 similar to
	109195 AA188932	AF047033 Hs.132904	solute carrier family 4, sodium bicarbon
	109390 AA219653	AW007485 Hs.87125	EH-domain containing 3
65	109456 AA232645	AW956580 Hs.42699	ESTs
00	109737 F10078	AA055415 Hs.13233	ESTs, Moderately similar to A47582 B-cel
		AW001579 Hs.9645	Homo sapiens mRNA for KIAA1741 protein.
	110411 H48032		
	110660 H82117	AA782114 Hs.28043	ESTs
	110906 N39584	AA035211 Hs.17404	ESTs
70	111018 N54067	Al287912 Hs.3628	mitogen-activated protein kinase kinase
, 0		AA300067 Hs.33032	hypothetical protein DKFZp434N185
	111356 N90933	BE301871 Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-
	111378 N93764	AW160993 Hs.326292	hypothetical gene DKFZp434A1114
	111741 R26124	AB020653 Hs.24024	KIAA0846 protein
75	111769 R27957	AW629414 Hs.24230	ESTs
, ,	440240 DEE470	AW083384 Hs.11067	ESTs, Highly similar to T46395 hypotheti
	112318 R55470	AWU83384 RS.1106/	CO15, FIGURY SILLING IO 140000 HYPOTHER

	112951 T16550	AA307634 Hs.6650	representation and the AFD formers become
	113057 T26674	AW194301 Hs.339283	vacuolar protein sorting 45B (yeast homo Human DNA sequence from done RP1-187J11
	113195 T57112	H83265 Hs.8881	ESTs, Weakly similar to S41044 chromosom
	113490 T88700	BE178110 Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT
5	113542 T90527	H43374 Hs.7890	Homo sapiens mRNA for KIAA1671 protein,
	113803 W42789	AW880709 Hs.283683	chromosome 8 open reading frame 4
	113847 W60002	NM_005032Hs.4114	plastin 3 (T Isoform)
	113910 W78175	AA113262 Hs.17901	Homo sapiens, done IMAGE:3937015, mRNA,
	113947 W84768	W84768	gb:zh53d03.s1 Soares_fetal_liver_spleen_
10	114047 W94427	AL035858 Hs.3807	FXYD domain-containing ion transport reg
	115061 AA253217	Al751438 Hs.41271	Homo sapiens mRNA full length insert cDN
	115819 AA426573	AA486620 Hs.41135	endomucin-2
	115870 AA432374	NM_005985Hs.48029	snail 1 (drosophila homolog), zinc finge
	115964 AA446622	AA987568 Hs.74313	KIAA1265 protein
15	116228 AA478771	Al767947 Hs.50841	ESTs
	116264 AA482594	D51174 Hs.272239	lysosomal
	116314 AA490588	AI799104 Hs.178705	Homo sapiens cDNA FLJ11333 fis, clone PL
	116589 D59570	Al557212 Hs.17132	ESTs, Moderately similar to 154374 gene
20	117023 H88157	AW070211 Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (f
20	117112 H94648	AW969999 Hs.293658	ESTs
	117156 H97538	W73853	ESTs
	117176 H98670 117280 N22107	H45100 Hs.49753	uveal autoantigen with coiled coil domai
		M18217 Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C
25	119559 W38197 119866 W80814	W38197 AA496205 Hs.193700	Empirically selected from AFFX single pr Homo sapiens mRNA; cDNA DKFZp58610324 (f
25	120655 AA287347	AA305599 Hs.238205	hypothetical protein PRO2013
	121314 AA402799	W07343 Hs.182538	phospholipid scramblase 4
	121335 AA404418	AA404418	gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_
	121822 AA425107	AI743860	metallothionein 1E (functional)
30	121835 AA425435	AB033030 Hs.300670	KIAA1204 protein
	122331 AA442872	AL133437 Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H
	122577 AA452860	AA829725 Hs.334437	hypothetical protein MGC4248
	123160 AA488687	AA488687 Hs.284235	ESTs, Weakly similar to 138022 hypotheti
	123486 AA599674	BE019072 Hs.334802	Homo sapiens cDNA FLJ14680 fis, clone NT
35	124059 F13673	BE387335 Hs.283713	ESTs, Weakly similar to S64054 hypotheti
	124339 H99093	H99093 Hs.343411	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
	124358 N22495	AW070211 Hs.102415	Homo saplens mRNA; cDNA DKFZp586N0121 (f
	124364 N23031	AF265555 Hs.250646	baculoviral IAP repeat-containing 6
40	124726 R15740	NM_003654Hs.104576 BE410405 Hs.76288	carbohydrate (keratan sulfate Gal-6) sul
40	124763 R39610 125167 W45560	AL137540 Hs.102541	calpain 2, (m/li) large subunit netrin 4
	125304 Z39833	AL359573 Hs.124940	GTP-binding protein
	125307 Z40583	AW580945 Hs.330466	ESTs
	125329 AA825437	AA825437 Hs.58875	ESTs
45			
	125598 R66613	T40064 Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr
70	125596 R66613 125609 AA868063	T40064 Hs.71968 AA868063 Hs.104576	Homo sapiens mRNA; cDNA DKFZp564F053 (fr carbohydrate (keratan sulfate Gal-6) sul
40	125609 AA868063 418245 AA128075	AA868063 Hs.104576 AA088767 Hs.83883	carbohydrate (keratan sulfate Gal-6) sul transmembrane, prostate androgen induced
70	125609 AA868063 418245 AA128075 127435 N66570	AA868063 Hs.104576 AA088767 Hs.83883 X69086 Hs.286161	carbohydrate (keratan sulfate Gal-6) sul transmembrane, prostate androgen induced Homo sapiens cDNA FLJ13613 fis, clone PL
	125609 AA868063 418245 AA128075 127435 N66570 127566 Al051390	AA868063 Hs.104576 AA088767 Hs.83883 X69086 Hs.286161 Al051390 Hs.116731	carbohydrate (keratan sulfate Gal-6) sul transmembrane, prostate androgen induced Homo sapiens cDNA FLJ13813 fis, clone PL ESTs
50	125609 AA868063 418245 AA128075 127435 N66570 127566 Al051390 127619 AA627122	AA868063 Hs.104576 AA088767 Hs.83883 X69086 Hs.286161 AI051390 Hs.116731 AA627122 Hs.163787	carbohydrate (keratan sulfate Gal-6) sul transmembrane, prostate androgen induosd Homo sapiens cDNA FLJ13613 fis, clone PL ESTs ESTs
	125609 AA868063 418245 AA128075 127435 N66570 127566 Al051390 127619 AA627122 128453 X02761	AA868063 Hs.104576 AA088767 Hs.83883 X69036 Hs.286161 Al051390 Hs.2161731 AA827122 Hs.163787 X02761 Hs.287820	carbohydrate (keratan sulfate Gal-6) sul transmembrane, prostate androgen induced Homo sapiens oDNA FL/13613 fis, clone PL ESTs ESTs fibronecin 1
	125809 AA868063 418245 AA128075 127435 N96570 127566 AI051390 127619 AA627122 128453 X02761 128495 AF010193	AA868063 Hs.104576 AA088767 Hs.83863 X69086 Hs.286161 AI051390 Hs.116731 AA627122 Hs.163787 X02761 Hs.287820 NM_005904Hs.100602	carbohydrate (keratan sulfate Gal-6) sul transmembrane, prostate androgen induoed Homo sapiens cDNA FL/13613 fis, clone PL EST3 EST5 fibroneclin 1 MAD (mothers against decapentaplegic, Dr
	125609 AA868063 418245 AA128075 127435 N66570 127656 AI051390 127619 AA627122 128453 X02761 128495 AF010193 128515 AA149044	AA868063 Hs.104576 AA083767 Hs.83863 X69086 Hs.286161 A051390 Hs.116731 AA827122 Hs.163787 X02761 Hs.287820 NM_005904Hs.100602 BE395085 Hs.10086	carbofydrate (keraten sulfale Gal-G) sul transmembrane, prostate androgen induced Homo saplans cDNA FL.113613 fis, clone PL ESTs fibronedin 1 MAD (mothers against decapentaplegic, Dr type I transmembrane protein Fn14
50	125609 AA868063 418245 AA128075 12735 N66570 127568 Al051390 127619 AA627122 128453 X02761 128495 AF010193 128515 AA149044 128580 U82108	AA888083 Hs.104576 AA088767 Hs.83883 K99086 Hs.286161 AU51390 Hs.116731 AA627122 Hs.163787 X02761 Hs.287820 NM_005904Hs.100602 BE395085 Hs.10086 U82108 Hs.101813	carbotydrate (keraten sulfate Gal-G) sul transmerbrane, prostale androgen induced Homo sapiens cDNA FLJ13513 fis, clone PL EST3 EST3 fibronedin 1 MAD (mothers against decapentaplegic, Dr type I transmerbrane protein Fn14 southe carter family 6 (sodium/ydrogen
	125609 AA868063 418245 AA128075 127435 N66570 127566 AI051390 127619 AA627122 128453 X02761 128495 AF010193 128515 AA149044 128580 U82108 128623 D76676	AA868063 Hs.104576 AA083767 Hs.83863 X69086 Hs.286161 AI051390 Hs.116731 AA827122 Hs.163787 X02761 Hs.287820 NM_005904Hs.100802 BE395065 Hs.10086 U82108 Hs.101810 BE076608 Hs.105808	carbohydrate (keratan sulfala Gal-6) sul transmenhrane, postale androgan induced Homo sapiens cDNA FLJ13513 fis, olone PL ESTS ESTS ESTS fibroneciin 1 MAD (molbera against decapenlaplogic, Dr type I transmentrane probein Fn14 solute carrier family 9 (sodium/hydrogen CTL2 gene
50	125809 AA660063 418245 AA128075 127455 N66570 127566 N051390 127619 AA627122 128453 X02761 128495 AF010193 128515 AA149044 128580 U82108 128623 D76676 128622 L35240	AA86093 Hs.104576 AA083767 Hs.83883 X59096 Hs.289161 AI051390 Hs.116731 AA827122 Hs.183787 X02761 Hs.287820 NM_005904Hs.100802 BE395065 Hs.10086 U82108 Hs.101813 BE076608 Hs.105506 Z28913 Hs.102546	carbohydrate (Jersten sulfale Cal-6) sul transmerbrane, postale androgen induced Homo septem cDNA FLJ13913 fis, olone PL ESTs ESTs ESTs (ST)
50	12:5609 A4868083 418:245 A4128075 127435 N96570 127568 A1051390 127519 A4827122 128453 X02761 128:495 A7010193 128:515 A4149044 128:580 U82108 128:623 D76576 128:624 L35:240 128:659 A4589737	AA86003 Hs.104576 AA983767 Hs.25863 X69086 Hs.286161 Al051390 Hs.116731 AA827122 Hs.163787 X02761 Hs.287820 MM_005904Hs.10080 U82108 Hs.101813 BE076508 Hs.105500 Z28913 Hs.102946 W28493 Hs.80014	carbohydrate (Jeratan sullate Gal-6) sul transmentrane, prostate androgen induced Homo sapiens cDNA FLJ13513 fis, clone PL ESTS ESTS ESTS Industrial sullation of the Compania of the Homoleura spaintst decapentaplogic, Dr type I transmentrane protein Fn14 soute carrier family 6 (sodiumflydrogen CTL2 gene enigma (LIM domain protein) early sullation of the enigma (LIM domain protein) early solation of the set shock 7000 protein 8
50	125909 AA68003 A162405 A4128075 127435 Ne6570 127566 A1051390 127569 A22712 128453 X02761 128455 AF010193 128515 A4149044 128580 U82108 128622 D76576 128642 L35240 128696 A659737 128903 R59417	AA86093 Hs.104576 AA08776 Hs.83883 X69096 Hs.268161 Al051390 Hs.116731 AA827122 Hs.163787 X02761 Hs.287820 NM_005904Hs.100802 BE395095 Hs.10596 U82108 Hs.101813 BE076509 Hs.10590 Z28913 Hs.102948 W28493 Hs.180414 AW150717 Hs.345728	catchydrate (leretan sulfae Gal-9) sul transmerbrine, positika androgen induzed Horno sepiers CDNA FLJ13913 fis, clone PL ESTs ESTs ESTs Significant supplies CDNA FLJ13913 fis, clone PL ESTs MAD (modellars supplies for MAD (modellars supplies for CDNA FLD Supplies CDNA FLD Supplies Supplie
50 55	125909 AA868083 418245 A4129075 127435 N66570 127565 A1061390 127619 AA827112 128495 A701193 128515 A4149044 128622 D76676 128642 L55240 128695 AA586737 128903 R59417 128914 AA228637	AA88083 Hs.28813 X69086 Hs.28813 X69086 Hs.288161 AUS1390 Hs.116731 X02761 Hs.287820 X02761 Hs.287820 X02761 Hs.287820 X02761 Hs.10824 X02108 Hs.10830 BE17808 Hs.10830 BE17808 Hs.10840 X02463 Hs.10840 X045747 Hs.345728 AVIST6717 Hs.345728	carbohydrate (jeraten sulfas Gal-6) sul transmerbnen, politike androgen indusid Horn septins CDMR FL17813 in, clone PL ESTS STA THE STAN STAN STAN STAN STAN STAN STAN STAN
50	125909 AA68003 A418245 A4128075 127435 N66570 127565 A4061390 127565 A4061390 127565 A4061390 128515 A4149044 128580 U32108 128623 D76576 128642 L35240 128593 R69417 128914 A222827 128913 R69417 128914 A222827 129987 W76955	AA88003 Hs.104576 AA088707 Hs.3683 X99086 Hs.269161 AI051390 Hs.16271 AA627122 Hs.162737 X02761 Hs.26782 X02761 Hs.26782 X02761 Hs.26782 X02761 Hs.10361 BEJ77600 Hs.10360 BEJ76606 Hs.10360 BEJ76606 Hs.10360 W2493 Hs.105404 W2493 Hs.105478 AW150771 Hs.345728 AW167741 Hs.107125 AW167741 Hs.107125	carchydrate (leretan suffee Gal-9) sul transmerbrine, positive and consistent of the ESTs ESTs ESTs ESTs ESTs Control of the ESTs ESTS
50 55	125909 AA868083 418245 A4129075 127435 N96570 127566 A40651390 127619 AA627112 128463 X02761 128469 X7010193 128515 A4149044 128580 U32108 128623 D76576 128649 X459047 128507 R69477 128507 R69477 128507 R69477 128507 R69477 129507 R79355 R69477 129507 R79355 R69477 129507 R79355 R69477 129518 A4598737 129507 R79355 R69477 R6947 R69477 R6947 R69477 R6	AA88003 Hs.104576 AA088707 Hs.3883 X89086 Hs.288161 AN051309 Hs.288161 AA827122 Hs.163787 AO27761 Hs.287820 NM_005904Hs.100602 BES39605 Hs.10086 U82108 Hs.101813 BEO75608 Hs.10560 Z28913 Hs.10540 Z28913 Hs.10540 AV85747 Hs.345738 AV857491 Hs.107125 AI448027 Hs.108507	cabchydrate (lerethen sulfee Gel-9) sul transmerbrinen, positival androgen indused Homo sepires CDMR FLJ13513 fis, clone PL EST19 EST19 Extransical 1 MoD (multima saginat decapentaglogic, CD typo: I transmerbrine protein Fnr14 substac carefar family 6 (odustrihydrogen CTL2 gene engines (LM domain protein) heat stock 7000 protein 8 STC1 flatback 9001 Frailback and careful STC1 flatback 9001 Frailback 1001 protein STC1 flatback 9001 Frailback 1001 protein STC1 flatback 9001 Frailback 1001 protein hypothetical protein PP1057
50 55	125909 AA68003 A418245 A4128075 127435 N66570 127565 A4061390 127565 A4061390 127565 A4061390 128515 A4149044 128580 U32108 128623 D76576 128642 L35240 128593 R69417 128914 A222827 128913 R69417 128914 A222827 129987 W76955	AA88003 Hs.104576 AA088707 Hs.3683 X99086 Hs.269161 AI051390 Hs.16271 AA627122 Hs.162737 X02761 Hs.26782 X02761 Hs.26782 X02761 Hs.26782 X02761 Hs.10361 BEJ77600 Hs.10360 BEJ76606 Hs.10360 BEJ76606 Hs.10360 W2493 Hs.105404 W2493 Hs.105478 AW150771 Hs.345728 AW167741 Hs.107125 AW167741 Hs.107125	carchydrate (leretan suffee Gal-9) sul transmerbrine, positive and consistent of the ESTs ESTs ESTs ESTs ESTs Control of the ESTs ESTS
50 55 60	125099 AA669083 412075 412075 412075 412075 127458 N66570 127568 Al01999 127519 AA627122 128495 XU2751 128495 XU2751 128508 R25108 128652 D78576 128698 AA568737 128914 AA2232637 129914 AA223263 129918 M30257 12918 M30257 12918 M30257 12918 M30257 129268 M86843	AA88003 Hs.104576 AA088707 Hs.3683 X99086 Hs.268161 AN51390 Hs.268161 AA627122 Hs.163787 AV07761 Hs.27820 NM .005904Hs.100572 BE395065 Hs.10087 BE395065 Hs.10087 BE395065 Hs.10087 BE395065 Hs.10087 AV16077 Hs.30172 AV16074 Hs.30172 AV16074 Hs.30172 AV16074 Hs.30172 AV16074 Hs.30172 BE22444 Hs.10657 NM .001078Hs.301256	carchydrate (leretan sulfae Gal-9) sul transmerbrine, positiva androgen induced Horno sepies CDNA FLH13913 fis, clone PL ESTs ESTs ESTs florenedin 1 MAD (mothers against decapentaplegic), Dr type I transmerbrinezee prolain Fm14 souths carrier family 5 (codium/pdrogen expires LUM demand protein) best shock 7000 protein 8 STA1 induced STA1 inibility 3 pissmelarma vesicle association of prophetical protein protein STA1 induced STA1 inibility 3 pissmelarma vesicle association of prophetical protein PP1057 vascular call adhresion milectate III shibility of RNA billing 2, dominant nog
50 55	125090 AA660083 142459 AA129075 127458 Ne6570 127658 Ne6570 127659 A6151390 127619 AA627122 128463 XUZ761 128463 XUZ761 128458 AF010193 128515 AA149044 128580 U82108 128623 D76676 128692 AA568737 128693 A858737 128903 R69417 128914 A822837 129026 M68843 129268 M68843	AA869032 Hs.104575 AA083707 Hs.3683 X99086 Hs.289618 AN051390 Hs.105731 AA627122 Hs.163773 AA627124 Hs.105712 BEZ9616 Hs.105912 BEZ9616 Hs.105912 AV86745 Hs.105712 AV86746 Hs.105712 AV86746 Hs.105712 BEZ2646 Hs.105712 BEZ2646 Hs.105712 BEZ2646 Hs.105712 BEZ2647 Hs.105713 BEZ2647 Hs.10575 BEZ2647 Hs.10575 AA503622 Hs.110576	carbohydrate (lerethen sulfae Gal-6) sulf transmerbrinen, posibile androgen induced Homo sepiera CDNR FL178513 fis, clone PL EST18 E
50 55 60	126969 AA68063 AA68063 12745 N62570 12745 AA627142 12845 AZC761 128465 AZC761 1	AA88808 3: h.10475 AA88767 ls.8385 X89085 ls.289161 AA82712 ls.18576 AA82712 ls.18576 AA82712 ls.18576 MIL (2017) ls.18576 MIL (carbohydrate (jeraten sulfas Gal-6) sul transmerbrine, positiva androgen indused Homo septins CDMR FLJ15313 in, clone PL EST3 EST3 MAD (mabbra saginat decapentaplegic, Dr typo I transmerbrane protein fir14 subbac carrier family 6 ordinarlystogen CTL2 gene suggest CLM domain protein) sergina CLM domain protein) sergina CLM domain protein STAT hacked STAT inhibitor STAT hacked STAT inhibitor State of the substantial of the succusar of an affection molecule 1 inhibitor of DAN binding 2, domainant tog inhall postflip y benefit securited protein, scilic, options of matterial protein protein securited protein, scilic, option of security protein, scilic, option of security protein, scilic, option of membrane protein scilic, option of membrining advanced and postflip y protein, scilic, option of membrining advanced and postflip y protein, scilic, option of membrining advanced and postflip y protein, scilic, option of membrining advanced protein scilic postflip y protein protein protein scilic postflip y protein scilic y prot
50 55 60	12989 AA65903 AA65903 T21745 N96570 N	AA88802 H-10477 6 AA8877 H-8-8583 X8908 H-289161 AA87712 H-8-8787 AA87712 H-8-8787 AA87712 H-8-8787 AA87712 H-8-8787 AA87712 H-8-8787 AA87712 H-8-8787 AA87814 H-8-8787 AA87814 H-8-8787 AA87874 H-8-8787	catchydrate (leretan sulfae Gal-9) sul transmerbrane, positiva androgen induced Horno sepiers CDNR FLJ13913 fis, clone PL ESTs ESTs ESTs Significant spiral decapentasilogic, Dr MOD (Instrumenturae protein Fin 4; south curied from 19/9 (codum/hydrogen CTLZ ogen capings CLM domain protein) heat shock 7000 protein 6 STAT Induced STAT (Finibler 3 plesmeterma vesicle associated protein hydrogen care of the company of the properties of the company of the similar CDNR object, dominant nor dual specificity proceptuals of scarcifor prioria, scaling cylindrical scarcifor prioria scarcifor prioria scarcif
50 55 60	12989 AASSONS (1294) 11245 NGS77 12745 NGS	AA88608 H-104776 AA88777 H-8.5858 X60068 H-269618 AA08777 H-8.5858 X60068 H-269618 AA07320 H-10731 AA07727 H-10731 BES7050 H-10961 BES7050 H-10962 BES2067 H-10961 BES7050 H-10961 BES7050 H-10961 BES7050 H-10962 BES2067 H-10961 BES7050 H-10961 BES7050 H-10961 BES7050 H-10962 BES7050 H-10961 BES7050 H-1	carbohydrate (jeraten sufles Gal-9) sul transmerbrine, positiva androgen inducid Homo sepires CDMR FL173513 fis, clone PL ESTs School (1998) and the substitution of the ESTs Extrement of the Modern superior of the Modern substitution of the School (1998) and Modern substitution of Home School (1998) and Home School (1998) and H
50 55 60 65	120808 AA680603 AA680	AA58608 H-10475 AA0877 H-8-5883 X6008 H-10276 AA0877 H-8-5883 X6008 H-2026 H-20276 H-20276 AA0877 H-20276 H-20	catchydrate (jersten sulfas Gal-9) sul transmerbrine, positiva androgen inducid Homo septims CDNN FLJ15315 in, clone PL ESS18 5575 and CDNN FLJ15315 in, clone PL ESS18 5576 and CDNN FLJ15315 in, clone PL ESS18 5576 and CDNN FLJ15315 in
50 55 60	120808 AASS8030 AASS8031 AASS80330	AASSE03 H-10475 AA0877 H-8-5863 X69085 H-10476 AA08777 H-8-5863 X69085 H-269161 AA08772 H-8-5863 X69085 H-269161 AA0872 H-8-5863 H-269161 AA0872 H-8-5863 H-10985 H-10	carbohydrate (lerethen sulfae Gal-6) sulf transmerbrinen, posible androgen induced Homo sepiers CDNR FLJ13513 fis, done PL ES114 ES114 ES114 Extraordia 1 and Estate (Legislation of Legislation of Legis
50 55 60 65	12988 AASS043 (1992) 12745 NBS570 NBS570 12745 NBS570 127	AA58508 3: h10475 AA08777	carbohydrate (jeraten sulfas Gal-9) sul transmerbrine, positiva androgen inducid Homo septins cDNN FLJ1513 in, clone PL EST3 EST3 MAD (mothers aspired decapentaplegic, Dr typo I transmerbrane probein Fri 14 subsize carter lamily 4 (odurahydrogen CTL2 gene CTL2 gene
50 55 60 65	12080 AA68003 AA68003 TI 12745 NG57 NG57 NG57 NG57 NG57 NG57 NG57 NG5	AA88608 H-104776 AA08777 H-8-5868 X69085 H-269161 AA05739 H-10476 AA05739 H-10476 AA05739 H-10476 AA05739 H-10476 AA05739 H-10476 AA05739 H-10476 BES7085 H-10486 BES7085 H-10	carbohydrate (jeretne suffee Gel-9) sul transmerbrine, positiva androgen induzed Homo sepires CDMR FLJ13513 fis, clone PL EST18 EST1
50 55 60 65	12989 AASS003 (2014) 16245 AASS013 (2014) 16245 AASS013 (2014) 16245 ASS013 (2014) 16245 ASS013 (2014) 16245 ASS013 (2014) 16245 ASS013 (2014) 16245 AASS013 (2014) 16245 AASS013 (2014) 16245 AASS013 (2014) 16245 ASS013 (2014)	AA88608 H-10475 AA88767 H-8.5883 X60688 H-10475 AA88767 H-8.5883 X60688 H-26861 H-2686	carbohydrate (jeraten sulfas Gal-6) sul transmerbrine, positiva androgen indused Homo sepins COMA FLJ15313 in, clone PL EST3 ST3 MDD (malbra saginat decapentaptiegic, Dr hybo I transmerbrine protein Fr14 substac carlier family 6 odocarrylargoen CTL2 gene sugar CLM domain protein) sergina CLM domain protein) sergina CLM domain protein STAT indused STAT inhibitor STAT indused STAT inhibitor STAT indused STAT inhibitor successful gradient protein successful gradient protein successful gradient successful gradient successful successful gradient successful gradient successf
50 55 60 65 70	129898 AABSP083 (1978) 127458 NBS5710 (1978) 127458 NBS5710 (1978) 127458 NBS5710 (1978) 127458 NBS5710 (1978) 127458 AABSP182 (1978) 127615 AABSP182 (1978) 127	AA88608 H-104776 AA08777 H-8-5868 X69085 H-269161 AA05739 H-10476 AA05739 H-10476 AA05739 H-10476 AA05739 H-10476 AA05739 H-10476 AA05739 H-10476 BES7085 H-10486 BES7085 H-10	carbohydrate (jersten sulfas 6.45) sulf transmerbrine, positiva androgen induced Homo septies CDNN FLJ15315 is, clone PL EST3 100 molecular and supplies CDNN FLJ15315 is, clone PL EST3 100 molecular against decapentuplegic, Dr hybo I lumanembrane protein Fin 4 substance training (Fin 4) contravelydogen entigne LDM domain protein) host standar TDN (Fin 4) substances TST inhibitor 3 STAT Induced STAT inhibitor 3 STAT
50 55 60 65	12989 AASS003 (2014) 16245 AASS013 (2014) 16245 AASS013 (2014) 16245 ASS013 (2014) 16245 ASS013 (2014) 16245 ASS013 (2014) 16245 ASS013 (2014) 16245 AASS013 (2014) 16245 AASS013 (2014) 16245 AASS013 (2014) 16245 ASS013 (2014)	AASS608 H-10475 AASS608 H-10475 AASS607 H-28-1619 AASS608 H-10619	carbohydrate (jeraten sulfas Gal-6) sul transmerbrine, positiva androgen indused Homo sepins COMA FLJ15313 in, clone PL EST3 ST3 MDD (malbra saginat decapentaptiegic, Dr hybo I transmerbrine protein Fr14 substac carlier family 6 odocarrylargoen CTL2 gene sugar CLM domain protein) sergina CLM domain protein) sergina CLM domain protein STAT indused STAT inhibitor STAT indused STAT inhibitor STAT indused STAT inhibitor successful gradient protein successful gradient protein successful gradient successful gradient successful successful gradient successful gradient successf

	130431 L10284	AW505214 Hs.155560	calnexin
	130495 AA243278	AW250380 Hs.109059	mitochondrial ribosomal protein L12
	130553 AA430032	AF062649 Hs.252587	pituitary tumor-transforming 1
	130638 H16402	AW021276 Hs.17121	ESTs
5	130639 D59711	Al557212 Hs.17132	ESTs, Moderately similar to 154374 gene
-	130657 T94452	AW337575 Hs.201591	ESTs
	130686 AA431571	BE548267 Hs.337986	Homo saplens cDNA FLJ10934 fis, clone OV
	130778 R79356	AF167706 Hs.19280	cysteine-rich motor neuron 1
	130818 AA280375	AW190920 Hs.19928	hypothetical protein SP329
10	130840 Z49269	BE048821 Hs.20144	small inducible cytokine subfamily A (Cy
	130699 Z41740	AI077288 Hs.296323	serum/qlucocorticoid regulated kinase
	131002 AA121543	AL050295 Hs.22039	KIAA0758 protein
	131080 J05008	NM_001955Hs.2271	endothelin 1
	131084 AA101878	NM_017413Hs.303084	apelin; peptide ligand for APJ receptor
15	131091 T35341	AJ271216 Hs.22880	dipeptidylpeptidase III
	131107 N87590	BE620886 Hs.75354	GCN1 (general control of amino-acid synt
	131182 AA256153	Al824144 Hs.23912	ESTs
	131207 W74533	AF104266 Hs.24212	latrophilin
	131319 U25997	NM_003155Hs.25590	stanniocalcin 1
20	131328 V01512	AW939251 Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131328 V01512	AW939251 Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131328 V01512	AW939251 Hs.25647	v-fos FBJ murine osteosarcoma viral onco
	131328 V01512	AW939251 Hs.25647	v-fos FBJ murine osteosarcoma viral onco
~-	131509 X56681	X56681 Hs.2780	jun D proto-oncogene
25	131555 AA161292	T47364 Hs.278613	interferon, alpha-inducible protein 27
	131564 AA491465	T93500 Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL
	131573 AA046593	AA040311 Hs.28959	ESTs
	131692 D50914	BE559681 Hs.30736	KIAA0124 protein
20	131756 D45304	AA443966 Hs.31595	ESTs
30	131859 M90657	AW960564	transmembrane 4 superfamily member 1
	131909 W69127	NM_016558Hs.274411	SCAN domain-containing 1
	131915 AA316186	Al161383 Hs.34549	ESTs, Highly similar to S94541 1 clone 4
	132048 AA384503 132050 AA136353	Al359214 Hs.179260 Al267615 Hs.38022	chromosome 14 open reading frame 4 ESTs
35	132151 AA044755	BE379499 Hs.173705	Homo sapiens cDNA: FLJ22050 fis, clone H
55	132164 U84573	Al752235 Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
	132187 AA058911	AA235709 Hs.4193	DKFZP586O1624 protein
	132303 AA620962	BE177330 Hs.325093	Homo sapiens cDNA: FLJ21210 fis, clone C
	132314 AA285290	AF112222 Hs.323806	pinin, desmosome associated protein
40	132358 X60486	NM_003542Hs.46423	H4 histone family, member G
40	132398 R31641	AA876616 Hs.16979	ESTs, Weakly similar to A43932 mucin 2 p
	132421 AA489190	AW163483 Hs.48320	double ring-finger protein, Dorfin
	132490 F13782	NM 001290Hs.4980	LIM domain binding 2
	132520 AA257993	AA257992 Hs.50651	Janus kinase 1 (a protein tyrosine kinas
45	132546 M24283	M24283 Hs.168383	intercellular adhesion molecule 1 (CD54)
	132610 AA443114	AA160511 Hs.5326	amino acid system N transporter 2; porcu
	132716 T35289	BE379595 Hs.283738	caseln kinase 1, alpha 1
	132840 N23817	BE218319 Hs.5807	GTPase Rab14
	132883 AA047151	AA373314 Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f
50	132968 N77151	AF234532 Hs.81638	myosin X
	132989 AA480074	AA480074 Hs.331328	hypothetical protein FLJ13213
	132999 Y00787	Y00787 Hs.624	Interleukin 8
	133071 T99789	BE384932 Hs.64313	ESTs, Weakly similar to AF257182 1 G-pro
	133076 W84341	AW946276 Hs.6441	Homo sapiens mRNA; cDNA DKFZp586J021 (fr
55	133099 L09209	W16518 Hs.279518	amyloid beta (A4) precursor-like protein
	133147 D12763	AA026533 Hs.66	interleukin 1 receptor-like 1
	133149 T16484	AA370045 Hs.6607	AXIN1 up-regulated
	133161 AA253193	AW021103 Hs.6631	hypothetical protein FLJ20373
60	133200 AA432248	AB037715 Hs.183639	hypothetical protein FLJ10210
60	133220 X82200	NM_006074Hs.318501	Homo sapiens mRNA full length insert cDN
	133260 AA063572	AA403045 Hs.6906	Homo sapiens cDNA: FLJ23197 fls, clone R
	133295 L00352	Al147861 Hs.213289	low density lipoprotein receptor (famili
	133349 N75791	AW631255 Hs.8110	L-3-hydroxyacyl-Coenzyme A dehydrogenase
65	133391 X57579	AW103364 Hs.727	inhibin, beta A (activin A, activin AB a
03	133398 X02612	NM_000499Hs.72912	cytochrome P450, subfamily I (aromatic c
	133436 H44631 133454 AA090257	BE294068 Hs.737 BE547647 Hs.177781	immediate early protein hypothetical protein MGC5618
			cardiac ankyrin repeat protein
	133478 X83703 133491 L40395	X83703 Hs.31432 BE619053 Hs.170001	eukaryotic translation initiation factor
70	133491 L4U395 133510 AA227913	AW880841 Hs.96908	p53-induced protein
70	133510 AA227913 133517 X52947	NM_000165Hs.74471	gap junction protein, alpha 1, 43kD (con
	133526 M11313	AU077051 Hs.74561	alpha-2-macroglobulin
	133538 L14837	NM_003257Hs.74614	tight junction protein 1 (zona occludens
	133562 M60721	M60721 Hs.74870	H2.0 (Drosophila)-like homeo box 1
75	133584 D90209	D90209 Hs.181243	activating transcription factor 4 (tax-r
, ,	133590 T67986	T70956 Hs.75106	clusterin (complement lysis inhibitor, S
			· · · · · · · · · · · · · · · · · · ·

	102012 44	440040	DEGAAGGA	11- 75240	ADD alternative feater like 2 internati
	133617 AA 133651 U9		BE244334 Al301740	Hs.173381	ADP-ribosylation factor-like 6 interacti dihydropyrimidinase-like 2
			AW503116	He 201210	zinc finger protein 146
	133678 KO		AW247252	110.001010	nucleoside phosphorylase
5	133681 D7		Al352558		tyrosine 3-monooxygenase/tryptophan 5-mo
-	133722 X5	3331	AW969976	Hs.279009	matrix Gla protein
	133730 S7	3591	BE242779	Hs.179526	upregulated by 1,25-dihydroxyvitamin D-3
				Hs.75873	zyxin
10			AW239400		G protein-coupled receptor kinase 6
10	133825 U4			Hs.285313	core promoter element binding protein
				Hs.180919	inhibitor of DNA binding 2, dominant neg
				Hs.178761 Hs.211582	26S proteasome-associated pad1 homolog myosin, light polypeptide kinase
	133960 M1			Hs.77899	tropomyosin 1 (alpha)
15				Hs.295944	tissue factor pathway inhibitor 2
				Hs.250666	hairy (Drosophila)-homolog
	134039 S7	8569	NM_002290	Hs.78672	laminin, alpha 4
	134075 U2		NM_012201		Golgi apparatus protein 1
			AL034349		protein tyrosine phosphatase, receptor t
20			AW245540		brain abundant, membrane attached signal
			AA161219		diphtheria toxin receptor (heparin-bindi
				Hs.160726	Homo sapiens cDNA FLJ11680 fis, clone HE
			AW580939 D86962	Hs.81875	complement component C1q receptor growth factor receptor-bound protein 10
25				Hs.81988	disabled (Drosophila) homolog 2 (mitogen
23				Hs.82028	transforming growth factor, beta recepto
	134381 U5	6637	Al557280	Hs.184270	capping protein (actin filament) muscle
	134403 MB	1199	AA334551		sperm specific antigen 2
	134416 M2			Hs.211579	melanoma cell adhesion molecule
30	134493 X1			Hs.289088	heat shock 90kD protein 1, alpha
	134558 S5		NM_001773		CD34 antigen
			AU076592		jun B proto-oncogene
	134983 D2 134989 AA		D28235 AW968058	Hs.196384	prostaglandin-endoperoxide synthase 2 (p nudix (nucleoside diphosphate linked mol
35	135052 AA	148923		Hs.93675	decidual protein induced by progesterone
55				Hs.93872	KIAA1682 protein
				Hs.93961	Homo saplens mRNA; cDNA DKFZp667D095 (fr
		8069		Hs.94	DnaJ (Hsp40) homolog, subfamily A, membe
				Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
40		282140	T53169	Hs.9587	Homo saplens cDNA: FLJ22290 fis, clone H
				Hs.9615	myosin regulatory light chain 2, smooth
	135348 AA 134404 AB			Hs.268177 Hs.82771	phospholipase C, gamma 1 (formerly subty vaccinia related kinase 2
				Hs.6582	Rho guanine exchange factor (GEF) 12
45				Hs.4295	proteasome (prosome, macropain) 26S subu
				Hs.57553	tousled-like kinase 2
				Hs.15113	homogentisate 1,2-dioxygenase (homogenti
	100104 AF	008937	AF008937		syntaxin 16
			AB011169		similar to S. cerevisiae SSM4
50			AF029674		KIAA1605 protein
			NM_001269		chromosome condensation 1
		0760 11139	AA469369		v-ral simian leukemia viral oncogene hom tissue inhibitor of metalloproteinase 1
				Hs.81892	KIAA0101 gene product
55	100169 D1	14878	AL037228		D123 gene product
	129718 D1	7716	NM_002410		mannosyl (alpha-1,6-)-glycoprotein beta-
	100190 D2			Hs.178658	RAD23 (S. cerevisiae) homolog B
	134742 D2		NM_001346		diacylglycerol kinase, gamma (90kD)
	100211 D2			Hs.123058	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
60	100238 D3			Hs.348	calcium/calmodulin-dependent protein kin
	130283 D3		NM_012288 D31765	Hs.170114	TRAM-like protein KIAA0061 protein
	134237 D3 100248 D3	31888	NM_015156	118.170114 Na 78308	KIAA0071 protein
		88128	D25418	Hs.393	prostaglandin 12 (prostacyclin) receptor
65		38500		Hs.278468	postmeiotic segregation increased 2-like
		8551	N92036	Hs.81848	RAD21 (S. pombe) homolog
		12087		Hs.184627	KIAA0118 protein
		19396		Hs.75454	peroxiredoxin 3
70		5640	D55640		gb:Human monocyte PABL (pseudoautosomal
70		33391 3477	AW247529 D63477	Hs.6793 Hs.84087	platelet-activating factor acetylhydrola KIAA0143 protein
		3477 33483	D86864	Hs.57735	acetyl LDL receptor; SREC
		34015		Hs.182741	TIA1 cytotoxic granule-associated RNA-bi
		79990	NM_014737		Ras association (RalGDS/AF-6) domain fam
75	100372 D7	9997	NM_014791	1Hs.184339	KIAA0175 gene product
	134304 D8	30010	BE613486		lipin 1

	100394	D84276	D84284	Hs.66052	CD38 antigen (p45)
	100405	D86425	AW291587		nidogen 2
	100418	D86978	D86978	Hs.84790	KIAA0225 protein
	133154	D87012	D87012	Hs.194685	topoisomerase (DNA) III beta
5	134347	D87075	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra
	444099	D87432	D87432	Hs.10315	solute carrier family 7 (cationic amino
	100438	D87448	AA013051	Hs.91417	topoisomerase (DNA) II binding protein
	134593	D87845	NM_000437		platelet-activating factor acetylhydrola
	100481		X70377	Hs.121489	cystatin D
10	100552	HG2167-HT2237		Hs.301946	lysosomal
	100591	HG2415-HT2511			Homo sapiens, Similar to hypothetical pr
	100652	HG2825-HT2949	BE613608	Hs.142653	ret finger protein
	100662	HG2887-HT3031	AI368680	Hs 816	SRY (sex determining region Y)-box 2
	100899	HG4660-HT5073		Hs.103042	microtubule-associated protein 1B
15	100905	HG4704-HT5146		Hs.172816	neureaulin 1
10	100945	HG884-HT884	AF002225	Hs.180686	ubiquitin protein ligase E3A (human papi
	100950	HG919-HT919	AF128542	Hs.166846	polymerase (DNA directed), epsilon
	100964	J00212	J00212	110.100010	Empirically selected from AFFX single pr
	135407	J04029	J04029	Hs.99936	keratin 10 (epidermolytic hyperkeratosis
20	130149	J04031	AW067805	Hs 172665	methylenetetrahydrofolate dehydrogenase
	131877	J04088	J04088	Hs.156346	topolsomerase (DNA) II alpha (170kD)
	101016	J04543	J04543	Hs.78637	annexin A7
	134786	L06139	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous
	134100	L07540	AA460085	Hs.171075	replication factor C (activator 1) 5 (36
25	134078	L08896	L08895	Hs.78995	MADS box transcription enhancer factor 2
23	101132	L11239	L11239	Hs.36993	gastrulation brain homeo box 1
	134849	L11353	BE409525	Hs.902	neurofibromin 2 (bilateral acoustic neur
	332736	L13773	Z83689	Hs.114765	myeloid/lymphoid or mixed-lineage leukem
		L13800	Al984825	Hs.9884	spindle pole body protein
30	135397	L14922	L14922	Hs.166563	replication factor C (activator 1) 1 (14
50	432642		BE297635		heat shock 70kD protein 9B (mortalin-2)
		L15388	NM_00530		G protein-coupled receptor kinase 5
	421155		H87879	Hs.102267	lysyl oxidase
		L27476	AF083892		tight junction protein 2 (zona occludens
35		L27624	C18356	Hs.295944	tissue factor pathway inhibitor 2
55	134739	L32976	NM_00241		mitogen-activated protein kinase kinase
	130155	L33404	AA101043	De 151354	kalikrein 7 (chymotryptic, stratum com
	440538	L35263	W76332	Hs.79107	mitogen-activated protein kinase 14
	409916	L37347	BE313625	Hs.57435	solute carrier family 11 (proton-coupled
40	101294	L40371	AF168418	Hs.116784	thyroid hormone receptor Interactor 4
40		L40391		HS.110704	transmembrane trafficking protein
	101300		BE535511 L41607	Hs.934	glucosaminyl (N-acetyl) transferase 2, I
	101310 130344	L41607 L77566	AW250122		DiGeorge syndrome critical region gene D
	101381	M13928	AW675039		aminolevulinate, delta-, dehydratase
45	101381	M13928	AW675039		aminolevulinate, delta-, dehydratase
43		M14016	AW005903		
	415678			Hs.76152	uroporphyrinogen decarboxylase
	133780	M14219 M15796	AA557660 BE267931		decorin proliferating cell nuclear antigen
	101396			П8.70990	gb:Human alpha satellite and satellite 3
50	101447 101458	M21305 M22092	M21305		gb:Human neural cell adhesion molecule (
30		M22898	M22092 NM_00054	211- 4040	tumor protein p53 (Li-Fraument syndrome)
	101470		NM_00088		
	134604	M22995			RAP1A, member of RAS oncogene family
	101478	M23379	NM_00289		RAS p21 protein activator (GTPase activa
55	133519	M24400	AW583032	HS.74502	chymotrypsinogen B1
33	131185	M25753	BE280074	HS.23900	cyclin B1
	134116	M27691	R84694	Hs.79194	cAMP responsive element binding protein
	133999	M28213	AA535244		RAB2, member RAS oncogene family
	130174		M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat
	129963		M29971	Hs.1384	O-6-methylguanine-DNA methyltransferas
60	132983		M30269		nldogen (enactin)
	133900		M31158	Hs.77439	protein kinase, cAMP-dependent, regulato
	101543		M31166	Hs.2050	pentaxin-related gene, rapidly induced b
	101545	M31210	BE246154	Hs.154210	endothelial differentiation, sphingolipi
	101620	M55420	S55271	Hs.247930	Epsilon , IgE
65	134691	M59979	AW382987	Hs.88474	prostaglandin-endoperoxide synthase 1 (p
	133595	M62810	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond
	101700	M64710	D90337	Hs.247916	natriuretic peptide precursor C
	101714	M68874	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,
	134246	M74524	D28459	Hs.80612	ubiquitin-conjugating enzyme E2A (RAD6)
70	101760	M80254	M80254	Hs.173125	peptidylprolyl isomerase F (cyclophilin
-	415022	M81780	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid
	415022	M81780	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid
	415022	M81780	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid
	415022	M81780	X59960	Hs.77813	sphingomyelin phosphodlesterase 1, acid
75	415022	M81780	X59960	Hs.77813	sphingomyelin phosphodiesterase 1, acid
		M83822	M83822	Hs.62354	cell division cycle 4-like
					•

	101812 M86934	BE439894 Hs.78991	DNA segment, numerous copies, expressed
	101813 M87338	NM_002914Hs.139226	replication factor C (activator 1) 2 (40
	133396 M96326	M96326 Hs.72885	azurocidin 1 (callonic antimicrobial pro
-	428161 M96954	M96954 Hs.182741	TIA1 cytotoxic granule-associated RNA-bi
5	129026 M98833	AL120297 Hs.108043	Friend leukemia virus integration 1
	101901 S66793	H38026 Hs.308	arrestin 3, retinal (X-arrestin)
	134831 S72370 134039 S78569	AA853479 Hs.89890	pyruvate carboxylase
	442355 S79873	NM_002290Hs.78672 AA456539 Hs.8262	laminin, alpha 4 lysosomal-associated membrane protein 2
10	101975 S83325	AA079717 Hs.283664	aspartate beta-hydroxylase
10	101977 \$83364	AF112213 Hs.184062	putative Rab5-interacting protein
	101978 S83365	BE561610 Hs.5809	putative transmembrane protein; homolog
	101998 U01212	U01212 Hs.248153	olfactory marker protein
	102003 U01922	U01922 Hs.125565	translocase of inner mitochondrial membr
15	102007 U02556	U02556 Hs.75307	t-complex-associated-testis-expressed 1-
	102009 U02680	BE245149 Hs.82643	protein tyrosine kinase 9
	416658 U03272 132951 U04209	U03272 Hs.79432 AW821182 Hs.61418	fibrilin 2 (congenital contractural ara microfibrilar-associated protein 1
	132951 U04209 135389 U05237	U05237 Hs.99872	fetal Alzheimer antigen
20	102048 U07225	U07225 Hs.339	purinergic receptor P2Y, G-protein coupt
	130145 U07620	U34820 Hs.151051	milogen-activated protein kinase 10
	303153 U09759	U09759 Hs.246857	mitogen-activated protein kinase 9
	420269 U09820	U72937 Hs.96264	alpha thalassemia/mental retardation syn
	102095 U11313	U11313 Hs.75760	sterol carrier protein 2
25	102123 U14518	NM_001809Hs.1594	centromere protein A (17kD)
	102126 U14575	AW950870 Hs.78961	protein phosphatase 1, regulatory (Inhib
	102133 U15173	AU076845 Hs.155596	BCL2/adenovirus E1B 19kD-interacting pro
	102139 U15932 102162 U18291	NM_004419Hs.2128 AA450274 Hs.1592	dual specificity phosphatase 5 CDC16 (cell division cycle 16, S. cerevi
30	102164 U18300	NM_000107Hs.77602	damage-specific DNA binding protein 2 (4
50	427653 U18383	AA159001 Hs.180069	nuclear respiratory factor 1
	131817 U20536	U20536 Hs.3280	caspase 6, apoptosis-related cysteine pr
	102200 U21551	AA232362 Hs.157205	branched chain aminotransferase 1, cytos
	102210 U23028	BE619413 Hs.2437	eukaryotic translation initiation factor
35	102214 U23752	U23752 Hs.32964	SRY (sex determining region Y)-box 11
	132811 U25435	U25435 Hs.57419	CCCTC-binding factor (zinc finger protei
	131319 U25997 102256 U28251	NM_003155Hs.25590 U28251 Hs.53237	stanniocalcin 1 ESTs, Highly similar to Z169_HUMAN ZINC
	132316 U28831	U28831 Hs.44566	KIAA1641 protein
40	102269 U30245	U30245	gb:Human myelomonocytic specific protein
	417526 U32315	AA568906 Hs.82240	syntaxin 3A
	102293 U32439	AF090116 Hs.79348	regulator of G-protein signalling 7
	102298 U32849	AA382169 Hs.54483	N-myc (and STAT) interactor
45	102325 U35139	Al815867 Hs.50130	necdin (mouse) homolog
45	428734 U36764 102361 U39400	BE303044 Hs.192023 AA223616 Hs.75859	eukaryotic translation initiation factor chromosome 11 open reading frame 4
	102367 U39657	U39656 Hs.118825	mitogen-activated protein kinase kinase
	102388 U41344	AA362907 Hs.76494	proline arginine-rich end leucine-rich r
	102394 U41766	NM 003816Hs.2442	a disintegrin and metalloproteinase doma
50	129829 U41813	AF010258 Hs.127428	homeo box A9
	102409 U43286	BE300330 Hs.118725	selenophosphate synthelase 2
	133746 U44378	AW410035 Hs.75862	MAD (mothers against decapentaplegic, Dr
	102423 U44754	Z47542 Hs.179312	small nuclear RNA activating complex, po
55	132828 U47011 132828 U47011	AB014615 Hs.57710 AB014615 Hs.57710	fibroblast growth factor 8 (androgen-ind fibroblast growth factor 8 (androgen ind
33	132828 U47011	AB014615 Hs.57710 AB014615 Hs.57710	fibroblast growth factor 8 (androgen-ind
	132828 U47011	AB014615 Hs.57710	fibroblast growth factor 8 (androgen-ind
	425322 U47077	U63630 Hs.155637	protein kinase, DNA-activated, catalytic
	102450 U48251	U48251 Hs.75871	protein kinase C binding protein 1
60	129350 U50535	U50535 Hs.110630	Human BRCA2 region, mRNA sequence CG006
	102534 U56833	U96759 Hs.198307	von Hippel-Lindau binding protein 1
	130457 U58091	AB014595 Hs.155976	cullin 4B
	135065 U58837	AA019401 Hs.93909	cyclic nucleotide gated channel beta 1
65	102560 U59289 102567 U59863	R97457 Hs.63984 U63830 Hs.146847	cadherin 13, H-cadherin (heart) TRAF family member-associated NFKB activ
05	417173 U67122	U61397 Hs.81424	ubiquitin-like 1 (sentrin)
	102638 U67319	U67319 Hs.9216	caspase 7, apoptosis-related cysteine pr
	132736 U68019	AW081883 Hs.211578	Homo sapiens cDNA: FLJ23037 fis, clone L
=-	133070 U69611	U92649 Hs.64311	a disintegrin and metalloproteinase doma
70	102663 U70322	NM_002270Hs.168075	karyopherin (importin) beta 2
	134660 U73524	U73524 Hs.87465	ATP/GTP-binding protein
	102735 U79267	AF111106 Hs.3382	protein phosphatase 4, regulatory subuni hypothetical protein MGC14433
	102741 U79291 130564 U82671	AW959829 Hs.83572 U82671 Hs.36980	melanoma antigen, family A, 2
75	130564 U82671	U82671 Hs.36980	melanoma antigen, family A, 2
	132164 U84573	AI752235 Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
			-

	102823 U90914	DOESOO IL EGET	and an analistana D
	102826 U91316	D85390 Hs.5057 NM_007274Hs.8679	carboxypeptidase D cytosolic acyl coenzyme A thioester hydr
	102831 U91932	AA262170 Hs.80917	adaptor-related protein complex 3, sigma
	102846 U96131	BE264974 Hs.6566	thyroid hormone receptor interactor 13
5	129777 U97018	U97018 Hs.12451	echinoderm microtubule-associated protei
-	134161 U97188	AA634543 Hs.79440	IGF-II mRNA-blinding protein 3
	134854 V00503	J03464 Hs.179573	collagen, type I, alpha 2
	429257 X04327	AW163799 Hs.198365	2,3-bisphosphoglycerate mutase
	413985 X06389	Al018666 Hs.75667	synaptophysin
10	419768 X07496	T72104 Hs.93194	apolipoprotein A-I
	102915 X07820	X07820 Hs.2258	matrix metalioproteinase 10 (stromelysin
	134656 X14787	Al750878 Hs.87409	thrombospondin 1
	413858 X15525	NM_001610Hs.75589	acid phosphatase 2, lysosomal
	102968 X16396	AU076611 Hs.154672	methylene tetrahydrofolate dehydrogenase
15	102971 X16609	X16609 Hs.183805	ankyrin 1, erythrocytic
	134037 X53586	Al808780 Hs.227730	integrin, alpha 6
	134037 X53586	Ai808780 Hs.227730	integrin, alpha 6
	103023 X53793	AW500470 Hs.117950	multifunctional polypeptide similar to S
20	103037 X54936	BE018302 Hs.2894	placental growth factor, vascular endoth
20	130282 X55740	BE245380 Hs.153952	5' nudeotidase (CD73)
	134542 X57025	M14156 Hs.85112	insulin-like growth factor 1 (somatomedi
	128568 X60673	H12912 Hs.274691 H12912 Hs.274691	adenylate kinase 3
	128568 X60673 103093 X60708	H12912 Hs.274691 S79876 Hs.44926	adenylate kinase 3 dipeptidylpeptidase IV (CD26, adenosine
25	413076 X62048	U10564 Hs.75188	wee1 (S. pombe) homolog
23	129063 X63097	X63094 Hs.283822	Rhesus blood group, D antigen
	424460 X63563	BE275979 Hs.296014	polymerase (RNA) II (DNA directed) polyp
	411077 X64037	AW977263 Hs.68257	general transcription factor IIF, polype
	103181 X69636	X69636 Hs.334731	Homo saplens, clone IMAGE:3448306, mRNA,
30	103184 X69878	U43143 Hs.74049	fms-related tyrosine kinase 4
	103194 X70649	NM 004939Hs.78580	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
	103208 X72841	AW411340 Hs.31314	retinoblastoma-binding protein 7
	129698 X74987	BE242144 Hs.12013	ATP-binding cassette, sub-family E (OABP
	131486 X83107	F06972 Hs.27372	BMX non-receptor tyrosine kinase
35	130729 X84194	Al963747 Hs.18573	acylphosphatase 1, erythrocyte (common)
	103334 X85753	NM_001260Hs.25283	cyclin-dependent kinase 8
	132645 X87870	Al654712 Hs.54424	hepatocyte nuclear factor 4, alpha
	135094 X89066	NM_003304Hs.250687	transient receptor potential channel 1
40	103352 X89398	H09366 Hs.78853	uracil-DNA glycosylase
40	103352 X89398	H09366 Hs.78853	uradi-DNA glycosylase
	103353 X89399	X89399 Hs.119274	RAS p21 protein activator (GTPase activa
	132173 X89426	X89426 Hs.41716	endothelial cell-specific molecule 1
	103371 X91247 131584 X91648	X91247 Hs.13046 AA598509 Hs.29117	thioredoxin reductase 1 punne-rich element binding protein A
45	103376 X92098	AL036166 Hs.323378	coated vesicle membrane protein
45	103378 X92110	AL119690 Hs.153618	HCGVIII-1 protein
	128510 X94703	X94703	RAB28, member RAS oncogene family
	103410 X96506	AA158294 Hs.295362	DR1-associated protein 1 (negative cofac
	133490 X97230	AF022044 Hs.274601	killer cell immunoglobulin-like receptor
50	332689 X97230	AF022044 Hs.274601	killer cell immunoglobulin-like receptor
	103438 X98263	AW175781 Hs.152720	M-phase phosphoprotein 6
	103440 X98296	X98296 Hs.77578	ubiquitin specific protease 9, X chromos
	103452 X99584	NM_006936Hs.85119	SMT3 (suppressor of mif two 3, yeast) ho
	133536 Y00264	W25797.comp	Hs.177486 amyloid beta (A4) precursor protein (pro
55	420234 Y07566	AW404908 Hs.96038	Ric (Drosophila)-like, expressed in many
	426502 Y07759	Y07759 Hs.170157	myosin VA (heavy polypeptide 12, myoxin)
	134662 Y07827	NM_007048Hs.284283	butyrophilin, subfamily 3, member A1
	132083 Y07867	BE386490 Hs.279663	Pirin
	103500 Y09443	AW408009 Hs.22580	alkylglycerone phosphate synthase
60	134389 Y09858	Y09858 Hs.82577	spindin-like
	132084 Y12394	NM_002267Hs.3886	karyopherin alpha 3 (importin alpha 4)
	103540 Z11559	NM_002197Hs.154721 Z11695 Hs.324473	aconitase 1, soluble milogen-activated protein kinase 1
	133152 Z11695 103548 Z15005	Z15005 Hs.75573	centromere protein E (312kD)
65	103612 Z46261	BE336654 Hs.70937	H3 histone family, member A
05	129092 AA011243	D56365 Hs.63525	poly(rC)-binding protein 2
	103692 AA018418	AW137912 Hs.227583	Homo sapiens chromosome X map Xp11.23 L-
	103695 AA018758	AW207152 Hs.186600	ESTs
	129796 AA018804	BE218319 Hs.5807	GTPase Rab14
70	434993 AA031993	AA306325 Hs.4311	SUMO-1 activating enzyme subunit 2
	132683 AA044217	BE264633 Hs.143638	WD repeat domain 4
	131887 AA046548	W17064 Hs.332848	SWI/SNF related, matrix associated, acti
	103723 AA057447	BE274312 Hs.214783	Homo sapiens cDNA FLJ14041 fis, clone HE
	453368 AA058376	W20296 Hs.288178	Homo sapiens cDNA FLJ11968 fis, clone HE
75	133260 AA083572	AA403045 Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R
	103765 AA085696	AA085696 Hs.169600	KIAA0826 protein

	103766 AA088744	Al920783 Hs.191435	ESTs
	103767 AA089688	BE244667	CGI-100 protein
	132051 AA091284	AA393968 Hs.180145	HSPC030 protein
5	103773 AA092700	AI219323 Hs.101077	ESTs, Weakly similar to T22363 hypotheti
5	135289 AA092968	AW372569 Hs.9788	hypothetical protein MGC10924 similar to
	409659 AA094800	AW970843 Hs.55682	eukaryotic translation initiation factor
	103794 AA100219	AF244135 Hs.30670	hepatocellular carcinoma-associated anti
	131471 AA114885	AA164842 Hs.192619	KIAA1600 protein
10	134319 AA129547	BE304999 Hs.285754	fumarate hydratase
10	103807 AA133016	AW958264 Hs.103832	similar to yeast Upf3, variant B homolog of mouse quaking QKI (KH domain
	446392 AA149507 129863 AA151005	AF142419 Hs.15020 BE379765 Hs.129872	sperm associated antigen 9
	103850 AA187101	AA187101 Hs.213194	hypothetical protein MGC10895
	103855 AA195179	W02363	hypothetical protein FLJ10330
15	103861 AA206236	AA206236 Hs.4944	hypothetical protein FLJ12783
13	130634 AA227621	Al769067 Hs.127824	ESTs, Weakly similar to T28770 hypotheti
	447735 AA248283	AA775268 Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L
	103909 AA249611	AA249611 Hs.47438	SH3 domain binding glutamic acid-rich pr
	458928 AA282640	AF043117 Hs.24594	ubiquitination factor E4B (homologous to
20	415824 AA287199	D42039 Hs.78871	mesoderm development candidate 2
20	129013 AA313990	AA371156 Hs.107942	DKFZP564M112 protein
	129435 AA314256	AF151852 Hs.111449	CGI-94 protein
	103988 AA314389	AA314389 Hs.342849	ADP-ribosylation factor-like 5
	104000 AA324364	Al146527 Hs.80475	polymerase (RNA) II (DNA directed) polyp
25	425284 AA329211	AF155568 Hs.348043	NS1-associated protein 1
	128629 AA399187	AL096748 Hs.102708	DKFZP434A043 protein
	133281 AA421079	AK001601 Hs.69594	high-mobility group 20A
	104104 AA422029	AA422029 Hs.143640	ESTs, Weakly similar to hyperpolarizatio
	332455 AA425230	NM_005754Hs.220689	Ras-GTPase-activating protein SH3-domain
30	132091 AA447052	AW954243	KIAA0251 protein
	135073 AA452000	W55956 Hs.94030	Homo saplens mRNA; cDNA DKFZp586E1624 (f
	131367 AA456687	AI750575 Hs.173933	nuclear factor I/A
	129593 AA487015	Al338247 Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f
	133505 C01527	Al630124 Hs.324504	Homo saplens mRNA; cDNA DKFZp586J0720 (f
35	132064 C01714	AA121098 Hs.3838	serum-inducible kinase
	442351 C01811	W52642 Hs.8261	hypothetical protein FLJ22393
	131427 C02352	AF151879 Hs.26706	CGI-121 protein
	433892 C02375	Al929357 Hs.323966	Homo sapiens clone H63 unknown mRNA
40	104282 C14448	C14448 Hs.332338	EST
40	134827 D16611	BE314037 Hs.89866	coproporphyrinogen oxidase (coproporphyr
	425330 D25216	D25216 Hs.155650	KIAA0014 gene product
	131742 D31352	AA961420 Hs.31433	ESTs
	456935 D58024	AA370362 Hs.57958	EGF-TM7-latrophilin-related protein
45	425218 D80897	NM_014909Hs.155182	KIAA1036 protein
45	104334 D82614	D82614 Hs.78771	phosphoglycerate kinase 1
	134593 D87845	NM_000437Hs.234392 D89377 Hs.89404	platelet-activating factor acetylhydrola
	134731 D89377	D89377 Hs.89404 NM_001310Hs.13313	msh (Drosophila) homeo box homolog 2 cAMP responsive element binding protein-
	445776 H06583 131670 H40732	H03514 Hs.15589	ESTs
50	131670 H40732 104394 H46617	AA129551 Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C
50	104402 H56731	H56731 Hs.132956	ESTs
	439130 H75570	AA306090 Hs.124707	ESTs
	129077 H78886	N74724 Hs.108479	ESTs
	104417 H81241	Al819448 Hs.320861	Kruppel-like factor 8
55	134927 L36531	L36531 Hs.91296	Integrin, alpha 8
-	129280 M63154	M63154 Hs.110014	gastric intrinsic factor (vitamin B synt
	134498 M63180	AW246273 Hs.84131	threonyl-tRNA synthetase
	104460 M91504	AW955705 Hs.62604	Homo sapiens, clone IMAGE:4299322, mRNA,
	104488 N56191	N56191 Hs.106511	protocadhenn 17
60	131248 N78483	Al038989 Hs.332633	Bardet-Biedl syndrome 2
	130017 R14652	AK000096 Hs.143198	Inhibitor of growth family, member 3
	104530 R20459	AK001676 Hs.12457	hypothetical protein FLJ10814
	104534 R22303	R22303	gb:yh26b09.r1 Soares placenta Nb2HP Horno
	104544 R33779	Al091173 Hs.222362	ESTs, Weakly similar to p40 [H.sapiens]
65	133328 R36553	AW452738 Hs.265327	hypothetical protein DKFZp761I141
	104567 R64534	AA040620 Hs.5672	hypothetical protein AF140225
	129575 R70621	F08282 Hs.278428	progestin induced protein
	130776 R79356	AF167706 Hs.19280	cysteine-rich motor neuron 1
70	104599 R84933	AW815036 Hs.151251	ESTs
70	104660 AA007160	BE298665 Hs.14846	Homo sapiens mRNA; cDNA DKFZp564D016 (fr
	104667 AA007234	Al239923 Hs.63931	ESTs
	104718 AA018409	Al143020 Hs.36250	ESTs, Weakly similar to 138022 hypotheti
	104764 AA025351	Al039243 Hs.278585	ESTs
75	104786 AA027168	AA027167 Hs.10031	KIAA0955 protein
75	104787 AA027317	AA027317 AK001751 Hs.171835	gb:ze97d11.s1 Soares_fetal_heart_NbHH19W
	134079 AA029423	MNUU1/01 IIS.1/1030	hypothetical protein FLJ10889

	104804 AA031357	Al858702 Hs.31803	ESTs, Weakly similar to N-WASP (H.sapien
	104865 AA045136	T79340 Hs.22575	B-cell CLL/lymphoma 6, member B (zlnc fi
	130828 AA053400	AW631469 Hs.203213	ESTs
_	104907 AA055829	AA055829 Hs.196701	ESTs, Weakly similar to ALU1_HUMAN ALU S
5	104943 AA065217	AF072873 Hs.114218	frizzled (Drosophila) homolog 6
	105013 AA116054	H63789 Hs.296288	ESTs, Weakly similar to KIAA0638 protein
	105024 AA126311	AA126311 Hs.9879	ESTS
	132592 AA129390 105038 AA130273	AW803564 Hs.288850 AW503733 Hs.9414	Homo sapiens cDNA: FLJ22528 fis, clone H KIAA1488 protein
10	105077 AA142919	W55946 Hs.234863	Homo sapiens cDNA FLJ12082 fis, clone HE
10	105096 AA150205	AL042506 Hs.21599	Kruppel-like factor 7 (ubiquitous)
	129215 AA176867	AB040930 Hs.126085	KIAA1497 protein
	105169 AA180321	BE245294 Hs.180789	S164 protein
	132796 AA180487	NM_006283Hs.173159	transforming, acidic coiled-coil contain
15	427210 AA187634	BE396283 Hs.173987	eukaryotic translation initiation factor
	105200 AA195399	AA328102 Hs.24641	cytoskeleton associated protein 2
	130114 AA234717	AA233393 Hs.14992 AW338625 Hs.22120	hypothetical protein FLJ11151 ESTs
	105330 AA234743 105337 AA234957	AW338625 PIS.22120 AI468789 PIS.347187	myolubularin related protein 1
20	422040 AA235604	AA172106 Hs.110950	Rag C protein
~~	105376 AA236559	AW994032 Hs.8768	hypothetical protein FLJ10849
	105397 AA242868	AA814807 Hs.7395	hypothetical protein FLJ23182
	431679 AA251776	AK000046 Hs.343877	hypothetical protein FLJ20039
	131991 AA251909	AF053306 Hs.36708	budding uninhibited by benzimidazoles 1
25	421305 AA252672	BE397354 Hs.324830	diptheria toxin resistance protein requi
	105489 AA256157	AA256157 Hs.24115	Homo sapiens cDNA FLJ14178 fis, clone NT
	105508 AA256680	AA173942 Hs.326416	Homo saplens mRNA; cDNA DKFZp564H1916 (f
	105539 AA258873 135172 AA262727	AB040884 Hs.109694 AB028956 Hs.12144	KIAA1451 protein KIAA1033 protein
30	131569 AA281451	AL389951 Hs.271623	nucleoporin 50kD
50	431129 AA281545	AL137751 Hs.263671	Homo saplens mRNA; cDNA DKFZp434i0812 (f
	105643 AA282069	BE621719 Hs.173802	KIAA0603 gene product
	105659 AA283044	AA283044 Hs.25625	hypothetical protein FLJ11323
	105666 AA283930	AA426234 Hs.34906	ESTs, Weakly similar to T17210 hypotheti
35	105674 AA284755	Al609530 Hs.279789	histone deacetylase 3
	105709 AA291268	Al928962 Hs.26761	DKFZP586L0724 protein
	105722 AA291927	Al922821 Hs.32433 AA299688 Hs.24183	ESTs ESTs
	105765 AA343514 115951 AA398109	BE546245 Hs.301048	sec13-like protein
40	130884 AA398109	BE546245 Hs.301048	sec13-like protein
	105962 AA405737	AW880358 Hs.339808	hypothetical protein FLJ10120
	105985 AA406610	AA406610	gb:zv15b10.s1 Soares_NhHMPu_S1 Homo sapi
	106008 AA411465	AB033888 Hs.8619	SRY (sex determining region Y)-box 18
45	457322 AA416886	Al815486 Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE
45	134222 AA424013	AW855861 Hs.8025	Homo sapiens clone 23767 and 23782 mRNA DKFZP434I116 protein
	446954 AA424148 106141 AA424558	AB037850 Hs.16621 AF031463 Hs.9302	phosducin-like
	447973 AA424961	AB011169 Hs.20141	similar to S. cerevisiae SSM4
	106157 AA425367	W37943 Hs.34892	KIAA1323 protein
50	428314 AA425921	AW135049 Hs.26285	Homo sapiens cDNA FLJ10643 fis, clone NT
	446727 AA426220	AB011095 Hs.16032	KIAA0523 protein
	106196 AA427735	AA525993 Hs.173699	ESTs, Weakly similar to ALU1_HUMAN ALU S
	457714 AA430673	AA083764	hypothetical protein MGC3178
55	133200 AA432248	AB037715 Hs.183639 AA398859 Hs.18397	hypothetical protein FLJ10210 hypothetical protein FLJ23221
22	106302 AA435896 106328 AA436705	AL079559 Hs.28020	KIAA0766 gene product
	450534 AA446561	Al570189 Hs.25132	KIAA0470 gene product
	106423 AA448238	AB020722 Hs.16714	Rho guanine exchange factor (GEF) 15
	439608 AA449756	AW864696 Hs.301732	hypothetical protein MGC5306
60	106477 AA450303	R23324 Hs.41693	DnaJ (Hsp40) homolog, subfamily B, membe
	106503 AA452411	AB033042 Hs.29679	cofactor required for Sp1 transcriptiona
	446999 AA454566	AA151520	hypothetical protein MGC4485
	106543 AA454667 442007 AA456437	AA676939 Hs.69285 AA301116 Hs.142838	neuropilin 1 nucleolar phosphoprotein Nopp34
65	106589 AA456646	AK000933 Hs.28661	Homo sapiens cDNA FLJ10071 fis, done HE
03	106593 AA456826	AW296451 Hs.24605	ESTs
	106596 AA456981	AA452379	ESTs, Moderately similar to ALU7_HUMAN A
	423064 AA458959	AF265208 Hs.8740	SWI/SNF related, matrix associated, acti
	106636 AA459950	AW958037 Hs.286	ribosomal protein L4
70	106654 AA460449	AW075485 Hs.286049	phosphosenne aminotransferase
	131353 AA463910	AW754182	gb:RC2-CT0321-131199-011-c01 CT0321 Homo
	106707 AA464603	AK000566 Hs.98135	hypothetical protein FLJ20559 pannexin 1
	452909 AA464606 106717 AA465093	NM_015368Hs.30965 AA600357 Hs.239489	pannexin 1 TIA1 cytotoxic granule-associated RNA-bi
75	453141 AA465692	AB014548 Hs.31921	KIAA0648 protein
,,,	106747 AA476473	NM_007118Hs.171957	triple functional domain (PTPRF interact
		-	•

	106773 AA478109	AA478109 Hs.188833	ESTs
	106781 AA478474	AA330310 Hs.24181	ESTs
		AA330310 HS.24101	FSTs
	106817 AA480889	D61216 Hs.18672	
	106846 AA485223	AB037744 Hs.34892	KIAA1323 protein
5	106848 AA485254	AA449014 Hs.121025	chromosome 11 open reading frame 5
	106856 AA486183	W58353 Hs.285123	Homo sapiens mRNA full length insert cDN
	418699 AA496936	BE539639 Hs.173030	ESTs, Weakly similar to ALU8_HUMAN ALU S
	107001 AA598589	Al926520 Hs.31016	putative DNA binding protein
10	442853 AA598831	AW021276 Hs.17121	ESTs
10	107054 AA600150	AI076459 Hs.15978	KIAA1272 protein
	107059 AA608545	BE614410 Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re
	107080 AA609210	AL122043 Hs.19221	hypothetical protein DKFZp566G1424
	107115 AA610108	BE379623 Hs.27693	peptidylprolyl isomerase (cyclophilin)-l
	107130 AA620582	AB033106 Hs.12913	KIAA1280 protein
15	107156 AA621239	AA137043 Hs.9663	programmed cell death 6-interacting prot
13			
	107174 AA621714	BE122762 Hs.25338	ESTs
	130621 AA621718	AW513087 Hs.16803	LUC7 (S. cerevislae)-like
	107190 D19673	AA836401 Hs.87860	ESTs
	132626 D25755	AW504732 Hs.21275	hypothetical protein FLJ11011
20	107217 D51095	AL080235 Hs.35861	DKFZP586E1621 protein
20	332584 D60272	AA357879 Hs.29423	ESTs; Weakly similar to macrophage lecti
	444655 T08879	AF088886 Hs.11590	cathepsin F
	107295 T34527	AA186629 Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp
	107299 T40327	BE277457 Hs.30661	hypothetical protein MGC4606
25	107315 T62771	AA316241 Hs.90691	nucleophosmin/nucleoplasmin 3
	107316 T63174	T63174 Hs.193700	Homo sapiens mRNA; cDNA DKFZp586l0324 (f
	107328 T83444	AW959891 Hs.76591	KIAA0887 prolein
	107334 T93641	T93597 Hs.187429	ESTs
	456340 U48263	U48263 Hs.89040	prepronociceptin
30	128636 U49065	U49065 Hs.102865	interleukin 1 receptor-like 2
	129938 U79300	AW003668 Hs.135587	Human clone 23629 mRNA sequence
	107375 U88573	BE011845 Hs.251064	high-mobility group (nonhistone chromoso
	130074 U93867	AL038596 Hs.250745	polymerase (RNA) III (DNA directed) (62k
		D86983 Hs.118893	Melanoma associated gene
25	107387 W01094	D00303 FIS.110033	Investigation associated gene
35	132036 W01568	AL157433 Hs.37706	hypothetical protein DKFZp434E2220
	107426 W26853	W28853 Hs.291003	hypothetical protein MGC4707
	135388 W27965	W27965 Hs.99865	epimorphin
	130419 W36280	AF037448 Hs.155489	NS1-associated protein 1
	107469 W47063	W47063 Hs.94668	ESTs
40	434203 W79060	BE262677 Hs.283558	hypothetical protein PRO1855
40	107503 W88550	AB028981 Hs.8021	KIAA1058 protein
		NM 003542Hs.46423	
	132358 X60486		H4 histone family, member G
	107522 X78931	X78931 Hs.99971	zinc finger protein 272
	456495 Z14077	NM_003403Hs.97496	YY1 transcription factor
45	107582 AA002147	AA002147 Hs.59952	EST
	107609 AA004711	R75654 Hs.164797	hypothetical protein FLJ13693
	107661 AA010383	AA010383 Hs.60389	ESTs
		AA015761 Hs.60642	ESTs
		AW008846 Hs.60857	ESTs
50	107775 AA018772		
50	107832 AA021473	AA021473	gb:ze66c11.s1 Soares relina N2b4HR Homo
	107859 AA024835	AW732573 Hs.47584	potassium voltage-gated channel, delayed
	107914 AA027229	AA027229 Hs.61329	ESTs, Weakly similar to T16370 hypotheti
	107935 AA029428	AA029428 Hs.61555	ESTs
	410196 AA035143	Al936442 Hs.59838	hypothetical protein FLJ10808
55	131461 AA035237	AA992841 Hs.27263	KIAA1458 protein
55			
	108007 AA039347	AA039347 Hs.61916	EST
	108029 AA040740	AA040740 Hs.62007	ESTs
	103040 AA041551	AL121031 Hs.159971	SWI/SNF related, matrix associated, acti
	108084 AA045513	AA058944 Hs.116602	Homo sapiens, clone IMAGE:4154008, mRNA,
60	108088 AA045745	AA045745 Hs.62886	ESTs
	108168 AA055348	Al453137 Hs.63176	FSTs
	130719 AA056582	AA679262 Hs.14235	hypothetical protein FLJ20008; KIAA1839
	108189 AA056697	AW376061 Hs.63335	ESTs, Moderately similar to A46010 X-lin
	108190 AA056748	AA056746 Hs.63338	EST
65	108203 AA057678	AW847814 Hs.289005	Homo sapiens cDNA: FLJ21532 fis, clone C
	108216 AA058681	AA524743 Hs.44883	ESTs
	108217 AA058686	AA058686 Hs.62588	ESTs
	108245 AA062840	BE410285 Hs.89545	proteasome (prosome, macropain) subunit,
		AA064859	gb:zm50f03.s1 Stratagene fibroblast (937
70	106277 AA064859	AA065069	gb:zm50i05.81 Stratagene infroblest (507 gb:zm12e11.s1 Stratagene pancreas (93720
70	108280 AA065069		guzanize i1.51 Strategene panciera (93/20
	108309 AA069923	AA069818	gb:zm67e03.r1 Stratagene neuroepithelium
	108340 AA070815	AA069820 Hs.180909	peroxiredoxin 1
	108403 AA075374	AA075374	gb:zm87a01.s1 Stratagene ovarian cancer
	108427 AA076382	AA076382	gb:zm91g08.s1 Stratagene ovarian cancer
75	108435 AA078787	T82427 Hs.194101	Homo sapiens cDNA: FLJ20869 ffs, clone A
		AA079096	abram03k04 at Cimbasona quarian cancer
	108439 AA078986	AA078986	gb:zm92h01.s1 Stratagene ovarian cancer

108500 AA083207 AA083207 Aa08206 String Carding Cardin				
108500 AA083207 AA083207 Aa08206 String Carding Cardin				
108507 AA083526 AA085276 108507 AA085276 AA085277 AA08578 AA085415 108502 AA085277 AA08578 AA010738 108502 AA052574 AA07578 AA		108469 AA079487		gb:zm97f08.s1 Stratagene colon HT29 (937
\$\ \text{100833} \text{ AA084416} \text{ 100859} \text{ AA085676} \text{ AA07078} \text{ 100859} \text{ AA082676} \text{ AA07078} \text{ 100859} \text{ AA082676} \text{ AA07078} \text{ AA07078} \text{ 100859} \text{ AA07072} \text{ AA07078} \text{ AA07078} \text{ 100857} \text{ AA170826} \text{ AA070787} \text{ AA170827} \text{ 100857} \text{ AA170827} \text{ AA070770} \text{ 1008577} \text{ 100857} \text{ AA1709770} \text{ 1008577} \text{ 100857} \text{ AA1709770} \text{ 1008577} \text{ 100857} \text{ 100857} \text{ AA170970} \text{ 1008570} \text{ 100857} \text{ 100858} \text{ AA170970} \text{ 100857} \text{ 100857} \text{ 100858} \text{ AA170970} \text{ 100857} \text{ 100858} \text{ AA170970} \text{ 100857} \text{ 100858} \text{ 100858} \text{ AA170970} \text{ 100857} \text{ 100859} \text{ 100859} \text{ AA150820} \text{ 100859} \text{ AA150820} \text{ 100859} \text{ 100859} \text{ 100859} \text{ AA150820} \text{ 100859} \text{ 100859} \text{ 100859} \text{ AA150820} \text{ 100859} \t				
105592 AA0856779	5			oh:zn06o09 s1 Stratagene hNT neumn /937
108599 AA0108275 AV7377 H. N26969 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1				gb:zm26c06.s1 Stratagene pancreas (93720
1		108589 AA088678		ESTs
10 193825 AA129077				stress-associated endoplasmic reticulum
108496 AA127017 AA127017 Pat 1/052 ESTs hypothetical probe PL 20044 ESTs 108505 AA13506 AA14506 AA14506 AA14506 AA14507 Pat 1/052 AA14506 AA14507 Pat 1/052 AA14506 AA14507 Pat 1/052 AA14506 AA14507 AA14506 AA14507 AA14506 AA1450	10			
108807 AA159806 A852236 Bh.48376 Bhypothetical prober PL/20044 Bh.42778 Bhypothetical prober PL/20044 Bhypotheti	10		AVV05/800 HS.105223	
108808 AA13980			AR127017 FIS.71032 AIR5223R He 49376	
15 108866 AA132802				
108897 AA133502				ESTs, Weakly similar to AF174605 1 F-box
131474 AA133843 L46353 H347276 108941 AA139840 AA148920 L46353 H34567 L16989 L1	15			DKFZP586G1517 protein
108894 AA139594 A0001431 Ha-5105 Implometrial probability 108986 AA15110 A304670 Ha-18880 EST ES				
10881 AA146950			AK001434 Ne 5405	
200 108966 AA151710			AA148650	gb:zo09e06.s1 Stratagene neuroepithelium
199001 AA156202 AA156203 AA166203 AA156203 AA	20		Al304870 Hs.188680	
191183 AA159299 AA15797 Ha.258107 hg.258107 hg				
109819 AA159879 AA159726 AA15729 AA157				
25 109022 AA157281 AA157281 haz2465				
109622 AA15728	25		AA150700 Hs.72100	
109606 AA164233 AA	20		AA157293 Hs.72168	
248881 AA167269 h. 246767 h. 146877		109068 AA164293	AA164293 Hs.72545	ESTs
1933-86 AA175899 1940-7959 1941-8079				
109162 AA179889 AA16984 AA16948 In 1442076 109172 AA109469 AA16948 In 1442076 120206 AA16974 AA16946 In 1442076 120206 AA16974 AA16947 BA169470 AA16947 In 142040 109405 AA230472 AA69276 AA16947 BE510020 Ha28455 In 142040 AA20040 A	20			
109172 A4160449 A4164000 A5016594.2271 A416040 A5016594.2271 A416040 A5016594.2271 A5016594 A	30			
228.63 AA187144 MM_001655Hs_2271 mcdobleni1				
122006 AA189170 A1897376 No.10941			NM_001955Hs.2271	endothelin 1
109300 AA030950 AA403276 AA170142		129208 AA189170	Al587376 Hs.109441	MSTP033 protein
109461 A.233472	35			
109465 AA234101 A17699 h.271613 h.27161				
109576 A2234110				
106557 P01969				
108677 F22206	40	109537 D80981	AI858695 Hs.34898	
109596 PR25254				
109585 F02544				
4.5 109625 F03016 H22400 H22897 ESTS prophosphatase (inorganic) 109626 F04050 H17900 H21916 H18901 H2191 H21				
#28376 F94258 AF19935 Hs.46011 pyrophorphates (morpanic) ESTs	45			
109671 F98998				
106989 F09905				
109820 F11115				
109833 1963371 872477 1420956 142742 110014 110039 110039 111039	50			
110014 H10956 AL109695 Har7422 Homo supplies nrBMA fall length insee histories and H10958 H10	50			Homo sapiens done 24993 mRNA sequence
100.99 H16568 R44657 Na2746 ESTs 10107 H1672 AV16969 Hs3444 ESTs 10155 H16591 H3694 Al556926 Hs35222 H10197 P20289 Al556926 Hs35222 H10197 P20289 Al556926 Hs35222 H10274 P10289 K21474 H18539 Hs15197 CTC1 gene methyl for KNA-1647 p10289 K21474 H18539 Hs1597 Hs1597 H18594 Hs1594 Hs15			AL109666 Hs.7242	Homo sapiens mRNA full length insert cDN
55 110107 H16772 AV151690 Has31444 Homo spilers mRNA for IMAA1647 pt 110157 H20859 12777 H20859 Has31627 AV080026 Has12270 H2022 AV080026 Has12270 H2022 AV080026 Has12270 H2022 AV080026 Has12270 H2022 H2022 AV080026 Has12270 H2022 H20				
10155 H16951 AISSS625 Ha59522 Has5922 Home supplies mRNA for IVAA 1647 g 110228 H23747 H19359 AV80928 Ha 12579 H19359 H23097 Has5959 H			R44557 Hs.23748	
110197 1201959 AWW30038 Tel. 12278 Aww30138 Tel. 12278	23		AW151660 Hs.31444	
110223 123747 119338 1431897 ESTs CTL game				
110396 143087 H38087 H480589 CTL2 gene 110396 143087 H480589 H480581 H				
11/3342 H40567		110306 H38087		CTL2 gene
11/3355 H46996	60			
116511 1493940				
119523 157154 ADM0354 http://dx.doi.org/10.2003/157154 http://dx.d				
19715 1967/12 1967/12 1967/12 1968/029 1975/14 1975/04 1975/				
428454 N25246 U55536 hts164576 symplosomasi-associated protein, 23 for 1924 states of 1924 state	65		H96712 Hs.269029	ESTs
451863 NZ7100 MM_076586916_267182 134253 N38916 AV87424 1548.086 70 11938 N49592 M45922 H383034 11938 N49597 M159578+102577 111981 N59435 A1165839 H3271614 111128 N61939 AV85954 H15973 11128 N61939 AV85954 H15973 75 11126 N68694 A1834273 H35711 75 11126 N68694 A1834296 H152804 EETs			AW302200 Hs.6336	KIAA0672 gene product
134233 NSS916 AW377445 144.096 RNA (Quartie-7) methytimanelisense of 11983 MSS916 AW37445 144.096 RNA (Quartie-7) methytimanelisense of 11983 NSS9157 NM_USSS78-14267 (AM1-12724 fis, d 411.494 NSS918 AW3745 HA-12724 (AM1-12724 fis, d 411.494 NSS918 AW3745 HA-12724 AW3745 (AM1-12724 fis, d 411.494 NSS918 AW3745 (AM1-12724 fis, d 411.494 NSS918 AW3745 AW3745 (AM1-12724 fis, d 411.494 NSS918 AW3745 (AM1-1		428454 N25249		synaptosomal-associated protein, 23kD
10938 N48982 M4982 H5.38034 Homo sapiens dDNA FLJ12924 fis, d 11982 N51957 M1019587Hs10297 ML1 problem ML1 probl			NM_U16569HS.207162 AM/073/43 He 8//86	RNA (numino 7.) methyltraneferoco
11083 N51957 NM_01587Hs.10267 ML1 profein 111081 N59435 A1146349 Hs.271614 OGI-112 protein 111128 N64139 AW503634 Hs.19074 L4TS (targe tumor suppressor, Drosc 431548 N66981 AI83427 Hs.9711 onvel protein 75 111216 N86840 AW139408 Hs.152940 ESTS	70			Homo sapiens cDNA FLJ12924 fis. clone NT
111081 N59435 A1146349 Hs.271614 CGI-112 protein 111128 N64139 AW505394 Hs.19074 LATS (large tumor suppressor, Drosc 431548 N66981 Al834273 Hs.9711 novel protein 75 111216 N88640 AW139408 Hs.152940 ESTS	, ,			
431548 N66981 AI834273 Hs.9711 novel protein 75 111216 N68640 AW139408 Hs.152940 ESTs		111081 N59435	AI146349 Hs.271614	CGI-112 protein
75 111216 N68640 AW139408 Hs.152940 ESTs				LATS (large tumor suppressor, Drosophila
	75	431548 N66981		
407002 100002 7,000,000 100000 DENDIT (Pap-diarraphilis) toxy	15	111210 N0004U 437562 N69352		DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
		-0/002 110002	001000 1101-200	vol out the toler tol out bulleth

	111000 B00100	A1110700770 11 40057	FMT-
	111399 R00138 111514 R07998	AW270776 Hs.18857 R07998	ESTS
	428744 R08929	BE267033 Hs.192853	gb:yf16g11.s1 Soares fetal liver spleen ubiquifin-conjugating enzyme E2G 2 (homo
	111574 R10307	Al024145 Hs.188526	ESTs
5	111804 R33354	AA482478 Hs. 181785	ESTs
	111831 R36083	R36095 Hs.268695	ESTs
	426773 R37938	NM_015556Hs.172180	KIAA0440 protein
	111904 R39330	Z41572	gb:HSCZYB122 normalized infant brain cDN
1.0	428371 R40816	AB012193 Hs.183874	cultin 4A
10	112033 R43162	R49031 Hs.22627	ESTs
	130987 R45698 112300 R54554	BE613269 Hs.21893 H24334 Hs.26125	hypothetical protein DKFZp761N0624 ESTs
	112513 R68425	R68425 Hs.13809	hypothetical protein FLJ 10648
	112514 R68568	R68568 Hs.183373	src homology 3 domain-containing protein
15	112522 R68763	R68857 Hs.265499	ESTs
	112540 R70467	R69751	gb:yi40a10.s1 Soares placenta Nb2HP Homo
	428655 R73565	H05769 Hs.188757	Horno sapiens, clone MGC:5564, mRNA, comp
	129534 R73640	AK002126 Hs.11260	hypothetical protein FLJ11264
20	112597 R78376	R78376 Hs.29733	EST
20	112732 R92453 451798 T03865	R92453 Hs.34590 BE297567 Hs.27047	ESTs hypothetical protein FLJ20392
	451798 T03865 112888 T03872	BE297567 Hs.27047 AW195317 Hs.107716	hypothetical protein FLJ20392
	131863 T10072	Al656378 Hs.33461	ESTs
	112911 T10080	AW732747 Hs.13493	like mouse brain protein E46
25	132215 T10132	AL035703 Hs.4236	KIAA0478 gene product
	112931 T15343	T02966 Hs.167428	ESTs
	112984 T23457	T16971 Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p
	112998 T23555	H11257 Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se
30	133376 T23670 113026 T23948	BE618768 Hs.7232 AA376654	acetyl-Coenzyme A carboxylase alpha eukaryotic translation initiation factor
50	113070 T33464	AB032977 Hs.6298	KIAA1151 protein
	410781 T34413	Al375672 Hs.165028	ESTs
	113074 T34611	AK001335 Hs.31137	protein tyrosine phosphatase, receptor t
	113095 T40920	AA828380 Hs.126733	ESTs
35	113179 T55182	BE622021 Hs.152571	ESTs, Highly similar to IGF-II mRNA-bind
	113337 T77453	T77453 Hs.302234	ESTs
	113421 T84039 113454 T86458	Al769400 Hs.189729 Al022166 Hs.16188	ESTs ESTs
	113481 T87693	T87693 Hs.204327	FST
40	453345 T89350	AA302862 Hs.90063	neurocalcin delta
	113557 T90945	H66470 Hs.16004	ESTs
	113559 T90987	T79763 Hs.14514	ESTs
	113589 T91883	Al078554 Hs.15682	ESTs
45	113591 T91881	T91881 Hs.200597	KIAA0563 gene product
43	113619 T93783 113683 T96687	R08665 Hs.17244 AB035335 Hs.144519	hypothetical protein FLJ 13605 T-cell leukemia/lymphoma 6
	113692 T96944	AL360143 Hs.17936	DKFZP434H132 protein
	113702 T97307	T97307	gb:ye53h05.s1 Soares fetal liver spleen
	113717 T97764	T99513 Hs.187447	ESTs
50	113824 W48817	Al631964 Hs.34447	ESTs
	113840 W58343	R72137 Hs.7949	DKFZP586B2420 protein
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	113902 W74644 113904 W74761	AA340111 Hs.100009 AF125044 Hs.19196	acyi-Coenzyme A oxidase 1, palmitoyi ubiqulfin-conjugating enzyme HBUCE1
55	113905 W74802	R81733 Hs.33106	ESTs
00	113931 W81205	BE255499 Hs.3496	hypothetical protein MGC15749
	113932 W81237	AA256444 Hs.126485	hypothetical protein FLJ12604; KIAA1692
	131965 W90146	W79283 Hs.35962	ESTs
	114035 W92798	W92798 Hs.269181	ESTs
60	114106 Z38412	AW602528	gb:RC5-BT0562-260100-011-A02 BT0562 Homo
	457308 Z38709 114161 Z38904	Al416988 Hs.238272 BE548222 Hs.299883	inosttol 1,4,5-triphosphate receptor, ty hypothetical protein FLJ23399
	424949 Z39103	AF052212 Hs.153934	core-binding factor, runt domain, alpha
	457548 Z39930	AW069534 Hs.279583	CGI-81 protein
65	128937 Z39939	AA251380 Hs.10726	ESTs, Weakly similar to ALU1_HUMAN ALU S
	432554 Z40012	Al479813 Hs.278411	NCK-associated protein 1
	114277 Z40377	Al052229 Hs.25373	ESTs, Weakly similar to T20410 hypotheti
	114304 Z40820	AI934204 Hs.16129	ESTs Homo sapiens mRNA; cDNA DKFZp566P013 (fr
70	114364 Z41680 432620 AA005112	AL117427 Hs.172778 AA777749 Hs.5978	LIM domain only 7
70	129034 AA005432	AA481157 Hs.108110	DKFZP547E2110 protein
	131881 AA010163	AW361018 Hs.3383	upstream regulatory element binding prot
	332421 AA026356	Al909968 Hs.108106	transcription factor
~-	114465 AA026901	BE621056 Hs.131731	hypothetical protein FLJ11099
75	451271 AA036867	AK001644 Hs.26156	hypothetical protein FLJ10782
	332498 AA044644	AA303661	lymphocyte-specific protein 1

	431555 AA046426	Al815470 Hs.260024	Cdc42 effector protein 3
	132944 AA054515	T96641 Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L.
	114618 AA084162 332509 AA085749	AW979261 Hs.291993	ESTs
5	114648 AA101056	AA128376 Hs.153884 AA101056	ATP binding protein associated with cell gb:zn25b03.s1 Stratagene neuroepithelium
,	114658 AA102746	AA102383 Hs.249190	tumor necrosis factor receptor superfami
	132456 AA114250	AB011084 Hs.48924	KIAA0512 gene product; ALEX2
	450847 AA126561	NM_003155Hs.25590	stanniocalcin 1
	132225 AA128980	AA128980	gb:zo09a11.s1 Stratagene neuroepithelium
10	437197 AA129757	W38586	guanine nucleotide binding protein (G pr
	114709 AA129921 456926 AA133331	AA397651 Hs.301959 AB018284 Hs.158688	proline synthetase co-transcribed (bacte KIAA0741 gene product
	114750 AA135958	AA887211 Hs.129467	ESTs
	426806 AA136524	T19228 Hs.172572	hypothetical protein FLJ20093
15	114763 AA147044	AA810755 Hs.102500	hypothetical protein dJ511E16.2
	114767 AA148885	Al859865 Hs.154443	minichromosome mainlenance deficient (S.
	114774 AA150043 129388 AA151621	AV656017 Hs.184325 AA662477 Hs.110964	CGI-76 protein hypothetical protein FLJ23471
	457742 AA155743	BE561824 Hs.273369	uncharacterized hematopoietic stem/proge
20	456200 AA156335	AA768242 Hs.80618	hypothetical protein
	130207 AA156336	AF044209 Hs.144904	nuclear receptor co-repressor 1
	114798 AA159181	AA159181 Hs.54900	serologically defined colon cancer antig
	114800 AA159825	Z19448 Hs.131887 AA252937 Hs.283522	ESTs, Weakly similar to T24396 hypotheti Homo sapiens mRNA; cDNA DKFZp434J1912 (f
25	114828 AA234185 114846 AA234929	BE018882 Hs.166196	ATPase, Class I, type 8B, member 1
23	114848 AA234935	BE614347 Hs.169615	hypothetical protein FLJ20989
	114902 AA236359	AV/275480 Hs.39504	hypothetical protein MGC4308
	132271 AA236466	AB030034 Hs.115175	stanle-alpha motif and leucine zipper c
30	114907 AA236535	N29390 Hs.13804	hypothetical protein dJ462O23.2
30	420170 AA236935 132204 AA236942	U43374 Hs.95631 AA235827 Hs.42265	Human normal keratinocyte mRNA ESTs
	114928 AA237018	AA237018 Hs.94869	ESTs
	132481 AA237025	W93378 Hs.49614	ESTs
2.5	114932 AA242751	AA971436 Hs.16218	KIAA0903 protein
35	314162 AA242760 131006 AA242763	BE041820 Hs.38516 AF064104 Hs.22116	Homo sapiens, clone MGC:15887, mRNA, com CDC14 (cell division cycle 14, S, cerevi
	131008 AA242763 114935 AA242809	H23329 Hs.290880	ESTs, Weakly similar to ALU1_HUMAN ALU S
	408908 AA243133	BE296227 Hs.250822	serine/threonine kinase 15
	437754 AA243495	R60366 Hs.5822	Homo sapiens cDNA: FLJ22120 fis, clone H
40	114957 AA243706	AW170425 Hs.87680	ESTs
	114974 AA250848	AV/966931 Hs.302649	nucleosome assembly protein 1-like 1
	114977 AA250868 114995 AA251152	AW296978 Hs.87787 AA769266 Hs.193657	ESTs ESTs
	115005 AA251544	AI760825 Hs.153042	ESTs
45	417177 AA251792	NM_004458Hs.81452	fatty-acid-Coenzyme A ligase, long-chain
	115026 AA252144	AA251972 Hs.188718	ESTs
	115045 AA252524	AW014549 Hs.58373	ESTs ESTs
	115068 AA253461 133138 AA255522	AV/512260 Hs.87767 AV657594 Hs.181161	Homo sapiens cDNA FLJ14643 fis, clone NT
50	332668 AA255522	AV657594 Hs.181161	ESTs
	115114 AA256468	AA527548 Hs.7527	small fragment nuclease
	129584 AA256528	AV656017 Hs.184325	CGI-76 protein
	115137 AA257976	AW968304 Hs.56156	ESTs
55	417187 AA258296 115166 AA258409	AE011151 Hs.334659 AF095727 Hs.287832	hypothetical protein MGC14139 myelin protein zero-like 1
33	115167 AA258421	AA749209 Hs.43728	hypothetical protein
	436719 AA262077	Y11192 Hs.5299	aldehyde dehydrogenase 5 family, member
	115239 AA278650	BE251328 Hs.73291	hypothetical protein FLJ10881
60	115243 AA278766	AA806600 Hs.116665 U49436	KIAA1842 protein KIAA1856 protein
00	428419 AA280791 115322 AA280819	L08895 Hs.78995	MADS box transcription enhancer factor 2
	413303 AA280828	AW836130 Hs.75277	hypothetical protein FLJ13910
	115372 AA282195	AW014385 Hs.88678	ESTs, Weakly similar to Unknown (H.sapie
	409962 AA283127	U82671 Hs.57698	Target CAT
65	130269 AA284694	F05422 Hs.168352 AA286914 Hs.183299	nucleoporin-like protein 1 ESTs
	456570 AA291137 332675 AA291708	BE439944	ESTS
	407864 AA293495	AF069291 Hs.40539	chromosome 8 open reading frame 1
	115536 AA347193	AK001468 Hs.62180	anillin (Drosophila Scraps homolog), act
70	408799 AA398474	AA059412 Hs.47986	hypothetical protein MGC10940
	115575 AA398512 115601 AA400277	AA393254 Hs.43619 AA148984 Hs.48849	ESTs ESTs, Weakly similar to ALU4_HUMAN ALU S
	115601 AA4002// 434428 AA400896	D14540 Hs.199160	myeloid/lymphoid or mixed-lineage leukem
	115683 AA410345	AF255910 Hs.54650	iunctional adhesion molecule 2
75	115715 AA416733	BE395161 Hs.1390	proteasome (prosome, macropain) subunit,
	132952 AA425154	Al658580 Hs.61426	Homo sapiens mesenchymal stem cell prote

	115810	AA426573	AA486620	He 41135	endomucin-2
	409124		AW292809		N-acetylglucosaminidase, alpha- (Sanfili
	115895	AA436182	AB033035	Hs.51965	KIAA1209 protein
_	458073	AA437099	AA192669	Hs.45032	ESTs
5		AA446585	AI636361	Hs.179520	hypothetical protein MGC10702
	115967	AA446887	A1745379	Hs.42911	ESTs
		AA447224	BE513442		hypothetical protein FLJ10631
		AA447709 AA453624	AA447709	Hs.268115	ESTs, Weakly similar to T08599 probable DKFZp434J1813 protein
10		AA455044	AA252468 BE384932		ESTs, Weakly similar to AF257182 1 G-pro
10		AA456045	AA043429	Hs.62618	ESTs
		AA460454	R19768	Hs.172788	ALEX3 protein
		AA476494	BE622792		ALEX3 protein
	116213	AA476738	AA292105	Hs.326740	hypothetical protein MGC10947
15	432645	AA481422	D14041	Hs.347340	H-2K binding factor-2
	116265		BE297412		hypothetical protein
	129334			Hs.343551	hypothetical protein FLJ22584
	116274		Al129767	Hs.182874	guanine nucleotide binding protein (G pr
20	426002 116331		N41300	Hs.165998 Hs.71616	PAI-1 mRNA-binding protein Homo sapiens mRNA; cDNA DKFZp586N1720 (f
20		AA491250	AF155827	Hs.203963	hypothetical protein FLJ10339
	132994	AA505133	AA112748	Hs.279905	clone HQ0310 PRO0310p1
	418538		BE244323		exportin, tRNA (nuclear export receptor
	116391		T86558	Hs.75113	general transcription factor IIIA
25	116394	AA599574	NM_00603	3Hs.65370	lipase, endothelial
	134531		Al742845	Hs.110713	DEK oncogene (DNA binding)
	116417	AA609309	AW499664		Human clone 23826 mRNA sequence
		AA609710	AF191018		putative nucleofide binding protein, est
30		AA610068 AA621399	AA251594 R80137	Hs.43913 Hs.302738	PIBF1 gene product Homo sapiens cDNA: FLJ21425 fis, clone C
30		AA621752		Hs.178761	26S proteasome-associated pad1 homolog
		C21523	AW449822		ESTs
	116541		D12160	Hs.249212	polymerase (RNA) III (DNA directed) (155
	132557			Hs.169531	ESTs
35	414964	D25801	AA337548	Hs.333402	hypothetical protein MGC12760
	116571		D45652	Hs.211604	gb:HUMGS02848 Human adult lung 3' direct
	451522		BE565817	Hs.26498	hypothetical protein FLJ21657
	421919	D80504	AJ224901	Hs.109526	zinc finger protein 198
40	116643 116661	F03010 F04247	Al367044 R61504	Hs.153638	myeloid/lymphoid or mixed-lineage leukem gb:yh16a03.s1 Soares Infant brain 1NIB H
70	116715	F10966	AL117440	Hs.170263	tumor protein p53-binding protein, 1
	116729	F13700	BE549407	Hs.115823	ribonuclease P, 40kD subunit
	318709	H05063	R52576	Hs.285280	Homo sapiens cDNA: FLJ22096 fis, clone H
	418999		NM_00012		erythropoletin receptor
45	116773		Al823410	Hs.343581	karyophenn alpha 1 (importin alpha 5)
	116780		H22566	Hs.63931	ESTs
	453884		AA355925	Hs.36232	KIAA0186 gene product
	116819 427278	H53073	H53073 AL031428	Hs.93698 Hs.174174	EST KIAA0601 protein
50	407833		AW955632		ESTs, Weakly similar to S19560 proline-r
50	116844		H64938	Hs.337434	ESTs, Weakly similar to A46010 X-linked
		H64973	AA649530		gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens
	116892	H69535	AI573283	Hs.38458	ESTs
	116925	H73110	H73110	Hs.260603	ESTs, Moderately similar to A47582 B-cel
55	116981	H81783	N29218	Hs.40290	ESTs
		H86259	AC005757		hypothetical protein
	117031 117034		H88353 U72209	Hs.347265	gb:yw21a02.s1 Morton Fetal Cochlea Homo YY1-associated factor 2
	431129		AL137751	Hs.263671	Homo sapiens mRNA; cDNA DKFZp434l0812 (f
60		H93708	AA334551	110.20007	sperm specific antigen 2
	117280		M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C
	117344	N24046	R19085	Hs.210706	Homo sapiens cDNA FLJ13182 fis, clone NT
	117422		Al355562	Hs.43880	ESTs, Weakly similar to A46010 X-linked
	117475		N30205	Hs.93740	ESTs, Weakly similar to 138022 hypotheti
65		N30621	N30621	Hs.44203	ESTs
	117937		AF044209 AF044209	Hs.144904 Hs.144904	nuclear receptor co-repressor 1 nuclear receptor co-repressor 1
	130207 117549		N33390	Hs.44483	FST
	117683		N40180	11244400	gb:yy44d02.s1 Soares_multiple_sclerosis_
70	117710	N45198	N45198	Hs.47248	ESTs, Highly similar to similar to Cdc14
	117791	N48325	N48325	Hs.93956	EST
	117822	N48913	AA706282		ESTs
	422544	N49394	AB018259	Hs.118140	KIAA0716 gene product
75	117895		AW450348	HS.93996	ESTs, Highly similar to SORL_HUMAN SORTI
75	452259	N50721	AA317439		signal sequence receptor, gamma (translo Homo sapiens clone 25218 mRNA sequence
	133057	N53143	AA465131	1004001	numu sapiens quite 252 to misses sequence

	118103 N55326	AA401733 Hs.184134	ESTs
	118111 N55493	N55493	gb:yv50c02.s1 Soares fetal liver spieen
	118129 N57493	N57493	gb:yy54c08.s1 Soares_multiple_sclerosis_
	118278 N62955	N62955 Hs.316433	Homo sepiens cDNA FLJ11375 fis, clone HE
5	118329 N63520	N63520	gb:yy62l01.s1 Soares_multiple_sclerosis_
	118336 N63604	BE327311 Hs.47166	HT021
	417098 N64166	AB017365 Hs.173859	frizzled (Drosophila) homolog 7
	118363 N64168	Al183838 Hs.48938	hypothetical protein FLJ21802
	118364 N64191	N46114 Hs.29169	hypothetical protein FLJ22623
10	118475 N66845	N66845	gb;za46c11.s1 Soares fetal liver spleen
	118491 N67135	AV647908 Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H
	118500 N67295	W32889 Hs.154329	ESTs
	118584 N68963	AW136928	gb:UI-H-BI1-adp-d-08-0-UI.s1 NCI_CGAP_Su
	456647 N69331	Al252640 Hs.110364	peptidylprolyl isomerase C (cyclophilin
15	118661 N70777	AL137554 Hs.49927	protein kinase NYD-SP15
	118684 N71364	N71313 Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K
	118689 N71545	AW390601 Hs.184544	Homo saplens, clone IMAGE:3355383, mRNA,
	118690 N71571	N71571 Hs.269142	ESTs
20	118766 N74456	N74456 Hs.50499 N75594 Hs.285921	EST ESTs, Moderately similar to T47135 hypot
20	118793 N75594 118817 N79035	Al668658 Hs.50797	ESTs, Moderately similar to 147 135 hypot ESTs
	118844 N80279	AL035364 Hs.50891	hypothetical protein
	118919 N91797	AW452696 Hs.130760	myosin phosphatase, target subunit 2
	129558 N92454	AW580922 Hs.180446	karyopherin (importin) beta 1
25	407604 N94581	AW191962 Hs.288061	collagen, type VIII, alpha 2
23	118996 N94746	N94746 Hs.274248	hypothetical protein FLJ20758
	119021 N98238	N98238 Hs.55185	ESTs
	119039 R02384	Al160570 Hs.252097	pregnancy specific bela-1-glycoprotein 6
	119063 R16833	R16833 Hs.53106	ESTs, Moderately similar to ALU1, HUMAN A
30	332622 R41828	R10674	CSR1 protein
	119111 R43203	T02865 Hs.328321	EST
	415115 R46395	AA214228 Hs.127751	hypothetical protein
	119146 R58863	R58863 Hs.91815	ESTs
	449224 R78248	AW995911 Hs.299883	hypothetical protein FLJ23399
35	119239 T11483	T11483	gb:CHR90049 Chromosome 9 exon Homo sapie
	119281 T16896	Al692322 Hs.65373	ESTs, Weakly similar to T02345 hypotheti
	119298 T23820	NM_001241Hs.155478	cyclin T2
	126502 T30222	T10077 Hs.13453	hypothetical protein FLJ14753
40	419983 W15275	W55956 Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
40	119558 W38194	W38194	Empirically selected from AFFX single pr
	429641 W42414	AW081883 Hs.211578	Homo sapiens cDNA: FLJ23037 fis, clone L
	419445 W49632	AA884471 Hs.90449	Human clone 23908 mRNA sequence
	119650 W57613 119654 W57759	R82342 Hs.79856 W57759	ESTs, Weakly similar to S65657 alpha-1C- gb:zd20g11.s1 Soares_fetal_heart_NbHH19W
45	119683 W61118	W65379 Hs.57835	ESTs
73	119694 W65344	AA041350 Hs.57847	ESTs, Moderately similar to ICE4_HUMAN C
	119718 W69216	W69216 Hs.92848	ESTs
	410365 W69379	Al287518	Homo sapiens mRNA; cDNA DKFZp586D0923 (f
	119938 W86728	AW014862 Hs.58885	ESTs
50	120128 Z38499	BE379320 Hs.91448	MKP-1 like protein tyrosine phosphatase
	120130 Z38630	AA045767 Hs.5300	bladder cancer associated protein
	120148 Z39494	F02806 Hs.65765	ESTs
	120155 Z39623	Z39623 Hs.65783	ESTs
	451979 Z40071	F06972 Hs.27372	BMX non-receptor tyrosine kinase
55	120183 Z40174	AW082866 Hs.65882	ESTs
	120184 Z40182	Z40182 Hs.65885	EST
	120211 Z40904	Z40904 Hs.66012	EST
	120245 AA166965	AW959615 Hs.111045	ESTs
C0	120247 AA167500	AA167500 Hs.103939	EST
60	120254 AA169599	W90403 Hs.111054	ESTs
	120259 AA171724	AW014786 Hs.192742	hypothetical protein FLJ12785
	120260 AA171739 120275 AA177105	AK000061 Hs.101590 AA177105 Hs.78457	hypothetical protein solute carrier family 25 (mitochondrial
	120284 AA182626	AA179656	gb:zp54e11.s1 Stratagene NT2 neuronal pr
65	417735 AA186324	AA188175 Hs.82506	KIAA1254 protein
05	422137 AA192099	AJ236885	zinc finger protein 148 (pHZ-52)
	120302 AA192173	AA837098 Hs.269933	ESTs
	120303 AA192415	Al216292 Hs.96184	ESTs
	120305 AA192553	AW295096 Hs.101337	uncoupling protein 3 (mitochondrial, pro
70	120319 AA194851	T57776 Hs.191094	ESTs
	408729 AA195520	AA195764 Hs.72639	ESTs
	120326 AA196300	AA196300 Hs.21145	hypothetical protein RG083M05.2
	133145 AA196549	H94227 Hs.6592	Homo sapiens, clone IMAGE:2961368, mRNA,
	120327 AA196721	AK000292 Hs.130732	hypothetical protein FLJ20285
75	120328 AA196979	AA923278 Hs.290905	ESTs, Weakly similar to protease (H.sapi
	120340 AA206828	AA206828	gb:zq80b08.s1 Stratagene hNT neuron (937

	417122	AA207123	AI906291	Hs.81234	immunoglobulin superfamily, member 3
	131522	AA214539	A1380040	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi
	421787	AA226914	AA227068	Hs.108301	nuclear receptor subfamily 2, group C, m
		AA227260	AF028706	Hs.111227	Zic family member 3 (odd-paired Drosophi
5		AA227469	AA227469	110.111.	gb:zr18a07.s1 Stratagene NT2 neuronal pr
-	120390		AA837093	Hs.111460	caldum/calmodulin-dependent protein kin
	410804	AA233334	U64820	Hs.66521	Machado-Joseph disease (spinocerebellar
	434223				
		AA233347	AI825842	Hs.3776	zinc finger protein 216
1.0	312771	AA233714	AA018515	Hs.264482	Homo sapiens mRNA; cDNA DKFZp761A0411
10	120396	AA233796	AA134006	Hs.79306	eukaryotic translation initiation factor
	120409	AA235050	AA235050		gb:zs38e04.s1 Soares_NhHMPu_S1 Homo sap
	120414	AA235704		Hs.181202	hypothetical protein FLJ10038
	120420	AA236031	Al128114	Hs.112885	spinal cord-derived growth factor-B
	120422	AA236352	AL133097	Hs.301717	hypothetical protein DKFZp434N1928
15	419326	AA236390	W94915	Hs.42419	ESTs
	120423	AA236453	AA236453	Hs.18978	Homo saplens cDNA: FLJ22822 fis, clone K
	120435	AA243370	AA243370	Hs.96450	EST
		AA250947	AA250947	Hs.170263	tumor protein p53-binding protein, 1
		AA251083	AA251720	Hs.104347	ESTs, Weakly similar to ALUC_HUMAN !!!!
20					
20		AA251113	AA488750	Hs.88414	BTB and CNC homology 1, basic leucine zi
	120473	AA251973	AA251973	Hs.269988	ESTs
	128922	AA252023	A1244901	Hs.9589	ubiquilin 1
	120477	AA252414	AA252414	Hs.43141	DKFZP727C091 protein
	120479	AA252650	AF006689	Hs.110299	mitogen-activated protein kinase kinase
25	120488	AA255523	AW952916	Hs.63510	KIAA0141 gene product
	120510	AA258128	AI796395	Hs.111377	ESTs
	120527	AA262105	AA262105	Hs.4094	Homo sapiens cDNA FLJ14208 fis, clone NT
	120528	AA262107	A1923511	Hs.104413	ESTs
	120529	AA262235	A1434823	Hs.104415	ESTs
30		AA278298			
30	120541		W07318	Hs.240	M-phase phosphoprotein 1
	120544	AA278721	BE548277	Hs.103104	ESTs
	120562	AA280036	BE244580	Hs.342307	hypothetical protein FLJ10330
	120569	AA280648	AA807544	Hs.24970	ESTs, Weakly similar to B34323 GTP-bindl
	120571	AA280738	AB037744	Hs.34892	KIAA1323 protein
35	120572	AA280794	H39599	Hs.294008	ESTs
	129434	AA280837	AW967495	Hs.186644	ESTs
	130529	AA280886	AA178953	Hs.309648	gb:zp39e03.s1 Stratagene muscle 937209 H
		AA280934	AW978022		hypothetical protein DKFZp762E1511; KIAA
	409339		AB020686	Hs.54037	eclonucleotide pyrophosphatase/phosphodi
40	120591		AF078847	Hs.191356	ecunicación pyrophicapridicación formation
40		AA281797	APU/004/	HS. 191300	general transcription factor IIH, polype
	120593		AA748355	Hs.193522	ESTs
		AA283002	Z11773	Hs.237786	zinc finger protein 187
	440303	AA283709	AA306166	Hs.7145	calpain 7
		AA283902	AW978721	Hs.266076	ESTs, Weakly similar to A46010 X-linked
45	409702	AA284108	Al752244		eukaryotic translation elongation factor
	456870	AA284109	AI241084	Hs.154353	nonselective sodium potassium/proton exc
	132614	AA284371	AA284371	Hs.118064	similar to rat nuclear ubiquitous casein
		AA284744	AA115496	Hs.336898	Homo sapiens, Similar to RIKEN cDNA 1810
		AA284784	BE617856	Hs.99756	mitochondrial ribosome recycling factor
50	120621	AA284840	AW961294		hypothetical protein FLJ23459
50		AA286844	AA286844		hypothetical protein FLJ13164
		AA287032	AW172431		ESTs
		AA287038	AI869129	Hs.96616	ESTs
	120660		AA286785	Hs.99677	ESTs
55		AA287553	BE622187	Hs.99670	ESTs, Weakly similar to 138022 hypotheti
	120661	AA287556	AA287556	Hs.263412	ESTs, Weakly similar to ALUB_HUMAN !!!!
	429828	AA287564	AB019494	Hs.225767	IDN3 protein
	452291	AA291015	AF015592	Hs.28853	CDC7 (cell division cycle 7, S. cerevisi
	120699	AA291716	Al683243	Hs.97258	ESTs, Moderately similar to S29539 ribos
60	100690	AA291749	AA383256	Hs.1657	estrogen receptor 1
00		AA293656	AA293655		ESTs
	120726			Hs.21198	
	120737	AA302430	AL049176	Hs.82223	chordin-like
	120745	AA302809	AA302809		gb:EST10426 Adipose tissue, white I Homo
	443574	AA302820	U83993	Hs.321709	punnergic receptor P2X, ligand-gated to
65		AA310499	Al191410	Hs.96693	ESTs, Moderately similar to 2109260A B c
	120761	AA321890	AA321890		branched chain keto acid dehydrogenase E
	120768	AA340589	AA340589	Hs.104560	EST
	120769		AI769467	Hs.9475	ESTs
		AA342457	AL038812	Hs.96800	ESTs, Moderately similar to ALU7_HUMAN A
70	120793	AA342864	AA342864	Hs.96812	ESTs
70				Hs.96820	ESTS
	120796	AA342973	A1247356	H9.900ZU	
		AA346495	AA346495		gb:EST52657 Fetal heart II Homo sapiens
	332633	AA347573	AL120071	Hs.48998	fibronectin leucine rich transmembrane p
	120825	AA347614	A1280215	Hs.96885	ESTs
75	120827	AA347717	AA382525	Hs.132967	Human EST clone 122887 mariner transposo
	120839	AA348913	AA348913		gb:EST55442 Infant adrenal gland II Homo

	120850 AA349647	AA349647 Hs.96927	Homo sapiens cDNA FLJ12573 fis, clone NT
	120852 AA349773	AA349773 Hs.191564	ESTs
	128852 AA350641	R40622 Hs.106601	ESTs
	135240 AA357159	AA357159 Hs.96986	EST
5	120870 AA357172	AA357172 Hs.292581	ESTs, Moderately similar to ALU1_HUMAN A
-	120894 AA370132	AA370132 Hs.97063	ESTs
	435737 AA370472	AF229839 Hs.173202	I-kappa-B-interacting Ras-like protein 1
	120897 AA370867	AA370867 Hs.97079	ESTs, Moderately similar to AF174605 1 F
	120915 AA377296	AL135556 Hs.97104	ESTs
10	120935 AA383902	AL048409 Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S
	120936 AA385934	AA385934 Hs.97184	EST, Highly similar to (defline not avail
	120937 AA386255	AA386255 Hs.97186	EST
	120938 AA386260	AA386260 Hs.104632	EST
	417632 AA386266	R20855 Hs.5422	glycoprotein M6B
15	120960 AA398014	AA398014 Hs.104684	EST '
	120985 AA398222	Al219896 Hs.97592	ESTs
	120988 AA398235	AA398235 Hs.97631	ESTs
	121008 AA398348	AA398348 Hs.130546	Human DNA sequence from clone RP11-251J8
	121029 AA398482	AA398482 Hs.97641	EST
20	121032 AA398504	AA393037 Hs.161798	ESTs
	121033 AA398505	AA398505 Hs.97360	ESTs
	121034 AA398507	AL389951 Hs.271623	nucleoporin 50kD
	121035 AA398523	AA398523 Hs.210579	ESTs
0.5	121058 AA398625	AA398625 Hs.97391	ESTs .
25	121060 AA398632	AA398632 Hs.97395	ESTs
	121061 AA398633	AA393288 Hs.97396	ESTs
	121091 AA398894	AA398894 Hs.97657	ESTs, Moderately similar to ALU8_HUMAN A
	121092 AA398895	AA398895 Hs.97658	EST
30	121094 AA398900	AA402505	gb:zt62h10.r1 Soares_testis_NHT Homo sap
30	121096 AA398904	AA398904 Hs.332690 AA398187 Hs.104682	ESTs ESTs, Weakly similar to mitochondrial ci
	121115 AA399122 121121 AA399371	AA399371 Hs.189095	similar to SALL1 (sal (Drosophila)-like
	121121 AA399373	Al126713 Hs.192233	ESTs, Highly similar to T00337 hypotheti
	121125 AA399441	AL042981 Hs.251278	KIAA1201 protein
35	121151 AA399636	AA399636 Hs.143629	ESTs
55	121153 AA399640	AA399640 Hs.97694	ESTs
	121163 AA399680	Al676062 Hs.111902	ESTs
	121176 AA400080	AL121523 Hs.97774	ESTs
	121192 AA400262	AA400262 Hs.190093	ESTs
40	121223 AA400725	Al002110 Hs.97169	ESTs, Weakly similar to dJ667H12.2.1 [H.
	121227 AA400748	AA400748 Hs.97823	Homo sapiens mRNA; cDNA DKFZp434D024 (fr
	121231 AA400780	AA814948 Hs.96343	ESTs, Weakly similar to ALUC_HUMAN !!!!
	121278 AA401631	AA037121 Hs.98518	Homo sapiens cDNA FLJ11490 fis, clone HE
	121279 AA401688	AA292873 Hs.177996	ESTs
45	121282 AA401695	AA401695 Hs.97334	ESTs
	121299 AA402227	AA402227 Hs.22826	tropomodulin 3 (ubiquitous)
	121301 AA402329	NM_006202Hs.89901	phosphodiesterase 4A, cAMP-specific (dun
	121302 AA402398	AA402587 Hs.325520	LAT1-3TM protein
	121304 AA402449	AA293863 Hs.97316	EST
50	121305 AA402468	AA402468 Hs.291557	ESTs
	134721 AA403268	AK000112 Hs.89306	hypothetical protein FLJ20105
	121323 AA403314	AA291411 Hs.97247	ESTs
	121324 AA404229	AA404229 Hs.97842	EST
5.5	444422 AA404260	Al768623 Hs.108264	ESTs
55	131074 AA404271	U16125 Hs.181581	glutamate receptor, ionotropic, kainate
	121344 AA405026 121348 AA405182	AA405026 Hs.193754 AA405182 Hs.97973	ESTs ESTs
	121350 AA405237	AA405237	gb:zt06e10.s1 NCI_CGAP_GCB1 Homo sapiens
	121400 AA406061	AA406061 Hs.98001	EST
60	121402 AA406063	AA406063 Hs.98003	ESTs
00	121403 AA406070	AA406070 Hs.98004	EST
	121408 AA406137	AA406137 Hs.98019	EST
	121431 AA406335	AA035279 Hs.176731	ESTs
	121471 AA411804	AA411804 Hs.261575	ESTs
65	121474 AA411833	AA402335 Hs.188760	ESTs, Highly similar to Trad [H.sapiens]
	121526 AA412219	AW665325 Hs.98120	ESTs
	121530 AA412259	AA778658 Hs.98122	ESTs
	121558 AA412497	AA412497	gb:zt95g12.s1 Soares_testis_NHT Homo sap
	121559 AA412498	Al192044 Hs.104778	ESTs
70	121584 AA416586	Al024471 Hs.98232	ESTs
	121609 AA416867	AA416867 Hs.98185	EST
	121612 AA416874	AA416874 Hs.98168	ESTs
	121737 AA421133	AA421133 Hs.104671	erythrocyte transmembrane protein
75	121740 AA421138	AA421138 Hs.143835	EST
75	436032 AA422079	AA150797 Hs.109276	latexin protein
	121784 AA423837	T90789 Hs.94308	RAB35, member RAS oncogene family

	121802 AA424328	Al251870 Hs.188898	ESTs
	121803 AA424339	Al338371 Hs.157173	ESTs
	135286 AA424469	AW023482 Hs.97849	ESTs
	332778 AA424469	AW023482 Hs.97849	ESTs
5	121806 AA424502	AA424313 Hs.98402	ESTs
-	129517 AA425004	AW972853 Hs.112237	FSTs
	121845 AA425734	Al732692 Hs.165066	ESTs, Moderately similar to ALU2_HUMAN A
	121853 AA425887	AA425887 Hs.98502	hypothetical protein FLJ14303
		AA426456 Hs.98469	FSTs
10	121891 AA426456		
10	121895 AA427396	AA427396	gb:zw33a02.s1 Soares ovary tumor NbHOT H
	121899 AA427555	R55341 Hs.50421	KIAA0203 gene product
	121917 AA428218	AA406397 Hs.139425	ESTs
	121918 AA428242	BE274689 Hs.184175	chromosome 2 open reading frame 3
	121919 AA428281	AA428281 Hs.98560	EST
15	121941 AA428865	AA428865 Hs.98563	ESTs
	121942 AA428994	AW452701 Hs.293237	ESTs
	121970 AA429666	AA429666 Hs.98617	EST
	121993 AA430181	AW297880 Hs.98661	ESTs
	418706 AA430184	U73524 Hs.87465	ATP/GTP-binding protein
20	122022 AA431293	AA431293 Hs.98716	ESTs, Moderately similar to T42650 hypot
20	122050 AA431478	Al453076	ELAV (embryonic lethal, abnormal vision,
	122051 AA431492	AA431492 Hs.98742	EST
	122055 AA431732	AA431732 Hs.98747	EST
25	122105 AA432278	AW241685 Hs.98699	ESTs
25	122125 AA434411	AK000492 Hs.98806	hypothetical protein
	135235 AA435512	AW298244 Hs.266195	ESTs
	122162 AA435698	AA628233 Hs.79946	cytochrome P450, subfamily XIX (aromatiz
	422072 AA435711	AB018255 Hs.111138	KIAA0712 gene product
	415106 AA435815	U40763 Hs.77965	peptidyl-prolyl isomerase G (cyclophilin
- 30	122186 AA435842	AA398811 Hs.104673	ESTs
	122235 AA436475	AA436475 Hs.112227	membrane-associated nucleic acid binding
	412970 AA436489	AB026436 Hs.177534	dual specificity phosphatase 10
	419288 AA442060	AA256106 Hs.87507	ESTs
	122310 AA442079	AW192803 Hs.98974	ESTs, Weakly similar to S65824 reverse t
35	122334 AA443151	BE465894 Hs.98365	ESTs, Weakly similar to LB4D_HUMAN NADP-
33	122382 AA446133		ESTS, Weakly Similar to EB40_HOWKN WODE
			KIAA0399 protein
	122425 AA447145		
	122431 AA447398	AA447398 Hs.99104	ESTs
40	122450 AA447643	AA447643 Hs.112095	hypothetical protein DKFZp434F1819
40	426284 AA447742	AJ404468 Hs.284259	dynein, axonemal, heavy polypeptide 9
	122477 AA448226	AA448226 Hs.324123	ESTs
	122500 AA448825	AA448825 Hs.99190	ESTs
	122522 AA449444	AA299607 Hs.98969	ESTs
	122536 AA450087	AF060877 Hs.99236	regulator of G-protein signalling 20
45	122538 AA450211	AA450211 Hs.99239	ESTs
	122540 AA450244	AA476741 Hs.98279	ESTs, Weakly similar to A43932 mucin 2 p
	122560 AA452123	AW392342 Hs.283077	centrosomal P4,1-associated protein; unc
	421919 AA452155	AJ224901 Hs.109526	zinc finger protein 198
	122562 AA452156	AA452156	gb:zx29c03.s1 Soares_total_fetus_Nb2HF8_
50	122585 AA453036	Al681654 Hs.170737	hypothetical protein FLJ23251
50	122608 AA453526	AA453525 Hs.143077	ESTs
	122635 AA454085	AA454085	gb:zx33a08.s1 Soares_total_fetus_Nb2HF8_
	122636 AA454103	AW651706 Hs.99519	hypothetical protein FLJ14007
55	122653 AA454642	AW009166 Hs.99376	ESTs
22	122660 AA454935	Al816827 Hs.180069	nuclear respiratory factor 1
	122703 AA456323	AA456323 Hs.269369	ESTs
	122724 AA457395	AA457395 Hs.99457	ESTs
	122749 AA458850	AA458850 Hs.293372	ESTs, Weakly similar to B34087 hypotheti
	122772 AA459632	AW117452 Hs.99489	ESTs
60	430242 AA459668	U66669 Hs.236642	3-hydroxyisobutyryl-Coenzyme A hydrolase
	429838 AA459679	AW904907 Hs.30732	hypothetical protein FLJ13409; KIAA1711
	122777 AA459702	AK001022 Hs.214397	hypothetical protein FLJ10160 similar to
	135362 AA460017	AA978128 Hs.99513	ESTs, Weakly similar to T17454 diaphanou
	122798 AA460324	AW366286 Hs.145696	splicing factor (CC1.3)
65	122837 AA461509	AA461509 Hs.293565	ESTs, Weakly similar to putative p150 [H
00	122860 AA464414	AA464414	gb:zx/78g01.s1 Soares ovary tumor NbHOT H
	122861 AA464428		ESTs
	122910 AA470084	AA470084 Hs.98358	ESTs
70	132899 AA476606	AA476606 Hs.59666	SMAD in the antisense orientation
70	122967 AA478521	AA806187 Hs.289101	glucose regulated protein, 58kD
	422845 AA478523	AA317841 Hs.7845	hypothetical protein MGC2752
	123009 AA479949	AA535244 Hs.78305	RAB2, member RAS encogene family
	128917 AA481252	Al365215 Hs.206097	oncogene TC21
	123081 AA485351	Al815486 Hs.243901	Homo sapiens cDNA FLJ20738 fis, clone HE
75	123133 AA487264	AA487264 Hs.154974	Homo sapiens mRNA; cDNA DKFZp667N064 (fr
	123184 AA489072	BE247767 Hs.18166	KIAA0870 protein

	332467 AA489630	NM_014700Hs.119004	KIAA0665 gene product
	123233 AA490225	AW974175 Hs.151875	ESTs, Weakly similar to MAPB_HUMAN MICRO
	123234 AA490227	NM_001938Hs.16697	down-regulator of transcription 1, TBP-b
5	123236 AA490255	AW968504 Hs.123073	CDC2-related protein kinase 7
5	123255 AA490890	AA830335 Hs.105273	ESTs FSTs
	430015 AA490916	AW768399 Hs.106357	
	448892 AA490925	AF084535 Hs.22464 AI744152 Hs.283374	epilepsy, progressive myoclonus type 2, ESTs, Weakly similar to CA15_HUMAN COLLA
	123259 AA490955 123284 AA495612	AI744152 Hs.283374 AA488988 Hs.293796	ESTs, Weakly similar to GA 15_HOWNY COLLA
10	123286 AA495824	AA495824 Hs.188822	ESTs. Weakly similar to A46010 X-linked
10	123286 AA495824 123315 AA496369	AA495824 HS.180822 AA496369	ab:zv37d10.s1 Soares ovary tumor NbHOT H
	457397 AA504125	AW969025 Hs.109154	ESTs
	433049 AA521473	AU076668 Hs.334884	SEC10 (S. cerevisiae)-like 1
	123421 AA598440	AA598440 Hs.291154	EST, Weakly similar to 138022 hypothetic
15	123449 AA598899	AL049325 Hs.112493	Homo saplens mRNA; cDNA DKFZp564D036 (fr
15	426981 AA599244	AL044675 Hs.173081	KIAA0530 protein
	409986 AA599694	NM 014777Hs.57730	KIAA0133 gene product
	123497 AA600037	AA765256 Hs.135191	ESTs, Weakly similar to unnamed protein
	123604 AA609135	AA609135 Hs.293076	ESTs
20	123712 AA609684	AA609684	Homo sapiens cDNA: FLJ21543 fis, clone C
20	123731 AA609639	AA609839 Hs.334437	gb:ae62f01.s1 Stratagene lung carcinoma
	123800 AA620423	AA620423 Hs.112862	EST
	123841 AA620747	AA620747 Hs.112896	ESTs
	123929 AA621364	AA621364 Hs.112981	ESTs
25	123978 C20653	T89832 Hs.170278	ESTs
	133184 D20085	AA001021 Hs.6685	thyrold hormone receptor interactor 8
	132835 D20749	Z83844 Hs.5790	hypothetical protein dJ37E16.5
	435147 D51285	AL133731 Hs.4774	Homo sapiens mRNA; cDNA DKFZp761C1712 (f
	128695 D59972	NM_003478Hs.101299	cultin 5
30	124029 F04112	F04112 Hs.312553	gb:HSC2JH062 normalized infant brain cDN
	124057 F13604	AA902384 Hs.73853	bone morphogenetic protein 2
	449318 H01662	Al609045 Hs.321775	hypothetical protein DKFZp434D1428
	130973 H05135	Al638418 Hs.1440	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep
	124106 H12245	H12245	gb:ym17a12.r1 Soares infant brain 1NIB H
35	124136 H22842	H22842 Hs.101770	ĒST
	124165 H30894	H30039 Hs.107674	ESTs
	429627 H43442	NM_015340Hs.2450	leucyl-tRNA synthetase, mitochondrial
	124178 H45996	BE463721 Hs.97101	putative G protein-coupled receptor
			ESTs
40	129948 H69281	Al537182 Hs.263988	
40	452114 H69485	N22687 Hs.8236	ESTs
40	452114 H69485 124+D826254	N22687 Hs.8236 H69899 H69899	ESTs gb:yu/70c12.s1 Weizmann Olfactory Epithel
40	452114 H69485 124+D826254 129056 H70827	N22687 Hs.8236 H69899 H69899 AI769958 Hs.108336	ESTs gb:yu70c12.s1 Weizmann Olfactory Epithel ESTs, Weakly similar to ALUE_HUMAN IIII
40	452114 H69485 124+D826254 129056 H70827 427580 H73260	N22687 Hs.8236 H69899 H69899 AI769958 Hs.108336 AK001507 Hs.44143	ESTs gb;yu70c12.s1 Weizmann Olfactory Epithel ESTs, Weakly similar to ALUE_HUMAN IIII Homo saplens done FLB6914 PRO1821 mRNA,
	452114 H69485 124+D826254 129056 H70827 427580 H73260 426793 H77531	N22687 Hs.8236 H69899 H69899 AI769958 Hs.108336 AK001507 Hs.44143 X89887 Hs.172350	ESTs gb.yu/70c12.s1 Weizmann Olfactory Epithel ESTs, Weakly similar to ALUE_HUMAN !!!! Homo saplens clone FLB6914 PRO1821 mRNA, HIR (histone cell cycle regulation delec
40 45	452114 H69485 124+D826254 129056 H70827 427580 H73260 426793 H77531 124274 H80552	N22687 Hs.8236 H69899 H69899 A1769958 Hs.108336 AK001507 Hs.44143 X99887 Hs.172350 H80552 Hs.102249	ESTs gbyu70c12.s1 Weizmann Olfactory Epithel ESTs, Weakly similar to ALUE_HUMAN IIII Homo saplens done FLB6914 PRO1821 mRNA, HIR (histone cell cycle regulation delec EST
	452114 H69485 124+D826254 129056 H70827 427580 H73260 426793 H77531 124274 H80552 129078 H80737	N22687 Hs.8236 H69899 H69899 AI769958 Hs.108336 AK001507 Hs.4143 X89887 Hs.172350 H80552 Hs.102249 AI351010 Hs.102267	ESTs gb.yu/70c12.s1 Weizmann Olfactory Epithel ESTs, Weakly similar to ALUE_HUMAN IIII Homo septems done FLB8914 PRO1821 mRNA, HIR (histone cell cycle regulation delec EST lysosomal
	452114 H69485 124+D826254 129056 H70827 427580 H73260 426793 H77531 124274 H80552 129078 H80737 457658 H93412	N22687 Hs.8236 H69899 Hs.108336 AK001507 Hs.44143 X89887 Hs.172350 H80552 Hs.102249 AJ35101 Hs.102249 AW952124 Hs.13094	ESTs gbyu/f0c12.s1 Weizmann Olladory Epithel ESTs, Wealdy similar to ALUE_HUNAN I III Homo saplens done FLB9314 PRO1821 mPNA, HR (histone cell cycle regulation delec EST lysseomial presentins associated rhomboid-like pro
	452114 H69485 124-0826254 129056 H70827 427580 H73280 426783 H77531 124274 H80552 129078 H80737 457668 H93412 124315 H94892	N22687 Hs.8236 H69899 H69899 A1769958 Hs.108336 AK001507 Hs.41413 X69887 Hs.172350 Hs.102269 A1351010 Hs.102267 AW952124 Hs.13094 M.0.0054024hs.288757	ESTs the systematic Collection of the Collection
45	452114 H69485 124-H0826254 129056 H70827 427580 H73260 426793 H77531 124274 H80552 129078 H80737 457668 H93412 124315 H94892 437712 H95643	N22687 Hs.8236 H69889 H69889 A1769956 Hs.108336 AK001507 Hs.44143 X59887 Hs.172350 H80552 Hs.102267 AW952124 Hs.13094 NM_0054024 Hs.28675 X04588 Hs.38544	ESTs gby470c12.s1 Weizmann Olfadory Epithel ESTs. Weizhy smilar to ALLE. HUMAH III Homo sagchers done FLBB614 PRO1022 mFNA, HR (histone cell cycle regulation delec EST lysosomal presentins associated rhomboti-like proversimiana leukemial virial concigene home unuricopatic home khases, receptor,
	452114 H69485 124-H0362524 129056 H70827 427580 H73280 425793 H77531 124274 H80552 129078 H80737 457688 H93412 124315 H94892 437712 H95643 124324 H95652	N22687 Hs 8236 H69899 H69899 A1769995 Hs 108336 AK001507 Hs 44143 X59887 Hs 172350 H80552 Hs 102267 AV952124 Hs 13094 NM_005402Hs 286757 X04568 Hs 85844 H96552 Hs 15947	ESTs gbyu70c12.s1 Weizmann Olfadory Epithel ESTs, Wealty similar to ALUE. HLMMM III Homo aspires of one FLBB914 PRO1822 rmAA, HR phistone cell cycle regulation delection of the Common and the Common an
45	452114 H69485 124-P026254 129056 H70827 427580 H73260 426783 H77531 124274 H80552 129078 H80737 457658 H93412 124315 H94682 437712 H95643 124324 H96552 452933 H97146	N22687 Hs. 8236 H69899 Hs. 108336 AK001507 Hs. 44143 X59887 Hs. 172350 H80562 Hs. 102246 AJ351010 Hs. 102267 AW9852124 Hs. 13094 NM_005402Hs. 288757 X04588 Hs. 159472 AW391423 Hs. 288644 H96552 Hs. 159472 AW391423 Hs. 288656	ESTs gbys/70c12.s1 Weizmann Olfactory Epithel ESTs, Wealty similar to ALLE, HUMAH III Homo sapiens clone FLB9914 PRO1821 mFNA, HIR (histone cell cycle regulation delec EST lysocomal presentins associated rhomboti-like pro v-ral similan leukeral's viral onogene hom enuoricopich priorie kinase, receptor, Homo sapiens CDNAF FLIZ2224 fis, chore H
45	45214 H68485 124+D826254 129056 H70827 427580 H73280 426739 H77531 124274 H80552 129078 H80737 457628 H83412 124315 H94892 437712 H95643 124324 H96552 45283 H97146 132231 H99131	N22687 Hs.8236 H69899 Hs.108336 AK001507 Hs.41413 X59887 Hs.172350 H80552 Hs.102267 AW952124 Hs.13094 NM_005402Hs.288757 X04588 Hs.8584 H96552 Hs.159472 AW981423 Hs.288655 AA862910 Hs.42835	ESTs gby/I/Oc12s1 Weizmann Olfadory Epithel ESTs, Westly emilar to ALUE, HUMAN till Homosospiere done PLBIGH PROISE2 mRNA, HR (Pathen cell order regulation delice EST) glossomal processional procession of the processional procession of the processional procession of the processional procession of homosospiere SUN PLIZZ226 fis, Chris H homo sepiere SUN PLIZZ26 fis, Chris H homosopiere SUN PLIZZ26 fi
45	452114 H89485 124-D826254 129056 H70827 427580 H73260 426738 H77531 124274 H80552 129078 H80737 457658 H93412 124315 H94882 437712 H95643 124324 H98552 452633 H99146 132231 H99131	N22887 Hs.8236 H69899 H69889 A1769936 Hs.10836 AK001507 Hs.41413 A89887 Hs.172350 H60552 Hs.102249 A1351010 Hs.102267 AW952124 Hs.13094 H6552 Hs.159472 AW95423 Hs.28855 AA862910 Hs.42855 AA862910 Hs.42855	ESTs gby/Tot2.s1 Weizmann Olfsdory Epithal ESTs, Weskly similar to ALUE, FLMANH III Homo sealens dome 11-Biol 14 PRO125 in IRVA, Homo sealens dome 11-Biol 14 PRO125 in IRVA, Homo sealens dome 11-Biol 14 PRO125 in IRVA, Homo sealens down dome 11-Biol 14 PRO125 in IRVA, Homo sealens down dome 11-Biol 14 Biol 14 B
45 50	452114 H88485 124-D926264 129086 H70827 427580 H73280 426783 H77531 124274 H80552 129078 H80737 457868 H834172 124315 H94682 437712 H89563 452833 H97146 124324 H99151 421877 H99462 443723 H99837	N22887 Hs 2236 H85999 Hs 109396 A1799958 Hs 109396 A1001507 Hs 102267 A001507 Hs 102267 AW952124 Hs 102267 AW952124 Hs 109267 AW952124 Hs 109267 AW952124 Hs 10926 AW9591423 Hs 268555 AW250380 Hs 109472 AW391423 Hs 268555 AW250380 Hs 109099 AW950380 Hs 109099 AW950380 Hs 109099	ESTs gby/I/Oc12s1 Weizmann Olfadory Epithel ESTs, Westly similar to ALUE, PLIMAN III Homosospiere done PLIGIGI PROVISE INFON, HR (Pathen cell cycle regulation delice EST Josephin associated fronthold-like pro- pressillam selection for the property provision of the provision for the property of the property through the property homosopiere CMN-R 122246 fis, chine H homosopiere CMN-R 122246 fis, chine H homosopiere CMN-R 122246 fis, chine H homosopiere CMN-R 122246 fis, chine H prophetical probin PCF2484 (4238 in Indicatorial reformal probin 1/12 putable Tamachine regulation nuclea
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5	124575 N68168	N68168	gb:za11c01.s1 Soares fetal liver spleen
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	124578 N68321	N68321 Hs.231500	EST
	124593 N69575	N69575 Hs.102788	ESTs
10	128501 N75007	AL133572 Hs.199009	protein containing CXXC domain 2
	332434 N75542	AI680737 Hs.289068	Homo sapiens cDNA FLJ11918 fis; clone HE
	128473 N90066	T78277 Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr
	128639 N91246	AW582962 Hs.102897	CGI-47 protein
	124652 N92751	W19407 Hs.3862	regulator of nonsense transcripts 2; DKF
15	133137 N93214	AB002316 Hs.65746	KIAA0318 protein
10	124671 N99148	AK001357 Hs.102951	Homo sapiens cDNA FLJ10495 fis, clone NT
	133054 R07876	AA464836 Hs.291079	ESTs, Weakly similar to T27173 hypotheti
	425266 R10865	J00077 Hs.155421	alpha-fetoprotein
	124720 R11056	R05283	gb:ye91c08.s1 Soares fetal liver spieen
20	124720 R11008	T97733 Hs.185685	
20			ESTs
	128944 R23930	AL137586 Hs.52763	anaphase-promoting complex subunit 7
	132965 R26589	Al248173 Hs.191460	hypothetical protein MGC12936
	426504 R37588	AW162919 Hs.170160	RAB2, member RAS oncogene family-like
26	438828 R37613	AL134275 Hs.6434	hypothetical protein DKFZp761F2014
25	124757 R38398	H11368 Hs.141055	Homo sapiens clone 23758 mRNA sequence
	124762 R39179	AA553722 Hs.92096	ESTs, Moderately similar to A46010 X-lin
	124773 R40923	R45154 Hs.338439	ESTs
	135266 R41179	R41179 Hs.97393	KIAA0328 protein
	427961 R41294	AW293165 Hs.143134	ESTs
30	414303 R42307	NM_004427Hs.165263	early development regulator 2 (homolog o
	128540 R43189	AW297929 Hs.328317	EST
	124785 R43303	W38537 Hs.280740	hypothetical protein MGC3040
	124792 R44357	R44357 Hs.48712	hypothetical protein FLJ20736
	124793 R44519	R44519	gb:yg24h04.s1 Soares infant brain 1NIB H
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	424123 R54950	AW966158 Hs.58582	Homo sapiens cDNA FLJ12789 fis, clone NT
	124835 R55241	R55241 Hs.101214	FST
40	124845 R59585	R59585 Hs.101255	ESTs
40	124847 R60044	W07701 Hs.304177	Homo sapiens clone FLB8503 PRO2286 mRNA,
	440630 R60872	BE561430 Hs.239388	Human DNA sequence from clone RP1-304B14
	124861 R66690	R87567 Hs.107110	ESTs
	332503 R67266	NM_004455Hs.150956	exostoses (multiple)-like 1
45	124879 R73588	R73588 Hs.101533	ESTs
73	124892 R79403	Al970003 Hs.23756	
	124992 R79403 124906 R87647	H75964 Hs.107815	hypothetical protein similar to swine ac ESTs
	124922 R93622	R93622 Hs.12163	eukaryotic translation initiation factor
	124940 R99599	AF068846 Hs.103804	heterogeneous nuclear ribonucleoprotein
50	124941 R99612	AF068846 Hs.103804 AI766661 Hs.27774	ESTs, Highly similar to AF161349 1 HSPC0
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50	124941 R99612 124943 T02688 124947 T03170	AF068846 Hs.103804 AI766661 Hs.27774 AW963279 Hs.123373 T03170 Hs.100165	ESTs, Highly similar to AF161349 1 HSPC0 ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs
50	124941 R99612 124943 T02888 124947 T03170 124954 T10465	AF068846 Hs.103804 AI766661 Hs.27774 AW963279 Hs.123373 T03170 Hs.100165 AW964237 Hs.6728	ESTs, Highly similar to AF161349 1 HSPC0 ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs KIAA1548 protein
	124941 R99612 124943 T02888 124947 T03170 124954 T10465 456862 T15418	AF068846 Hs.103804 Al766661 Hs.27774 AW963279 Hs.123373 T03170 Hs.100165 AW964237 Hs.6728 U55184 Hs.154145	ESTs, Highly similar to AF161349 1 HSPC0 ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs KIAA1548 protein hypothetical protein FLJ11585
50	124941 R99612 124943 T02888 124947 T03170 124954 T10465 456862 T15418 410653 T15597	AF068846 Hs.103804 AI766661 Hs.27774 AW963279 Hs.123373 T03170 Hs.100165 AW9634237 Hs.6728 U55184 Hs.154145 BE383768 Hs.65238	ESTs, Highly similar to AF161349 1 HSPC0 ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs KIAA1548 protein hypothetical protein FLI11585 95 kDa retinoblastoma protein binding pr
	124941 R99612 124943 T02888 124947 T03170 124954 T10465 456852 T15418 410653 T15597 418133 T15652	AF068846 Hs.103804 AI766661 Hs.27774 AW963279 Hs.12373 T03170 Hs.100165 AW934237 Hs.6728 U55184 Hs.154145 BE383768 Hs.65238 . R43504 Hs.6181	ESTs, Highly similar to AF161349 1 HSPC0 ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs KIAA1548 protein hypothetical protein FLJ11355 95 kDa relinoblastoma protein binding pr ESTs
	124941 R99612 124943 T02888 124947 T03170 124954 T10465 456852 T15418 410653 T1597 418133 T15652 440014 T16898	AF068846 Hs.103804 AI766661 Hs.27774 AW983279 Hs.123373 T03170 Hs.100165 AW984237 Hs.6728 U55184 Hs.154145 BE383768 Hs.65238 - R43504 Hs.6181 AW980782 Hs.6856	ESTs, Highly similar to AF161349 1 HSPC0 ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs KIAA1548 protein hypothetical protein FLI11585 95 kDa retinoblastoma protein binding pr
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55	124941 R99612 124943 T02888 124947 T03170 124954 T10465 456852 T15418 410653 T1597 418133 T15652 440014 T16898	AF06846 Hs.103804 AI766661 Hs.27774 AW983279 Hs.123373 T03170 Hs.100165 AW984237 Hs.6728 U55184 Hs.65238 . R45504 Hs.66238 . R45504 Hs.6856 AI091121 Hs.246218 T40841 Hs.98681	ESTs, Highly similar to AF161349 1 HSPC0 ESTs, Weakly similar to ALU1_HUMAN ALU S ESTs KIAA1548 protein hypothetical protein FLJ11585 95 kDa relinoblastoma protein binding pr ESTs ash2 (absent, small, or homeotic, Drosop
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55	124941 R99612 124943 T02888 124947 T03170 124954 T10465 456862 T15418 410653 T15597 418133 T15652 440014 T16898 131082 T26644 124980 T40841 124984 T47566	AF06846 Hs.103804 AI766661 Hs.27774 AW963279 Hs.123373 T03170 Hs.100165 AW994237 Hs.6728 U55184 Hs.154145 BE383768 Hs.65238 R43504 Hs.6181 AW960732 Hs.6858 AI091121 Hs.246218 T40041 Hs.98681 BE313210 Hs.334798	ESTS, Highly similar to AFIG13/9 it HSPC0 ESTS, Weakly similar to ALU1_HUMAN ALU S ESTS KRA15469 protein hypothetical protein FLJ11585 binding pr EST EST (Sebent, small, or homeofic, Drosop Homeospheris CDNA; FLJ21781 fis, chore H ESTs
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55	124941 PS9S12 124947 T03170 124954 T10465 456882 T15418 410853 T15587 418133 T15682 440014 T18888 131082 T28644 124980 T4084 124980 T4084 124980 T4084 124980 T50116 457222 T50145	AF068846 hs.103804 AF06861 hs.2777 AW963279 hs.123373 T03170 hs.100163 AW954227 hs.1700 hs.100163 E333768 hs.6728 CASS04 hs.6728 AW86072 hs.6528 AW96072 hs.8528 AW96072 hs.8586 AW91121 hs.246218 E315210 hs.334798 T50116	ESTS, Highly similar to AFIG13/9 it HSPC0 ESTS, Weakly similar to ALU1_HUMAN ALU S ESTS KRA15469 protein hypothetical protein FLJ11585 binding pr EST EST (Sebent, small, or homeofic, Drosop Homeospheris CDNA; FLJ21781 fis, chore H ESTs
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55 60	124941 PS9S12 124943 T0288 124947 T03170 124954 T10485 456852 T15418 410653 T15597 418133 T18652 440014 T16862 440014 T16862 124980 T40944 124890 T40944 124980 T4094 457222 T50145 125000 T58615 125930 T59340	AF068846 Ns. 103804 Ns. 103804 Ns. 103804 Ns. 103804 Ns. 103805279 Ns. 1038170	ESTs, Highly shrifter to API615426 11 RSPC0 SETS, Weakly shrifter to ALUT_HUMAN ALU S ESTs SETS, Weakly shrifter to ALUT_HUMAN ALU S ESTs (AAL1548 protein hypothetical protein FLJ 11585 SE (Aze referobletstome protein binding pr ESTs aard (afteent, small, or homeolic, Drosop Home supeliers CANN-FLZ 1737 fis, clone H Home supeliers CANN-FLZ 1737 fis, clone H FSFID region gene 1 ESTs Demon septem CANN-FLZ 1733 fis, clone K
55	124941 PS9S12 124947 T03770 124554 T10465 456852 T19416 410653 T15587 44014 T16858 431082 T26644 124980 T40841 124980 T40841 124981 T50116 457222 T50145 132532 T59394 444484 T63595	AF068846 hs.103804 AF06861 hs.2777 AW983279 hs.123373 T03170 hs.103156 AW984237 hs.6728 U55184 hs.6728 R45904 hs.5181 AW98072 hs.6938 AW91121 hs.6858 AU91121 hs.58681 BE313210 hs.334798 BE313210 hs.334798 T0316 hs.252887 AW11828 hs.6933 AW11828 hs.6933 AW11828 hs.6933 AW11828 hs.6933 AW11828 hs.6933	ESTs, Highly shrillar to API61549 it 19F0.0 ESTs, Weakly shrillar to ALUT, HUMAN ALU S ESTs Weakly shrillar to ALUT, HUMAN ALU S ESTs was also also also also also also also al
55 60	124941 PS9S12 124943 T0288 124947 T03170 124954 T10485 459852 T15418 410653 T15597 418133 T15892 440014 T16888 131082 T28644 124890 T40841 124890 T40841 124890 T40841 125980 T59116 457222 T90145 125000 T58615 125932 T993940 444484 T63595	AF068046 Hs.103804 AF06804 Hs.2777 AW986279 Hs.123573 T03170 Hs.103167 AW984237 Hs.50786 U55184 Hs.50165 AW984237 Hs.5728 U55184 Hs.54145 EE383788 Hs.55281 AW509122 Hs.5858 AW50041 Hs.38588 T30118 NH.204274 Hs.28587 T30118 NH.20427715 T3615 Hs.235887 AW118226 Hs.6033 AK002126 Hs.11280 T91251	ESTs, Highly shrifter to API615426 11 RSPC0 SETS, Weakly shrifter to ALUT_HUMAN ALU S ESTs SETS, Weakly shrifter to ALUT_HUMAN ALU S ESTs (AAL1548 protein hypothetical protein FLJ 11585 SE (Aze referobletstome protein binding pr ESTs aard (afteent, small, or homeolic, Drosop Home supeliers CANN-FLZ 1737 fis, clone H Home supeliers CANN-FLZ 1737 fis, clone H FSFID region gene 1 ESTs Demon septem CANN-FLZ 1733 fis, clone K
55 60	124941 R98912 124943 10288 124947 102370 10288 1249547 102370 124954 110485 456852 115418 410653 115597 416133 115652 440014 116858 131082 126644 124984 174756 124991 1750116 457222 1750145 132832 1759940 444484 163595 125000 176815 132832 1759940 144484 163595 125000 1764524	AF068846 Hs.103804 AF06861 Hs.2777 AW983279 Hs.123373 T03170 Hs.103165 AW984237 Hs.50738 U55184 Hs.104165 BE393768 Hs.60238 Hs.61514 AW980722 Hs.6355 AW98122 Hs.6355 AW19122 Hs.6355 T36116 T36116 T36116 Hs.34798 T36116 Hs.34798 T36116 Hs.23887 AW11826 Hs.3693 AW11826 Hs.23887 AW11826 Hs.23887 AW11826 Hs.23887 AW11826 Hs.23887 AW11826 Hs.1260 T31251	ESTs, Highly shritins to API61549 it 19F00 ESTs, Weakly shritin of AULT L-MAMN ALU S ESTs weekly shritin of AULT L-MAMN ALU S ESTs weekly shritin of AULT L-MAMN ALU S ESTs weekly shriting to the AULT L-MAMN ALU S ESTs weekly shriting to the AULT L-MAMN ALU S ESTs weekly shriting the AULT L-MAMN ALU S ESTs when AULT L-MAMN ALU S ESTs weekly shriting the AULT L-MAMN ALU S ESTs when AULT L-MAMN ALU S ESTs
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55 60 65	12444 1996/12 12444 1996/12 12444 170388 124447 170370 12454 170456 45882 175418 140653 175597 410153 17559 41015	AF068846 Hs.103804 AF06881 Hs.2777 AW952279 Hs.123773 T03170 Hs.103160 U55184 Hs.103160 U55184 Hs.103160 U55184 Hs.103160 Hs.5238 Hs.5238 R43004 Hs.5181 AW98072 Hs.6258 AU981121 Hs.26281 T05161 Hs.264718 T05161 Hs.264718 T05161 Hs.264718 T05161 Hs.264718 T05161 Hs.264718 T05161 Hs.264718 T05161 Hs.26586 T05161 Hs.265	ESTs, Highly shrifter to APIG14249 it 19F00. SETS, Weakly shrifter AULT_HUMAN ALU S ESTS SETS, Weakly shrifter AULT_HUMAN ALU S ESTS (ANA1546 protein FLJ 11535 SS (Can refinoblestoms protein binding pr SS (Can refinoblestoms protein bi
55 60	12444 PS9612 20288 124447 T03770 20288 124447 T03770 20288 124494 T03476 45882 T15418 45882 T15418 11553 T15597 419133 T15552 419133 T15552 419133 T15552 419133 T15552 419133 T15552 419133 T15552 419134 11553 4191	AF989246 1-10.03047 1-10.047 1	ESTS, Highly shrillar to API61549 it 19500. ESTS, Weally shrillar to AULI) - LIMMAN ALU S EST9 ESTS, Weally shrillar to AULI) - LIMMAN ALU S EST9 EST8 EST8 EST8 EST8 EST8 EST8 EST8 EST8
55 60 65	12444 PS9612 12443 T0288 124447 T03170 2788 124457 T03170 14455 124554 T04455 14582 115418 14582 115418 14582 115418 14582 115418 14582 115418 14582 115418 14582	APROBADE Hs. 103804 Hs. 10381 APROBADE Hs. 27774 AWS95273 Hs. 12373 Hs. 1237	ESTs, Highly shrifter to API61549 f 19F00 ESTs, Weakly shrifter AULI J-ILMAN ALU S EST weakly shrifter AULI J-ILMAN ALU S EST S (API6454) and API6454 f 19F00 EST S (API6454) and API6454 f 19F000 EST S (API6454) and API6454 f 19F0000 EST S (API6454) and API6454 f 19F00000 EST S (API6454) and API6454 f 19F00000 EST S (API6454) and API6454 f 19F000000 EST S (API6454) and API6454 f 19F000000000000000000000000000000000000
55 60 65	124941 PS9612 124943 PS9612 124943 PS9612 124943 PS9612 124945 PS9612 124945 PS9612 PS	AFREEDRIS H-103094 H-	ESTS, Highly almitins for API61540 ft 19500. ESTS, Weakly simitin of AULT HUMAN ALU S EST9 EST8, Weakly simiter of AULT, HUMAN ALU S EST9 EST8, Weakly simiter of AULT, HUMAN ALU S EST8 EST8 EST8 EST8 EST8 EST8 EST8 EST
55 60 65	124941 PS9612 124943 PS9612 124943 T02888 124947 T03170 124954 T10495 45882 T15418 141953 T1552	APRESEN H-103804 H-103804 H-103804 H-10374 AVR55277 H-123777 H-123777 H-12377	ESTS, Highly shrillar to APRIG 148 PGO ESTS, Weally shrillar to AUSI 148 PGO ESTS and (allows the shrill shrillar to PGO ESTS and (allows the shrill shrillar to PGO ESTS and (allows the shrillar to Homeosia, Chrosophemosaphero GNM: PLZ 1787 lise, Gnore HE GOOD ESTS and Control of PGO ESTS and P
55606570	124941 PS9612 124943 T02888 124947 T03570 124943 T02888 124947 T03570 124954 T04956 124941 T04956 124941 T04956 124991 T05116 124994 T07722 T05146 T0	AF06826 h-10.0304 h-10.0304 h-10.0304 h-10.0304 h-10.0305 h-10.030	ESTs, Highly shrillar to API61549 1 HSPC0 ESTs, Weakly shrillar to AULT HUMAN ALU S ESTs weekly shrillar to AULT HUMAN ALU S ESTs weekly shrillar to AULT HUMAN ALU S ESTs, Weekly Shrillar to AULT HISBS SCALL Calcabilitation probib finding pr 5400, calcabilitation probib finding pr 5400, and 5400, FLZ 1737 fis, Cone H ESTs acknowled translation elongation factor glosy74-01.01 st Drategane wavy (EST277) ESPO region general PLZ 12278 fis, Cone K hypothesical probib PLZ 12278 probibly set come or midleg homology of hypothesical probibly fishingene blue (GST224) set come or midleg homology (GST210) H hypothesical probibly ESTS
55 60 65	124941 R98612 124947 T0370788 124947 T0370788 124947 T037078 124947 T037078 124947 T037078 124947 T037078 124947 T03108 T	APRESENDE 1-10.000 1-	ESTS, Highly almitins to API61540 ft 18PCO STST, Weally simiter to AULT 1-MAMN ALU S ESTS and AUGUST 15 ft 18 ft 1
55606570	124941 PS9612 124943 T02888 124947 T03570 124943 T02888 124947 T03570 124954 T04956 124941 T04956 124941 T04956 124991 T05116 124994 T07722 T05146 T0	AF06826 h-10.0304 h-10.0304 h-10.0304 h-10.0304 h-10.0305 h-10.030	ESTs, Highly shrillar to API61549 1 HSPC0 ESTs, Weakly shrillar to AULT HUMAN ALU S ESTs weekly shrillar to AULT HUMAN ALU S ESTs weekly shrillar to AULT HUMAN ALU S ESTs, Weekly Shrillar to AULT HISBS SCALL Calcabilitation probib finding pr 5400, calcabilitation probib finding pr 5400, and 5400, FLZ 1737 fis, Cone H ESTs acknowled translation elongation factor glosy74-01.01 st Drategane wavy (EST277) ESPO region general PLZ 12278 fis, Cone K hypothesical probib PLZ 12278 probibly set come or midleg homology of hypothesical probibly fishingene blue (GST224) set come or midleg homology (GST210) H hypothesical probibly ESTS

	125063 T85352	T85352	gb:yd82d01.s1 Soares fetal liver spieen
	125064 T85373	T85373	gb:yd62f07.s1 Soares fetal liver spleen
	125066 T86284	T86284	gb:yd77b07.s1 Soares fetal liver spleen
	416507 T89579	AL045364 Hs.79353	transcription factor Dp-1
5	125080 T90360	T90360 Hs.268620	ESTs, Highly similar to ALU6_HUMAN ALU S
	125097 T94328	AW576389 Hs.335774	EST, Moderately similar to \$65657 alpha-
	125104 T95590	T95590	qb;ve40a03.s1 Soares fetal liver spleen
	135107 T97257	T97257 Hs.94560	ESTs, Moderately similar to 138022 hypot
	423122 T97599	AA845462 Hs.124024	deltex (Drosophila) homolog 1
10	125118 T97620	R10606 Hs.269890	gb:yf35f11.s1 Soares fetal liver spieen
	125120 T97775	T97775 Hs.100717	EST
	134160 T98152	T98152 Hs.79432	fibrillin 2 (congenital contractural ara
	125136 W31479	AW962364 Hs.129051	ESTs
	125144 W37999	AB037742 Hs.24336	KIAA1321 protein
15	125150 W38240	W38240	Empirically selected from AFFX single pr
	450142 W40150	AW207469 Hs.24485	chondroitin sulfate proteoglycan 6 (barna
	131987 W45435	AW453069 Hs.3657	activity-dependent neuroprotective prote
	125178 W58202	W93127 Hs.31845	ESTs
	125180 W58344	W58469 Hs.103120	ESTs
20	125182 W58650	AA451755 Hs.263560	ESTs
	446888 W68736	AL030996 Hs.16411	hypothetical protein LOC57187
	125197 W69106	AF086270 Hs.278554	heterochromatin-like protein 1
	133497 W69111	BE617303 Hs.74266	hypothetical protein MGC4251
	429922 W69399	Z97630 Hs.226117	H1 histone family, member ()
25	129232 W69459	R98881 Hs.109655	sex comb on midleg (Drosophila)-like 1
	422166 W72424	W72424 Hs.112405	S100 calcium-binding prolein A9 (calgran
	125209 W72724	W72724 Hs.103174	ESTs, Weakly similar to TSP2 HUMAN THROI
	125212 W72834	AA746225 Hs.103173	ESTs
	456631 W73955	BE383436 Hs.108847	hypothetical protein MGC2749
30	125223 W74701	AI916269 Hs.109057	ESTs, Weakly similar to ALU5_HUMAN ALU S
	125225 W76540	W74169 Hs.16492	DKFZP564G2022 protein
	125228 W79397	AA033982 Hs.110059	ESTs, Weakly similar to 138022 hypotheti
	132393 W85888	AL135094 Hs.47334	hypothetical protein FLJ14495
	125238 W86038	N99713 Hs.109514	ESTs
35	125247 W86881	AA694191 Hs.163914	ESTs
	129296 W87804	AI051967 Hs.110122	ESTs
	125263 W88942	AA098878	gb:zn45g10.r1 Stratagene HeLa cell s3 93
	125266 W90022	W90022 Hs.186809	ESTs, Highly similar to LCT2_HUMAN LEUKO
	450862 W92272	U91543 Hs.25601	chromodomain helicase DNA binding protei
40	452401 W92764	NM_007115Hs.29352	tumor necrosis factor, alpha-induced pro
	428243 W93040	H05317 Hs.283549	ESTs
	125277 W93227	W93227 Hs.103245	EST
	125278 W93523	Al218439 Hs.129998	enhancer of polycomb 1
10	125280 W93659	Al123705 Hs.106932	ESTs
45	448205 W94003	W93949 Hs.33245	ESTs
	131844 W94401	Al419294 Hs.324342	ESTs
	125284 W94688	NM_002666Hs.103253	perilipin
	417111 W94787	AW016321 Hs.82306	destrin (actin depolymenzing factor)
60	445424 Z38294	AB028945 Hs.12696	cortactin SH3 domain-binding protein
50	125289 Z38311	T34530 Hs.4210	Homo saplens cDNA FLJ13069 fis, clone NT
	446313 Z38465	H06245 Hs.106801	ESTs, Weakly similar to PC4259 ferritin
	431342 Z38525	AW971018 Hs.21659	ESTs
	433227 Z38538	AB040923 Hs.106808	kelch (Drosophila)-like 1
55	428306 Z38551	AB037715 Hs.183639	hypothetical protein FLJ10210
22	424624 Z38783	AB032947 Hs.151301	Ca2+dependent activator protein for secr
	125295 Z39113	AB022317 Hs.25887	sema domain, immunoglobulin domain (lg),
	125298 Z39255 125300 Z39591	AW972542 Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H
		Z39591 Hs.101376	EST
60	448378 Z39783 444582 Z39920	BE622770 Hs.264915	Homo sapiens cDNA FLJ12908 fis, clone NT
00		R55344 Hs.22142	cytochrome b5 reductase b5R.2
	130882 Z40166 128888 Z40388	AA497044 Hs.20887	hypothetical protein FLJ10392
	126868 240368 125310 Z40646	Al760853 Hs.241558	ariadne (Drosophila) homolog 2
	125310 Z40646 125315 Z41697	R59161 Hs.124953 R38110 Hs.106296	ESTs ESTs
65	125317 Z99349	Z99348 Hs.112461	ESTs, Weakly similar to 138022 hypotheti
03	135096 Z99394	AA081258	zinc finger protein 36 (KOX 18)
	100000 200004	ANDU IZAU	zaic iniger protein 50 (NOX 16)

TABLE 3A

Table 3A shows the accession numbers for those pixeys looking unigeneID's for Table 3. The pixeys in Table 7 looking unigeneID's are represented within Tables 1AA. For each probased we have listed the gener cluster number from which the oligonucleotides were designed. Gene clusters were compiled using sequences derived from Centeant KSTs and mRNAs. These sequences were clustered based on sequence similarity using Cutastring and Alignment Tools Choddle Wst, Oakland California). The Centeant accession numbers for sequences comprising each cluster are failed in the "Accession" 5 column.

10	Pkey: Unique E CAT number: Gene clu		cos probeset identifier number ster number				
			accession numbers				
15	Pkey	CAT Number	Accession				
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                                 AA430735 R68963 R22453 H70385 AW129369 AW467320 AW519082 AA345018 AA582183 AI961789 R65918 N30611
                                 A1979189 A1280889 AW273191 R66531 A1285845 A1675927 A1421990 AW190879 H37794 AA699667 H68427 AA954386
75
                                 AI188757 AI140048 AA430382 AI204151 AW247864 AA559099 AI431420 AA548276 AI149466 AA772669 AA694388
                                 AA724168 AA301651 AA281952 AA779925 AA234760 W86290 AA913603 AW511745 Al500697 AA814922 AA835040
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"LIFISE A SEGGE A MOTISON PERSITTO AUTOTION ATTOICS DEGIGNER AND SENSOR A LIFISTOR A MOTITOR A MOTITOR AND TASK AND THE RESEASE THE TOTAL TREBUTO A MOTITOR AND TASK AND THE RESEASE THE TOTAL TREBUTO A MOTISON AND THE TOTAL THE RESEASE THE TOTAL T

	119416	genbank_T97186 T97186	
	119558	NOT_FOUND_entrez_W38194	W38194
10	119559	NOT FOUND entrez W38197	W38197
	119654	genbank_W57759W57759	
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TABLE 4:

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106124 AA423987

5	Pkey: Accession: ExAcon: UnigenelD:	Unique Eos probeset identifier number Accession number used for previous palent filings Exemplar Accession number, Genbank accession number Uniquen enumber
	UnigenelL:	Unigene number

Unigene Title: Unigene gene title 10 Pkey Accession ExAccn UniGene UnigeneTitle 100405 D86425 AW291587 Hs.82733 nidogen 2 100420 D86983 D86983 Hs.118893 Melanoma associated gene 15 100481 HG1098-HT1098 X70377 Hs.121489 cystatin D 100484 HG1103-HT1103 NM_005402Hs.288757 v-ral simian leukemia viral oncogene hom 100718 HG3342-HT3519 BE295928 Hs.75424 inhibitor of DNA binding 1, dominant neg 100991 J03764 J03836 Hs.82085 serine (or cysteine) proteinase inhibito BE245301 Hs.89414 chemokine (C-X-C motif), receptor 4 (fus 101097 L06797 20 101168 L15388 NM_005308Hs.211569 G protein-coupled receptor kinase 5 L20971 Hs.188 phosphodiesterase 4B, cAMP-specific (dun D30857 Hs.82353 protein C receptor, endothelial (EPCR) 101194 L20971 101261 L35545 NM_005795Hs.152175 calcitonin receptor-like 101345 L76380 101447 M21305 M21305 gb:Human alpha satellite and satellite 3 AA296520 Hs.89546 selectin E (endothelial adhesion molecul 101485 M24736 M31166 Hs.2050 pentaxin-related gene, rapidly induced b Y00630 Hs.75716 serine (or cysteine) proteinase Inhibito 101543 M31166 101550 M31551 AW958272 Hs.347326 intercellular adhesion molecule 2 101560 M32334 NN_002291Hs.82124 laminin, beta 1 M68874 Hs.211587 phospholipase A2, group IVA (cytosolic, 101674 M61916 30 101714 M68874 101741 M74719 NM 003199Hs.326198 transcription factor 4 BE243845 Hs.75511 connective tissue growth factor BE550723 Hs.153179 fatty acid binding protein 5 (psoriasis-101838 M92934 101857 M94856 BE259035 Hs.118400 singed (Drosophila)-like (sea urchin fas 102012 U03057 35 102024 U03877 AA301867 Hs.76224 EGF-containing fibulin-like extracellula 102164 U18300 NM_000107Hs.77602 damage-specific DNA binding protein 2 (4 102241 U27109 NM_007351Hs.268107 multimerin 102283 U31384 AW161552 Hs.83381 guanine nucleotide binding protein 11 U33053 Hs.2499 protein kinase C-like 1 U59423 Hs.79067 MAD (mothers against decapentaplogic, Dr 102303 U33053 4∩ 102564 U59423 NM_002270Hs.168075 karyopherin (importin) beta 2 NM_005100Hs.788 A kinase (PRKA) anchor protein (gravin) syndecan binding protein (syntenin) 102663 U70322 102759 U81607 102778 U83463 102804 U89942 NM_002318Hs.83354 NsvI oxidase-like 2 45 J03836 Hs.82085 serine (or cysteine) proteinase inhibito 102887 X04729 102898 X06256 NM 002205Hs.149609 Integrin, alpha 5 (fibronectin receptor, X07820 Hs.2258 malrix metalloproteinase 10 (stromelysin M13509 Hs.83169 matrix metalloproteinase 1 (interstitial 102915 X07820 103036 X54925 BE018302 Hs.2894 placental growth factor, vascular endoth NM_005424Hs.78824 tyrosine kinase with immunoglobulin and 103037 X54936 50 103095 X60957 BE242587 Hs.118651 hematopoletically expressed homeobox 103158 X67235 103166 X67951 AA159248 Hs.180909 peroxiredoxin 1 NM_006825Hs.74368 transmembrane protein (63kD), endoplasmi 103185 X69910 U84722 Hs.76206 cadherin 5, type 2, VE-cadherin (vascula Al878826 Hs.74034 caveolin 1, caveolae protein, 22kD 103280 X79981 55 103554 Z18951 103850 AA187101 AA187101 Hs.213194 hypothetical protein MGC10895 AA039243 Hs.26185 ESTs
AA027167 Hs.10031 KIAA0955 protein 104465 N24990 104592 R81003 104764 AA025351 60 104786 AA027168 104850 AA040465 AL133035 Hs.8728 hypothetical protein DKFZp434G171 T79340 Hs.22575 B-cell CLLI/lymphoma 6, member B (zinc fi 104865 AA045136 104894 AA054087 AF065214 Hs.18858 phospholipase A2, group IVC (cytosolic, 104952 AA071089 AW076098 Hs.345588 desmoplakin (DPI, DPII) 65 104974 AA085918 Y12059 Hs.278675 bromodomain-containing 4 105178 AA187490 AA313825 Hs.21941 AD036 protein AW388633 Hs.6682 solute carrier family 7, (cationic amino 105263 AA227926 105330 AA234743 AW338625 Hs.22120 ESTs 105376 AA236559 AW994032 Hs.8768 hypothetical protein FLJ10849 70 105729 AA292694 H46612 Hs.293815 Homo sapiens HSPC285 mRNA, partial cds 105826 AA398243 AA478756 Hs.194477 E3 ubiquitin ligase SMURF2 105977 AA406363 AK001972 Hs.30822 hypothetical protein FLJ11110 10600B AA411465 AB033888 Hs.8619 SRY (sex determining region Y)-box 18 X64116 Hs.171844 Homo sapiens cDNA: FLJ22296 fis, clone H 106031 AA412284

H93366 Hs.7567 Homo sapiens cDNA: FLJ21962 fis, clone H

	106155	AA425309	AA425414	Hs.33287	nuclear factor I/B
		AA435896		Hs.18397	hypothetical protein FLJ23221
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	107216		D51069	Hs.211579	
	107295		AA186629	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp
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10		AA132983	AA127221 AL117452	Hs.44155	DKFZP586G1517 protein
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		AA156125	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to
		AA179845	AA219691	Hs.73625	RAB6 interacting, kinesin-like (rabkines
		AA232645	AW956580		ESTs
15		F10399	F06838	Hs.14763	ESTs
		H16772	AW151660	Hs.31444	ESTs
		N39584		Hs.17404	ESTs
		N52006	AW613287		UDP-N-acetyl-alpha-D-galactosamine:polyp
••		N53375			Homer, neuronal immediate early gene, 3
20		N54067	Al287912	Hs.3628	mitogen-activated protein kinase kinase
	111133	N64436 R26892	AW580939 BE551929	Hs.268754	complement component C1q receptor
		T33637	N39342	Hs.103042	Homo sapiens cDNA FLJ11949 fis, clone HE microtubule-associated protein 1B
		T57112	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
25		W80763	AW953484		hypothetical protein FLJ22041 similar to
23		AA046808			40S ribosomal protein S27 isoform
		AA253217	AI751438	Hs.41271	Homo saplens mRNA full length insert cDN
		AA255991	AI683069	Hs.175319	
	115145	AA258138	AA740907	Hs.88297	ESTs
30		AA426573	AA486620	Hs.41135	endomudn-2
		AA443793	R47479	Hs.94761	KIAA1691 protein
		AA490588	Al799104	Hs.178705	Homo sapiens cDNA FLJ11333 fis, clone PL
		AA496257	AK000290	Hs.44033	dipeptidyl peptidase 8
25		AA609717	AK001531	Hs.66048	hypothetical protein FLJ10669
35		D59570 F13787	Al557212 AL157424	Hs.17132	ESTs, Moderately similar to 154374 gene synaptojanin 2
		H88157	AU107424 AW070211	Hs.61289 Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 (
		H98988	H98988	Hs.42612	ESTs, Weakly similar to ALU1_HUMAN ALU S
		N34287	AF055634	Hs.44553	unc5 (C.elegans homolog) c
40		N52090	N52090	Hs.47420	EST
	118475	N66845	N66845		gb:za46c11.s1 Soares fetal liver spleen
		N68905	N68905		gb:za69b09.s1 Soares_fetal_lung_NbHL19W
		R32894	BE245360	Hs.279477	ESTs
		R61715	R61715	Hs.310598	ESTs, Moderately similar to ALU1_HUMAN A
45		R71234	R71234		gb:yi54c08.s1 Soares placenta Nb2HP Homo
		R98105	C14322	Hs.250700	tryptase beta 1
		T97186	T97186 AA496205	11- 400700	gb:ye50h09.s1 Soares fetal liver spleen Homo sapiens mRNA; cDNA DKFZp586i0324 (f
		W80814 AA404418	AA496205 AA404418	HS.193/00	gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_
50		AA405747	AW088642	Hs.97984	hypothetical protein FLJ22252 similar to
50		AA488687	AA488687		ESTs, Weakly similar to 138022 hypotheti
		AA599143	AA599143	Tioned Head	gb:ae52d04.s1 Stratagene lung carcinoma
		AA608588	AA608588		gb:ae54e06.s1 Stratagene lung carcinoma
	123533	AA608751	AA608751		gb:ae56h07.s1 Stratagene lung carcinoma
55		C13961	C13961		gb:C13961 Clontech human aorta polyA+mR
		D60302	Al147155	Hs.270016	ESTs
		H94892		2Hs.288757	v-ral simian leukemia viral oncogene hom
		N93521	AI680737		Homo sapiens cDNA FLJ11918 fis, clone HE
60		N95477	Al571594		hypothetical protein MGC12916
60		R60044	W07701	Hs.304177	Homo sapiens done FLB8503 PRO2286 mRNA
		R70506 T91518	AI887664 T91518	HS.200014	sprouty (Drosophila) homolog 4 gb:ye20105.s1 Stratagene lung (937210) H
		T95333	AA570056	Hs.122730	
		R45630	R60547	He 170098	KIAA0372 gene product
65		R20839	R20840	110.110000	gb:yg05c08.r1 Soares infant brain 1NIB H
•••		R23858	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,
		R23858	R23858		Homo sapiens, clone IMAGE:3840937, mRNA,
	126511	Al024874	T92143	Hs.57958	EGF-TM7-latrophilin-related protein
	100286	W26247	BE247550	Hs.86859	growth factor receptor-bound protein 7
70	126563		AA516391	Hs.181368	
		AA856990	AA001860		
		AA856990	AA001860	Hs.279531	
		AA136653	AW450979	11- 4404 :	gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su
75		AA136653	BE180876	ns.11614	HSPC065 protein gb:UI-H-BI3-ala-a-12-0-UI.s1 NCI_CGAP_Su
13		AA136653	AW450979	He 227040	SEC13 (S. cerevisiae)-like 1
	12/402	AA358869	MM330003	110-22/349	SEC 10 (S. COIONNAD/MRB I

	177051	AI123976	*********	D- 40rcs0	MSTP031 protein
		Al123976 Al123976			MSTP031 protein
		AA379500			neural proliferation, differentiation an
	128992	R49693	H04150	Hs.107708	FSTs
5		AA195678			actin binding protein; macrophin (microf
	129188	M30257	NM_001078	3Hs.109225	vascular cell adhesion molecule 1
	129314	AA028131	BE622768	Hs.290356	mesoderm development candidate 1
	129371	M10321	X06828		von Willebrand factor
10	129468	J03040			secreted protein, acidic, cysteine-rich
10	129765 129805	M86933	M86933	Hs.1238	amelogenin (Y chromosome)
	129884	AA012933 AA286710	AA012848 AF055581		tubulin-specific chaperone d lysosomal
	130495	AA243278	AW250380		mitochondrial ribosomal protein L12
	130639		Al557212	Hs.17132	ESTs, Moderately similar to 154374 gene
15	130657	T94452	AW337575		ESTs
	130828	AA053400	AW631469		ESTs .
		AA370302	D81886	Hs.21739	Homo sapiens mRNA; cDNA DKFZp586I1518 (f
	131080	J05008	NM_00195		endothelin 1
20	131137	U85193 AA256153	W27392 Al824144	Hs.33287 Hs.23912	nuclear factor VB ESTs
20	131182 131486	X83107	F06972	Hs.27372	BMX non-receptor tyrosine kinase
	131573	AA046593	AA040311		ESTs
	131647	AA410480	AA359615	Hs.30089	ESTs
	131756	D45304	AA443966		ESTs
25	131859	M90657	AW960564		transmembrane 4 superfamily member 1
	131881	AA010163	AW361018	Hs.3383	upstream regulatory element binding prot
	132050	AA136353	Al267615	Hs.38022	ESTs
	132083 132164	Y07867	BE386490		Pirin
30	132358	U84573	AI752235 NM 003543	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio H4 histone family, member G
50		AA132969	AW361383		metalloprotease 1 (pitrilysin family)
		AA114250	AB011084		KIAA0512 gene product; ALEX2
	132490		NM_00129		LIM domain binding 2
		AA283035	N92589	Hs.261038	ESTs, Weakly similar to 138022 hypotheti
35		AB002301	AB002301		KIAA0303 protein
	132718	AA056731 U68019	NM_004600	JHS-554 Me 241579	Sjogren syndrome antigen A2 (60kD, ribon Homo sapiens cDNA: FLJ23037 fis, clone L
	132760		AA125985	Hs.56145	flymosin, beta, identified in neuroblast
	132933	AA598702		Hs.6101	hypothetical protein MGC3178
40	132968	N77151	AF234532	Hs.61638	myosin X
	132994	AA505133	AA112748		clone HQ0310 PRO0310p1
	133061 133147	AB000584 D12763	Al186431 AA026533	Hs.296638	prostate differentiation factor interleukin 1 receptor-like 1
	133161	AA253193	AW020333		hypothetical protein FLJ20373
45		AA432248	AB037715		hypothetical protein FLJ10210
	133260	AA083572	AA403045		Homo sapiens cDNA: FLJ23197 fis, clone R
	133363	AA479713	AI866286	Hs.71962	ESTs, Weakly similar to B36298 proline-r
	133491	L40395	BE619053	Hs.170001	eukaryotic translation initiation factor
50	133517 133550	X52947 W80846	NM_000169 Al129903	Hs.74669	gap junction protein, alpha 1, 43kD (con vesicle-associated membrane protein 5 (m
50	133607	M34539	BE273749	110.1 1000	FK506-binding protein 1A (12kD)
	133614	D67029	NM_003000	3Hs.75232	SEC14 (S. cerevisiae)-like 1
	133627	U09587	NM_002047		glycyl-tRNA synthetase
	133691	M85289	M85289	Hs.211573	heparan sulfate proteoglycan 2 (perlecan
55	133696	D10522	Al878921	Hs.75607	myristoylated alanine-rich protein kinas
	133913	W84712 D29992	AU076964	Hs.295944	calumenin tissue factor pathway inhibitor 2
	133985		C18356 L34657	Hs.78146	platelet/endothelial cell adhesion molec
	134039		NM_002291		laminin, alpha 4
60	134088		Al379954	Hs.79025	KIAA0096 protein
	134161		AA634543	Hs.79440	IGF-II mRNA-binding protein 3
		AA487558	AW580939		complement component C1q receptor
		M28882 X70683	X68264	Hs.211579 Hs.83484	melanoma cell adhesion molecule SRY (sex determining region Y)-box 4
65	116470 134656		AI272141 AI750878	Hs.87409	thrombospondin 1
05	134989	AA236324	AW968058		nudix (nucleoside diphosphate linked moi
	135051	C15324	AI272141	Hs.83484	SRY (sex determining region Y)-box 4
	135073	AA452000	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f
70		D83174	AA114212		senne (or cysteine) proteinase inhibito
70	100114		X02308 NM_000304	Hs.82962	thymidylate synthetase peripheral myelin protein 22 ~
		D11428	AU076465		KIAA0015 gene product
		D14874	H73444	Hs.394	adrenomedullin
		D26129	NM_00293	3Hs.78224	ribonuclease, RNase A family, 1 (pancrea
75		D28476			thyroid hormone receptor interactor 12
	100405	D86425	AW291587	Hs.82733	nidogen 2

	100420	D86983	D86983	Hs.118893	Melanoma associated gene
	100455	D87953	AW888941	Hs.75789	N-myc downstream regulated
	100529	HG1862-HT1897	BE313693	Hs.334330	calmodulin 2 (phosphorylase kinase, delt
	100618	HG2614-HT2710		Hs.114599	collagen, type VIII, alpha 1
5	100619				RNA binding motif, single stranded inter
,			N24433	Hs.241567	
	100658	HG2855-HT2995	U56725	Hs.180414	heat shock 70kD protein 2
	100676	HG3044-HT3742	X02761		fibronectin 1
	100718	HG3342-HT3519	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg
	100752	HG3543-HT3739	T81309		insulin-like growth factor 2 (somatomedi
10	100828	HG4069-HT4339	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch
	100850	HG417-HT417	AA836472	Hs.297939	cathepsin B
	100991	J03764	J03836	Hs.82085	serine (or cysteine) proteinase inhibito
	101097	L06797	BE245301	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus
	101110	L08246	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r
15	101142	L12711	L12711	Hs.89643	transketplase (Wemicke-Korsakoff syndro
13					
	101156	L13977	AA340987		prolylcarboxypeptidase (angiotensinase C
	101168		NM_00530		G protein-coupled receptor kinase 5
	101184	L19871	NM_001674		activating transcription factor 3
	101192	L20859	BE247295		solute carrier family 20 (phosphale tran
20	101317	L42176	L42176	Hs.8302	four and a half LIM domains 2
	101336	L49169	NM_006732	2Hs.75678	FBJ murine osteosarcoma viral oncogene h
	101345	L76380	NM_00579	Hs.152175	calcitonin receptor-like
		M15990	M15990	Hs.194148	v-yes-1 Yamaguchi sarcoma viral oncogene
	101475	M23254	BE410405	Hs.76288	calpain 2, (m/ll) large subunit
25	101485	M24736	AA296520	Hs.89546	sciectin E (endothelial adhesion molecul
23	101496	M26576	X12784	Hs.119129	
					collagen, type IV, alpha 1
	101505	M27396	AA307680	Hs.75692	asparagine synthetase
	101543	M31166	M31166	Hs.2050	pentaxin-related gene, rapidly induced b
	101557	M31994	BE293116	Hs.76392	aldehyde dehydrogenase 1 family, member
30	101560	M32334	AW958272		Intercellular adhesion molecule 2
	101587	M35878	AI752416	Hs.77326	insulin-like growth factor binding prote
	101592	M36429	AF064853	Hs.91299	guanine nucleotide binding protein (G pr
	101633	M57730	NM 004428		ephrin-A1
	101634	M57731	AV650262		GRO2 oncogene
35	101667	M60858	NM_00538		nucleolin
55	101682	M62994	AF043045		filamin B, beta (actin-binding protein-2
	101714			Hs.211587	
		M68874	M68874		phospholipase A2, group IVA (cylosolic,
	101720	M69043	M69043	Hs.81328	nuclear factor of kappa light polypeptid
	101741	M74719	NM_003199		transcription factor 4
40	101744	M75126	A1879352	Hs.118625	hexokinase 1
	101793	M84349	W01076	Hs.278573	CD59 antigen p18-20 (antigen identified
	101837	M92843	M92843	Hs.343586	zinc finger protein homologous to Zfp-36
	101838	M92934	BE243845	Hs.75511	connective tissue growth factor
	101840	M93056	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito
45	101857	M94856	BE550723	Hs.153179	falty acid blinding protein 5 (psoriasis-
	101864	M95787	BE392588		transgelin
	101931	S76965	NM 006823	Ha.75200	protein kinase (cAMP-dependent, catalyti
	101966	S81914	X96438	Hs.76095	immediate early response 3
**	102012	U03057	BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas
50	102013	U03100	BE616287	Hs.178452	catenin (cadherin-associated protein), a
	102024	U03877	AA301867	Hs.76224	EGF-containing fibulin-like extracellula
	102059	U08021	AI752666	Hs.76669	nicotinamide N-methyltransferase
	102121	U14391	NM_004998	3Hs.82251	myosin IE
	102283	U31384	AW161552		guanine nucleotide binding protein 11
55	102300	U32944	Al929721	Hs.5120	dynein, cytoplasmic, light polypeptide
-	102378	U40369	AU076887	Hs.28491	spermidine/spermine N1-acetyltransferase
	102395	U41767	AU077005	Hs.92208	a disintegrin and metalloproteinase doma
	102355			Hs.211582	
		U48959	U48959	HS.211062	myosin, light polypeptide kinase
C0	102491	U51010	U51010		gb:Human nicotinamide N-methyltransferas
60	102499	U51478	BE243877	Hs.76941	ATPase, Na+K+ transporting, beta 3 poly
	102523	U53445	U53445	Hs.15432	downregulated in ovarian cancer 1
	102560	U59289	R97457	Hs.63984	cadherin 13, H-cadherin (heart)
	102564	U59423	U59423	Hs.79067	MAD (mothers against decapentaplegic, Dr
	102589	U62015	AU076728	Hs.8867	cysteine-rich, angiogenic Inducer, 61
65	102600	U63825	Al984144	Hs.66713	hepatitis delta antigen-interacting prot
	102645	U67963	AL119566	Hs.6721	lysosomal
	102687	U73379	NM_007019		ubiquitin carrier protein E2-C
	102693		AA532780		eukaryotic translation initiation factor
70	102709	U77604	AA122237	Hs.81874	microsomal glutathione S-transferase 2
70	102759	U81607	NM_00510		A kinase (PRKA) anchor protein (gravin)
	102804		NM_00231		lysyl oxidase-like 2
	102882	X04412	A1767736	Hs.290070	gelsolin (amyloidosis, Finnish type)
	102907	X06985	BE409861		heme oxygenase (decycling) 1
	102915	X07820	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin
75	102927	X12876	BE512730	Hs.65114	keratin 18
		X15729	AI904738	Hs.76053	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeg
	102800	V10179	W1204170	110.70000	person i Mahamanahu iia) nor boilhet

	103011	X52541	AJ243425	Hs.326035	early growth response 1
	103020	X53416 X54489	X53416 AW800726	Hs.195464	filamin A, alpha (actin-binding protein-
	103029		M13509	Hs.83169	GRO1 oncogene (melanoma growth stimulati matrix metalloproteinase 1 (interstitial
5	103056	X57206	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B
	103080	X59798	AU077231	Hs.82932	cyclin D1 (PRAD1: parathyroid adenomatos
	103095	X60957	NM_005424	Hs.78824	tyrosine kinase with Immunoglobulin and
	103138	X65965	X65965		gb:H.sapiens SOD-2 gene for manganese su
10	103176	X69111	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg
10	103195 103347	X70940	AA351647	Hs.2642 Hs.171271	eukaryotic translation elongation factor catenin (cadherin-associated protein), b
	103347	X87838 X91247	AU077309 X91247	Hs.13046	thioredoxin reductase 1
	103432	X97748	X97748	115.10040	gb:H.sapiens PTX3 gene promotor region.
	103471	Y00815	Y00815	Hs.75216	protein tyrosine phosphatase, receptor t
15	103967	AA303711	AL120051	Hs.144700	
	104447	L44538		Hs.156044	
	104764 104783	AA025351 AA027050	AI039243 AA533513	Hs.278585 Hs.93659	protein disulfide isomerase related prot
		AA029462	AW952619		Homo sapiens clone TCCCIA00176 mRNA sequ
20		AA045136	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi
	104877	AA047437	AI138635	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se
	104894	AA054087	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic, desmoplakin (DPI, DPII)
	104952	AA071089	AW076098		desmoplakin (DPI, DPII)
25	105113	AA156450	AB037816	Hs.8982	Homo sapiens, done IMAGE:3506202, mRNA,
23	105178 105196	AA187490 AA195031	AA313825 W84893	Hs.21941 Hs.9305	AD036 protein angiotensin receptor-like 1
	105196	AA205724	AA205759	Hs.10119	hypothetical protein FLJ14957
	105263	AA227926	AW388633		solute carrier family 7, (cationic amino
	105271	AA227986	AA807881	Hs.25329	ESTs
30		AA234743	AW338625		ESTs
	105461	AA253216	BE539071	Hs.69388	hypothetical protein FLJ20505
	105492	AA256210	AI805717	Hs.289112 Hs.10283	CGI-43 protein RNA binding motif protein 8B
	105493 105594	AA255268 AA279397	AL047586 AB024334	Hs.25001	tyrosine 3-monoxygenase/tryptophan 5-mo
35	105727	AA292379	AL135159	Hs.20340	KIAA1002 protein
	105732	AA292717		Hs.274344	hypothetical protein MGC12942
	105767	AA346551	AW370946		ESTs
	105882	AA400292	W46802	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
40	105936 106031	AA404338 AA412284	Al678765 X64116	Hs.21812	ESTs Homo sapiens cDNA: FLJ22296 fis, clone H
+0	106124	AA423987	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H
	106222	AA428594	AA356392	Hs.21321	Homo sapiens clone FLB9213 PRO2474 mRNA
	106241	AA430108	BE019681	Hs.6019	Homo sapiens cDNA: FLJ21288 fis, clone C
	106263	AA431462	W21493	Hs.28329	hypothetical protein FLJ14005
45	106264	AA431470	AL046859	Hs.3407 Hs.336429	protein kinase (cAMP-dependent, catalyti RIKEN cDNA 9130422N19 gene
	106366 106454	AA443758 AA449479	AA186715 NM_014038	HS.330429	HSPC028 protein
	106634	AA459916	W25491	Hs.288909	hypothetical protein FLJ22471
	106724	AA465226	N48670	Hs.28631	Homo sapiens cDNA: FLJ22141 fis, clone H
50	106793	AA478778	H94997	Hs.16450	ESTs
	106799	AA479037	BE313412	Hs.7961	Homo sapiens clone 25012 mRNA sequence
	106842	AA482597	AF124251	Hs.26054	novel SH2-containing protein 3
	106868 106890	AA487561 AA489245	BE185536 AA489245	Hs.88500	molecule possessing ankyrin repeats indu mitogen-activated protein kinase 8 inter
55	106961	AA504110	AW243614	Hs 18063	Homo sapiens cDNA FLJ10768 fis, clone NT
-	106974	AA520989	AI817130	Hs.9195	Homo sapiens cDNA FLJ13696 fis, clone PL
		AA599434	AL117424	Hs.25035	chloride intracellular channel 4
	107061	AA608649	BE147611	Hs.6354	stromal cell derived factor receptor 1
CO	107086	AA609519	NM_01233	Hs.26458	methionine sulfoxide reductase A
60	107216	D51069	D51069 NM_00539	HS.211579	melanoma cell adhesion molecule podocalyxin-like
	107385 107444	U97519 W28391	W28391	Hs.343258	proliferation-associated 2G4, 38kD
	107985	AA035638	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fi
	108507	AA083514	AI554545	Hs.68301	ESTs
65	108695	AA121315	AB029000	Hs.70823	KIAA1077 protein
	108931	AA147186	AA147186		gb:zo38d01.s1 Stratagene endofnelial cel
	109001	AA156125	AI056548	Hs.72116 Hs.132904	hypothetical protein FLJ20992 similar to
	109195	AA188932 AA219653	AF047033 AW007485		solute carrier family 4, sodium blcarbon EH-domain containing 3
70	109390	AA232645	AW956580		ESTs
, ,	109737	F10078	AA055415	Hs.13233	ESTs, Moderately similar to A47582 B-cel
	110411	H48032	AW001579	Hs.9645	Homo saplens mRNA for KIAA1741 protein,
		H82117	AA782114	Hs.28043	ESTs
75		N39584	AA035211	Hs.17404	ESTs
75		N54067 N59858	Al287912 AA300067	Hs.3628 Hs.33032	mitogen-activated protein kinase kinase hypothetical protein DKFZp434N185
	111091	NU8000	AA300007	113.33032	19 poucesal protein DATZ proviv 103

	111356	N90933	BE301871	Hs.4867	mannosyl (alpha-1,3-)-glycoprotein beta-
	111378	N93764	AW160993		hypothetical gene DKFZp434A1114
	111741	R26124	AB020653		KIAA0846 protein
5		R27957	AW629414		ESTS
3	112318	R55470 T16550	AW083384 AA307634		ESTs, Highly similar to T46395 hypotheti vacuolar prolein sorting 45B (yeast homo
	113057	T26674	AW194301	He 330283	Human DNA sequence from clone RP1-187J11
	113195	T57112	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom
	113490	T88700	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT
10	113542	T90527	H43374	Hs.7890	Homo sapiens mRNA for KIAA1671 protein,
	113803	W42789	AW880709		chromosome 8 open reading frame 4
	113847	W60002	NM_00503		plastin 3 (T isoform)
	113910	W78175	AA113262	Hs.1/901	Homo sapiens, clone IMAGE:3937015, mRNA, gb:zh53d03.s1 Soares_fetal_liver_spleen_
15	113947 114047	W84768 W94427	W84768 AL035858	Hs.3807	FXYD domain-containing ion transport reg
13	115061		AI751438	Hs.41271	Homo sapiens mRNA full length insert cDN
	115819	AA426573	AA486620		endomucin-2
	115870		NM_00598	5Hs.48029	snail 1 (drosophila homolog), zinc finge
	115964		AA987568		KIAA1265 protein
20	116228		A1767947	Hs.50641	ESTs
	116264	AA482594	D51174	Hs.272239	lysosomal
	116314 116589	AA490588 D59570	Al799104 Al557212	Hs.17132	Homo sapiens cDNA FLJ11333 fis, clone PL ESTs, Moderately similar to I54374 gene
	117023	H88157	AW070211	He 100/15	Homo sapiens mRNA; cDNA DKFZp586N0121
25	117112	H94648		Hs.293658	
	117156	H97538	W73853		ESTs
	117176	H98670	H45100	Hs.49753	uveal autoantigen with coiled coil domai
	117280	N22107	M18217	Hs.172129	Homo sapiens cDNA: FLJ21409 fis, clone C
	119559	W38197	W38197		Empirically selected from AFFX single pr
30	119866		AA496205	Hs.193700	Homo sapiens mRNA; cDNA DKFZp58610324 (I
		AA287347	AA305599		hypothetical protein PRO2013
		AA402799	W07343	Hs.182538	phospholipid scramblase 4
		AA404418 AA425107	AA404418 AI743860		gb:zw37e02.s1 Soares_total_fetus_Nb2HF8_ metallothionein 1E (functional)
35		AA425435		Hs 300670	KIAA1204 protein
55	122331	AA442872	AL133437	Hs.110771	Homo sapiens cDNA: FLJ21904 fis, clone H
	122577	AA452860	AA829725	Hs.334437	hypothetical protein MGC4248
	123160	AA488687	AA488687	Hs.284235	ESTs, Weakly similar to 138022 hypotheti
40	123486	AA599674	BE019072	Hs.334802	Homo sapiens cDNA FLJ14680 fis, clone NT
40	124059	F13673	BE387335		ESTs, Weakly similar to \$64054 hypotheti
	124339	H99093	H99093	Hs.343411	
	124358 124364	N22495 N23031 ·		Hs.102415	Homo sapiens mRNA; cDNA DKFZp586N0121 baculoviral IAP repeat-containing 6
	124726	R15740			carbohydrate (keratan sulfate Gal-6) sul
45	124763	R39610	BE410405		calpain 2, (m/ll) large subunit
	125167	W45560	AL137540	Hs.102541	
	125304	Z39833	AL359573	Hs.124940	GTP-binding protein
	125307	Z40583	AW580945	Hs.330466	
50	125329	AA825437	AA825437	Hs.58875	ESTs
50	107985	R66613	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (f
	125598 125609	R66613 AA868063	T40064 AA868063	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (f carbohydrate (keratan sulfate Gal-6) sul
	116024	AA128075	AA088767	Hs.83883	transmembrane, prostate androgen induced
	418000	AA128075	AA932794		quanine nucleotide binding protein-like
55	126399	AA128075	AA088767		transmembrane, prostate androgen induced
	127435		X69086	Hs.286161	Homo sapiens cDNA FLJ13613 fis, clone PL
	127566	AI051390	AI051390	Hs.116731	ESTs
		AA627122	AA627122	Hs.163787	
	434190		AA627122		
60	128453		X02761		fibronectin 1
	128495 128515	AF010193 AA149044	NM_00590 BE395085		MAD (mothers against decapentaplegic, Dr type I transmembrane protein Fn14
		U82108	U82108		solute carrier family 9 (sodium/hydrogen
	128623	D78676	BE076608	Hs.105509	CTL2 gene
65	128642	L35240	Z28913		enigma (LIM domain protein)
	128669	AA598737	W28493	Hs.180414	
	128903	R69417			STAT induced STAT inhibitor 3
	128914	AA232837		Hs.107125	
70	129087	N72695	AI348027	Hs.108557	
70	129188	M30257	NM_00107	8Hs.109225	vascular cell adhesion molecule 1
	129226		BE222494		inhibitor of DNA binding 2, dominant neg
	129265	X68277	AA530892 R22497	He 110574	dual specificity phosphatase 1 growth arrest and DNA-damage-inducible,
	129345	AA292440 J03040			secreted protein, acidic, cystelne-rich
75		AA228107	AW966728		methionine adenosyltransferase II, beta
, 5		AA449789	BE243845		connective tissue growth factor
					-

	440704 441	110700	BE243845	Hs.75511	annually forms who feeler
	413731 AA/ 129557 W0			Hs.46366	connective tissue growth factor KIAA0948 protein
	129619 AA6				tetraspan NET-6 protein
	129627 AA2	258308	T40064	Hs.71968	Homo sapiens mRNA; cDNA DKFZp564F053 (fr
5	129762 AA4	160273		Hs.12372	tripartite motif protein TRIM2
	129884 AA2	286710		Hs.13131	hysosomal
	130018 T68	873	AA353093		metallothionein 1L
	130147 D63		D63476	Hs.172813	PAK-interacting exchange factor beta
	130178 M62	2403	U20982	Hs.1516	insulin-like growth factor-binding prote
10	130282 X55				5' nucleotidase (CD73)
				Hs.155560	
	130495 AA2	243278	AW250380	Hs.109059	mitochondrial ribosomal protein L12
	130553 AA	130032		Hs.252587	pituitary tumor-transforming 1
1.0	130638 H16	3402	AW021276		ESTs
15	130639 D59		Al557212	Hs.17132	ESTs, Moderately similar to 154374 gene
	130657 T94 130686 AA4			Hs.201591	ESTs Homo sapiens cDNA FLJ10934 fis, clone OV
	130776 R79			Hs.19280	cysteine-rich motor neuron 1
	130818 AA2		AW190920		hypothetical protein SP329
20	130840 Z49		BE048821		small inducible cytokine subfamily A (Cy
	130899 Z41	740	Al077288	Hs.296323	serum/glucocorticoid regulated kinase
	131002 AA1			Hs.22039	KIAA0758 protein
	131080 J05		NM_001955		endothelin 1
			NM_017413		apelin; peptide ligand for APJ receptor
25	131091 T35	341	AJ271216	Hs.22880	dipeptidylpeptidase III
	131107 N87	7590	BE620886	Hs.75354	GCN1 (general control of amino-acid synt
	131182 AA2	256153	Al824144	Hs.23912	ESTs
	131207 W7	4533	AF104266	Hs.24212	latrophilin
20	131319 U25	5997	NM_003155	Hs.25590	stanniocalcin 1
30	131328 V01		AW939251		v-fos FBJ murine osteosarcoma viral onco
	131509 X56		X56681	Hs.2780	jun D proto-oncogene
	131555 AA1		T47364		interferon, alpha-inducible protein 27 Homo sapiens cDNA FLJ11041 fis, clone PL
	131564 AA4	191465	T93500 AA040311	Hs.28792 Hs.28959	ESTs
35	131573 AAC 131692 D50			Hs.30736	KIAA0124 protein
33	131756 D45			Hs.31595	ESTs
			AW960564	110.0 1000	transmembrane 4 superfamily member 1
			NM_016558	Hs.274411	SCAN domain-containing 1
				Hs.34549	ESTs, Highly similar to S94541 1 clone 4
40			Al359214	Hs. 179260	chromosome 14 open reading frame 4
	132050 AA	136353	AI267615	Hs.38022	ESTs
					Homo sapiens cDNA: FLJ22050 fis, clone H
	132164 U84		AJ752235	Hs.41270	procollagen-lysine, 2-oxoglutarate 5-dio
	132187 AAG			Hs.4193	DKFZP586O1624 protein
45	132303 AA6			Hs.325093	Homo sapiens cDNA; FLJ21210 fis, clone C
	132314 AAG	285290	AF112222	Hs.323806	pinin, desmosome associated protein
	132358 X60		NM_003542		H4 histone family, member G
	132398 R31	1641	AA876616	H8.16979	ESTs, Weakly similar to A43932 much 2 p
50	132421 AA/ 132490 F13	189190	AW163483 NM_001290	H\$.4002U	double ring-finger protein, Dorfin LIM domain binding 2
30	132490 F13		AA257992	III E00E1	Janus kinase 1 (a protein tyrosine kinas
	132520 AR		M24283	Hs.168383	
			AA160511		amino acid system N transporter 2; porcu
	132716 T35				caseln kinase 1, alpha 1
55			BE218319	Hs.5807	GTPase Rab14
	132883 AA	047151	AA373314	Hs.5897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f
	132968 N77	7151	AF234532	Hs.61638	myosin X
	132989 AA	480074	AA480074	Hs.331328	hypothetical protein FLJ13213
	132999 Y00		Y00787	Hs.624	interleukin 8
60	133071 T99		BE384932		ESTs, Wealdy similar to AF257182 1 G-pro
	133076 W8		AW946276		Homo sapiens mRNA; cDNA DKFZp586J021 (fr
	133099 L09		W16518		amyloid beta (A4) precursor-like protein
	133147 D12	2763	AA026533		interleukin 1 receptor-like 1
65	133149 T16	3484	AA370045		AXIN1 up-regulated
00		253193	AW021103		hypothetical protein FLJ20373
	133200 AA		AB037715		hypothetical protein FLJ10210
	133220 X82			Hs.318501	Homo sapiens mRNA full length insert cDN Homo sapiens cDNA: FLJ23197 fis, clone R
		083572 0352	AA403045 AI147861	Hs.213289	low density lipoprotein receptor (famili
70			AW631255		L-3-hydroxyacyi-Coenzyme A dehydrogenase
70		5791 7579	AW103364		inhibin, beta A (activin A, activin AB a
	133398 X02	2612	NM_00049		cytochrome P450, subfamily I (aromatic c
	133436 H4		BE294068		immediate early protein
	133454 AAI		BE547647		
75	133478 X83		X83703	Hs.31432	cardiac ankyrin repeat protein
	133491 L40				eukaryotic translation initiation factor

		AA227913	AW880841	Hs.96908	p53-induced protein
	133517	X52947	NM_00016	5Hs.74471	gap junction protein, alpha 1, 43kD (con
		M11313	AU077051		alpha-2-macroglobulin
	133538	L14837	NM_00325	7Hs.74614	tight junction protein 1 (zona occludens
5	133562	M60721	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1
	133584	D90209	D90209	Hs.181243	activating transcription factor 4 (tax-r
	133590	T67986	T70956	Hs.75106	clusterin (complement lysis inhibitor, S
	133617	AA148318	BE244334	Hs.75249	ADP-ribosylation factor-like 6 interacti
		U97105	Al301740	Hs.173381	
10		T25747		Hs.301819	
		K02574	AW247252		nucleoside phosphorylase
		D78577	Al352558		tyrosine 3-monoxygenase/typtophan 5-mo
		X53331		Hs.279009	matrix Gla protein
		S73591		Hs. 179526	
15		X95735	BE410769		zwin
13		L16862	AW239400		G protein-coupled receptor kinase 6
		U44975		Hs.285313	
		M97796			inhibitor of DNA binding 2, dominant neg
		U86782	U86782		26S proteasome-associated pad1 homolog
20			U48959		myosin, light polypeptide kinase
20		AA099391 M19267	M19267	Hs.77899	tropomyosin 1 (alpha)
				Hs.295944	
		D29992	C18356		
		L19314	Al125639		hairy (Drosophila)-homolog
25		S78569	NM_00229		laminin, alpha 4
25		U28811	NM_01220		Golgi apparatus protein 1
		L77886	AL034349		protein tyrosine phosphatase, receptor t
		C14407	AW245540		brain abundant, membrane attached signal
		M60278	AA161219		diphtheria toxin receptor (heparin-bindi
		R81509		Hs.160726	Homo sapiens cDNA FLJ11680 fis, clone HE
30		AA487558	AW580939		complement component C1q receptor
		D86962	D86962	Hs.81875	growth factor receptor-bound protein 10
		AA478971	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen
		D50683	D50683	Hs.82028	transforming growth factor, beta recepto
	134381	U56637	Al557280	Hs.184270	
35		M61199	AA334551		sperm specific antigen 2
		M28882	X68264	Hs.211579	
		X15183	M30627		heat shock 90kD protein 1, alpha
		S53911	NM_00177		CD34 antigen
	134817	U20734	AU076592	Hs.198951	
40	134983	D28235	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p
	134989	AA236324	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi
	135052	AA148923	AL136653	Hs.93675	decidual protein induced by progesterone
	135062	AA174183	AK000967	Hs.93872	KIAA1682 protein
	135069	AA456311	AA876372	Hs.93961	Homo sapiens mRNA; cDNA DKFZp667D095 (fr
45		L08069	W27190	Hs.94	DnaJ (Hsp40) homolog, subfamily A, membe
		AA452000	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (1
		AA282140	T53169	Hs.9587	Homo sapiens cDNA: FLJ22290 fis, clone H
		J02854	C03577	Hs.9615	myosin regulatory light chain 2, smooth
		AA442054	U80983	Hs.268177	phospholipase C, gamma 1 (formerly subty

TABLE 4A

Table 4A shows the accession numbers for those pieze lacking unigeneID's for Table 4. The plays in Table 7 locking unigeneID's are represented within Tables F4A. For each probeet we have listed the gene cluster number from which the oligonuclacidists were designed. Gene clusters were compiled useling sequences derived from endemant ESTs and mRNUs. These sequences were clustered based on sequence similarly unity Calastring and Algrement Tools (DoubleTailst, Oakland California). The Genthank accession numbers for sequences comprising each cluster are listed in the "Accession"

10	Pkev:	Unique Eos probeset identifier numb
	CAT number:	Gene cluster number

15	Pkey	CAT Number	Accession	
20	100752	33207_21	TRISING BERHORDS REMAIN BERDINGS HAN MODEL JUSCE AN MAY 1220 BERDONG BEZZETAR REMAIN ZAMADOINE TRISING BERHORDS HAR STANDAMEN TRISING BERHORD HAR STANDAMEN TRISING BERHORD HAR STANDAMEN TRISING BEZGRAF WINDOWN JONGTON JUSCESSA FROM SINT MISS MATTERS 14 TESSET 71 1615 BEZGRAF WINDOWN JONGTON JUSCESSA FROM SINT MISS MATTERS 14 TESSET 71 1615 BEZGRAF WINDOWN JONGTON JUSCESSA FROM SINT MASS MATTERS AND STANDAMEN JUSCESSA MATTERS AND STAN	98
25			Heads III WAYG MASSO AWYTUUN ORREI I 1989 (1985) 1985 (1985) 11839 (1986) 1986	943 1 .
30			H94199 AAGGS208 BE205776 AAMG0137 H77492 R08222 H37000 AAGT9294 H40041 H74238 H47230 H73231 *14861 AACDEAG AMOSEZ H45896 B15808 H50505 H75025 H75033 150600 AA411561 H50500 H74225 AAAGS25 AA9557501 TASA AAAMADAT H5725 H55806 H75027 H54550 N74625 R9505 H67047 H50758 M68556 H64758 N68256 H5726 H5585 H55806 N68825 N62453 H55004 H569270 H76027 B62525 R63375 T50516 H54339 H58455 H54066 H7509 H7504 H7505 H568256 R57057 H56056 R56335 B6605 H75037 H7505 H7502 H5005 H50	316 31
35			H-6357 W6557 AA5598 R1928 M5264 W7390 R0587 R2174 R17372 N7321 AW8559 AW8563 A466 H H-1708 R5572 AA54916 A46276 H73710 R5138 H6311 R6276 TF54512 R6934 H7033 H5761 R1864 H63 N5263 H5365 19776 H5106 AA4022 T4691 H6120 R6312 R5914 R591 T6756 H824 H63 AA5494 H5357 H6273 D62562 B62562 H6365 A46026 K7469 H6165 AA4044 N645 A4461 N R1052 R4920 A466537 AA54946 H5357 H6273 D62562 B62562 H6306 K7676 H6306 H7376 A4604 N645 A4461 N R1052 R4920 N6556 W6566 H6361 K7676 H6365 M5566 H6365 M5566 H6366 H6367 H637 H63	
40			AWASSH 14 N7867T H71702 FBGGS H71916 R51915 R78017 R60960 A153328 AQ247866 AA27445 AWS51050 AA7036F AA204713 AWS75060 AWS1116 AWS75264 FH26 M54556 BE16-184 FAV787060 VANOZ VAWS51050 AW685492 AW550515 AA334867 AW878715 W06882 AW550222 AW685381 H70865 AW381773 H47851 AW685682 H5306 AW68466 AW876173 AW678656 R32874 AW876564 AA276762 AW67865 AW376764 AW767864 AW678666 AW67866 AW678676 AW67866 AW678676 AW67866 AW6786 AW	
45			AWATRES AMERITA AWATRES AWASOSA AWASOSTA AWASOST	
50	117156	145392_1	W7385 AA928112 W77887 AW889237 AA148524 AI746182 AI754442 A133892 A1253102 A1079403 A1370541 ABS7 H97538 AW188021 A1827868 W72716 A1051402 A188071 A1338900 N21488 AW170478 W92522 A1891028 A1913512 A1144448 W73315 A4604358 N28800 W85221 A1868132 H93645 AA146783	2
55	131859	3672_1	AW690694 AA02467 T65690 D66120 T82652 A815967 DE 182608 DE 182505 AW090238 M09057 AA647258 AW96 AW176464 A304671 AW68375 T61714 A361698 AW46915 A362332 AA088458 A468005 W52295 W39480 M5 D82638 W25640 W52847 D62729 D65990 D6619162 A315186 A4390835 A4112474 W76162 A408854 H52265 A301031 H99082 A411378 D6520997 AW681691 A343799 B616369 E694718 D656665 F1933 AA75800	
33			AAJUSJ 180496, ANT 15 00 CECUSISY AND 1801 ANASOS 1801 ANASOS 1803 1803 1804 1804 ANT 1805 ANT 1804 ANT 1805 ANT 1804 ANT 1805 AN	510
60			AA73301 A ISG1934 R75930 R80023 AA45190 A4626059 AA44688 AW375550 A A88901 B AM74275 AW305837 AW305837 AM305270 AW305137	
65	125565 133607	1704098_1 1227_6	AAS2077 AA05979 I D82607 T48574 AW752038 C06300 R20840 R20839 BEZ77459 BES7761 BE387189 AL037858 AL037878 AB63094 BE299216 AA011333 AL036169 BE562225 AA25116 BE517431 BES577641 BE387 18195 AL037859 AL037878 AB63094 BE299216 AA011333 AL036169 BE562225 AA25116 BE617431 INSEST A145093 AL037810 INSEST A145093 AL037878 AB79819 MIL 200801 AA31740 D16371 AA156904 AA037114 AA312803 INSPAN BANGSON AL048591 BE38878 AA202697 AA03948 BES78788 AA95971 C160156 PRA175 FAA115065	9
70			AIGSTRO ESTRACS ECOROT ANICAGAD ESCADOR AGROPATA ANI TOZZO ANICATERA 33500 ESESSARI MINISTI SESTATI AAZTOTI AAZTOTI ESE 1651 (261 AASIOTA 2 ANICASSA DE ASSAS DI AASSO ANICASSA DE ASSAS ANICASSA ANICASSA DE ASSAS ANICASSA ANICAS	6726 4
75			AV662092 AW904105 AA011375 BE315214 H99302 BE537833 N32299 AW855829 AI291320 BE078322 AI301395 AA303362 N32719 AA368328 AA357877 AI952540 H58279 H02758 H02048 AW805233 R82224 AA410772 AA291352	2

5			EET 110 NEXOS DE 11/026A AJS1173 HAVET BESTATST DEZESO AAGBAUX WUSSIS REZIS INSERT MAZGA PET/LON HAVORI HAVOR HAVO
10			RIPSTS ASANSKO AAASSISSA AAGSISSA RAKSISSA (1824 TA AAACITAS ANTITYISSA KASISSIZ AAASSICA AASSICSI AASSICSI AA AASSICTI AAASSICA AAASSICA AARSICA AATSIGA KATISSA (1844 TA AASSICA AAASSICA AAAASSICA AAASSICA AAASSICA AAASSICA AAASSICA AAASSICA AAASSICA AAAASSICA AAASSICA AAASSICA AAASSICA AAASSICA AAASSICA AAAASSICA AAAASSICA AAASSICA AAASSICA AAASSICA AAASSICA AAASSICA AAASSICA AAAASSICA AAAASSICA AAAASSICA AAAASSICA AAAASSICA AAAASSICA AAAASSICA AAAASSICA AAAAAAAAAA
15			AAT-6864 NACISSES AB 1668 AND 1661 FROSES AND 1646 NACISSON AND 1617 AND 1672 AND 16
20			AA7515 SA A722793 A7984A7 A468946 AA251003 A894583 AA01737 AA05186 ESD43308 A8968273 A3022110 MD0724 M95322 ESD53074 (20085) A85177 AA765269 A8967237 NORTHA A6832476 AA90644 KAN097373 ANSQORFS 153369 WH6027 R87970 A5064165 AW259265 A465414 AW0669678 NORTH 150698 CY2140 A3825647 AA930068 AFFORT MASTE HAST HA A7065187 135914 AA762547 A482524 A49074 VA23578 (20084 A687578 A687578 A68758
25			W47374 T64155 AA269002 ABS98028 AA5581658 AA269008 ANT94259 H01953 AA149267 AA485075 AA975555 H44938 AA035358 A965555 H46293 A4655161 AR51222 AA269008 ANT94259 H01953 AA149267 AA745300 AA2530 AR52750 AF75125 AA095165 AR5126 AA09516 AR5126 AA09516 AR5126 AA26906 AR5126 AA09516 AR5126 AA26906 AR5126 AA09516 AR5126 AA26906 AR5126 AA09516 AR5126 AA26906
30			ABS2920* AASSEM ANDOLOGO ALGESERS DYA!*TO 1915*T TISSIAS ANNEAGAB ESELECT TISSIAS ANNEAGA ANCERE TISSIAS TISSIAS TISSIAS ANNEAGA ANCERE TISSIAS ANCERE TISSIAS TISSIAS TISSIAS ANCERE TISSIAS
35	133881	13893_1	MISS242 AGGINGS ANDIOTRO (1904) ANDITRO (1904) ANDITRO(1904) ANDITRO(190
40			H78924 T117-18 W85826 AWR9H6S AWR9H6S BETAHE BETTOH 5 ACAD4626 AWR0ETS AWR9H526 AL 158881 AL 151087 ERECOVERA ALGEBRA BESSED AWR5505 BETSSSS AWR5505 BETSSSS AWR5506 AWR5505 BETSSSS AWR5506 A
45			ADBESEA SAMBESTER ADBESTER ADBESTER ADBESTER ADBESEA SALESSER ADBESTER ADBE
50			ALASSES NIZIEZ AZTYTE WASSE AATTEST REZOZA MERCEZ I ARRESES NELTSÖN AATEERT DEZES WISSEST ARREST AMISSES ARREST KRISHE AMISSET TENERA TÜRMÜGET WERSTE ÜRÜS AMARSTVA ARREST MESSES WITATI SI WERTE AZZEZI AMISSES ARREST SADERTI BECSBOO AMISSES TERISE TÜRÜK ARREST SER BERSTE SATEST AMISSES AMIZSES ANTEST SER MESSES AMISSES AMISSE
55	134403	17037_1	AA003551 AW03549A ABB05051 KES26S AA513281 AW71197 H1517 M7999E A1174398 A1904207 A904208 BE514558 VAHVETZ WESS-38 AZZZEZ AA70070 BA19952 ALRESHA VAHVETZ BEST AVEZ ALRESHA AZZZEZ AA304551 BE5195229 AA007557 AV9651165 AW056959A AW056958 MAI 0.005737 AW0561165 AW056959A AW056959 AW056959A AW05695A AW056959A AW05695A AW06695A AW05695A AW05695A AW06695A AW05695A AW05695A AW06695A AW06695A AW05695A AW05695A AW06695A AW06695
60			HIOTIOT HORSET AGASATSA SAFTIGIO ANICEZANO ANI
65	126872	142696_1	AALUDI 26 ABB 64 DI 100 KR 958 B 100 R 100
70	121335 130018 121822	279548_1 18986_1 244391_1	AAA0414 A217248 AASSOSSA ANSATSTAT AWSTZ468 AESGOTS5 AIZ89110 AW135512 XSI7261 T68873 AI7A880 M49513 AWIZZ7759 E554967 AESGOZB HECKSSTS FASDIZZ AASTOST AWS55302 ALD4Z109 N53092 A811424 AIJ75962 AMSD503 ABZ0805 ABZ08045 E5644025 E664750 AK16141 AB11407 A811452 W59547 AIZ84566 AISAS38 AW185058 ABZ0805 ABZ0805 AM74502 AA697315 AA628161 AWX051728 AH5022 A440015T AA697379 AIZ2355 AISAS38 AW185058 ABZ0805 ABZ0805 AM74502 AA697315 AA628161 AWX051728 AH5022 A440015T AA697379 AIZ2355 ABZ0862 ABZ08174 AA62414 AA698464 ABZ08353 AAM1505 AA63751 ABC08756 AWZ637 AA63736 AA73706
75	123523	genbank_AA608	AA370301 AA429328 AW272055 AI580502 AI832944 AI038530 AA425107 AI014986 AI148349 AW237721 AW779756 AW137877 AI125293 AA400404 R28554

	123533 125091 123964	genbant_NA663751 AA608751 genbant_T91518 T91518 genbant_C19361
5	102491 118475 118581 113947 101447	genatic_clased clased enter_classified Ustroto genatic_N8846 N68465 genatic_N8846 N68465 genatic_N84768 N64766 enter_classified N64768
10	101667	ETINUE_LICASUM NICOSSE1 IMBORSS ANYST3722 ANWST35289 ANWST3529 ANWST3609 ANYST3760 ANYST3606 ANYS06940 ANYST420T 105229 AAC16003 ANY805555 AA09899 AA098625 AAC15461 ALDSST57 ANYST371 ANY80354 ANY80540 ANYST7404 T27299 BASSES F06657 ANYST61 AASAST79 AASASSE AA015461 ALDSST57 ANYST371 ANY80354 ANY80540 ANYSECT21 BASSES ANYSECTION ASSES ANYSECTION ASSES ANYSECTION ANYSECT
15		ANYSBAST AASTE 142 T25041 AB00061 ANYST002 AATUS914 AA666830 AB59203 AN45772 AAT4334 AB17066 ARSC002 ANYS0442 AB35902 AW08303 ANX68502 ANA66655 ANA5664 AA65662 AA55605 AA5662 AA6562 AA67040 AA561654 ARST154 ANV6002 ARGS164 H17424 AB2520 ANA66635 AA5662 AA65626 AA6662 AA66646 AA5664 AA6664
20		A-A41 1922, AWARD-965 A-A688-910, AAATROM 1-ABSCARTS AWINGSTAR A-AGUTEZ AUZTUZA AWIZ-265 AA41 1933 AISS221-6 AIT19965 AIB15002 AA182881 AUZTUSBO AA13508 AIT36857 WRODZS AWARDAS AA136423 AWARDAS FOH188 NIS9690 AWARD-76 AIT3965 AUZTUSBO AAZTUSBO NISSZAR T-33500 AA436657 AA285106 AA42896 NISSZOTO POZISZ AWARDAS AA13642 AWARD-865 AWARDAS AWARDA
25		AWH68988 A.12/0075 AWIGGGSS NCHSTW REVTAB. AASIGAVE. AL127958 H14907 A1487152 WYSGSA AAADBEED AA152976 AWIGS1940 AWIST3883 ABAGEZA AWIST4683 T56500 N24529 ABH0720 AWIST4983 AWIST4947 AWIST91913 A.1383373 AWIST3241 AWIGS244 F26905 AWI47022 AWISZ058 F54250 AWIST6907 AWISS18515 WYTH 4T AWI F16589 AA666757 AWISS1624 AAX06040 AR146574 AWISO0691 AR186579 AKS8973 A0065271 AA433818 AA6112807 AWIS1809 ABH44409 AA168683 AWIST2884
30	108931 103138 103432 119174 133678	gerbani, A.417166 A447168 entera Z.00265 X50955 X509
35		A 20/26760 A 20/2680 A WHIGTOSO TREACH MISSES TAYES HEADOS A AZOTROSO A AZOTROSO A PRINCESO TO TREACH VIZODO S A AZOTROSO A WHIGTOSO TREACH A THE SECONDA TO THE SECONDA TO THE SECONDA TO THE SECONDA
40		A188757 A1140048 AA430382 A224151 AW24T884 AA550399 AW51420 AA540276 A1149465 AA472599 A486H4388 AX724168 AA261651 AA261892 AA77825 AA254701 W66226 AA43503 W8151765 A1800397 AA4862 AA35040 T47964 H5098 AA960N R80710 A18700 N17022 R98040 AW25071 H80226 A1870767 A497076 A277248 A137115 R25262 H16737 R80070 AX73129 R85520 A45544 A481832 H16964 X17567 T595122 W6455 AA437065 A451989 A4915726 W65314 A787476 A426777 A4271477 N8644 A789164 K77826 B98363 H84013 A770057
45		A 415 166 A 1/259627 H-MOD2 HEBYZE RESS110 AMTYONE A 187.3318 A 17.35713 HEBSET COLEATY A MTRESS T27.551 A IMERITYA MUNUSIEN HEBTET 9 A BASHITY HESZEZ SA MESSES A KOROST A MAZIGES HI HIBSIS R 32240 A 187.3776 A 1/35002 NTRISS B A 126055 A 19.41172 A 34/36142 A 100/361 A 1823348 A A 145500 T 51257 N 504.54 H 13850 N 73.164 A 1708053 A 2781506 A 3425006 A 3435906 R 150804 H HERTS WO 1468 B 114500
50	119416 119559 123473	genbank_197168_197186 NOT_FOUND_motrex_w38197 W38197 genbank_AA599143 AA599143

TABLE 5:

5 Pkey: Accession: ExAccn: Unique Eos probeset identifier number Accession number used for previous patent filings Exemplar Accession number, Genbank accession number

Unigene Title: Unigene gene title

Uni

10

Pkey Accession ExAcon UniGene UnigeneTitle

15819 AA426573 AA486820 Hs.41135 AA486820 101545 M31210 E2461654 Hs.57988 A370682 101545 M31210 E2461654 Hs.157988 A370682 102688 X06256 MM.002208Hs.149608 MM.002206 101192 L20859 BE247295 Hs.78452 BE247295 102915 X07820 X07820 Hs.2288 X07820

102689 X106299 MM_0022894s.149909 MM_002289 101912 L02695 SEA217285 FRATARSE SEA21728 20 102515 X017262 X017260 MS25 KSA21728 X017260 101350 L027419 X107260 MS25 KSA21726 X017260 101350 L027419 X107260 KSA2178 KSA2178 MS25025 101350 L027419 MS25025 KSA2178 KSA2178 MS25025 101350 X54278 MS2502 KSA2178 KSA2178 MS2502 101050 X542625 MS2502 Hs2318 MS2502 25 1018685 XA64258 MS2502 Hs23216 MS2502 1018685 XA64258 MS2502 Hs23216 MS2502 1018685 XA64258 MS2502 Hs23217 KSA2178 MS2502 1018685 XA64258 MS2502 Hs23217 KSA2178 MS2502

25 104865 A0465136 T79340 Hs.22575 T79340 106124 A4423987 H33366 Hs.7567 H33366 105330 A02434743 N47348265 Hs.22130 A023465 H35366 Hs.7216 A055646 104764 A04025551 A033243 Hs.278585 A035243 133200 A4422246 B0377715 Hs.183639 A8037715

133200 AA432246 AB037715 Is.183639 AB037715 105263 AA227926 AW386833 Is.6682 AW386853 105176 AA187490 AA313825 Is.21941 AA313825 109456 AA232645 AW956580 Is.42699 AW956560

TABLE 5A

Table 5A shows the accession numbers for those plays lacking unigeneID's for Table 5. The plays in Table 7 lacking unigeneID's are represented within Tables 1-5A. For each probeset we have lated the gene cluster number from which the disponutabeties were despined. Gene clusters were compiled using sequences contend from electric 581s and mRNNs. These sequences were clustered cased on sequences similarly unign Clustering and Alignment Tools (DoubleTwist, Cakand California). The Genbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10	Pkey: CAT number: Accession:	Gene du	os probeset identifier number ster number accession numbers	
15	Pt 041	T Number		

15	Pkey	CAT Number	Accession
20	115819	10241_1	AA466020 AF205940 AA297524 AB034085 AA081335 NM_016242 AA188323 AA297537 H88204 AV953081 W31695 AVM852203 AA246250 AW661271 AA26250 AA6464607 AA26155 K44414 AA34739 AA770667 A333225 N36136 AV665574 AA761394 ALTSYSTO AW00254 ALS34846 AA668615 K8205 W04627 AA457065 AU51414 AA9161838
20	102024	14505_1	AA42677 AA425620 AW436654 AA050513 BE1672784 BE1672781 AR01728 AA301687 AW597861 R27614 AA155089 AB52099 A770171 AA301026 AA301015 Al220981 AI857670 AI537140 AW1012010 AA030000 W46880 1444021 AI556967 AI651736 AA058476 AA146932 T58265 R85800 AA047810 AA017387 AW1020050 AA971733 AI827256 AI606416 AB55999 A1172678 H46030 U33377 RML,004105 AA17357 H742405
25			A.14686 A.162709 A.162769 A.000478 A.A.1722 A.261687 A.15091 A.33058 F.62322 A.3021130 A.1950200 A.002157 A.0029129 A.302078 A.0029150 E.01581 T.4688 A.302483 DET-58557 EET-51191 Y.193949 A.4187200 EET-52520 A.1023037 A.1036022 A.0102067 A.10750072 EET-5300 A.1036030 A.10371085 A.107502644 A.1036064 A.1036058 A.1036250 H.16157 A.10360075 A.1056009 B.4373297 EED/5779 EED/5779 E.007279 A.1036309 H.16150254 A.1036009 H.161502 A.1036009 A.1036
30			A.A.1726 PIGSSEZ VINGERS AA29413 AITGSOO, AIRGAGE AWXCZOSA AWXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
35			AIBB1148 AX355651 AA004448 A1720067 AR75244 AA015305 A4157260 W80702 AISS14590 AI098450 TG4493 A446590 AA465566 AA73605 AA0036151 AA07477 A8665858 A445565 W8070500 AY005050 D56685 H52038 A445552 R30864 AN022036 A500600 W87456 A7755226 A1753263 A1453768 A4147615 H88101 A352414 H88025 A144771 AA0241 AN022036 A500600 W87456 A7755226 A1753263 A1453768 A4147615 H88101 A352414 H88025 A144771 AA0241 AN022036 A500600 W87456 A175226 A407560 A175236 A17530 A475415 A22146 A4077060 N52358 H383566 T31103 A4456741 AA017736 A4152027 A407693 A815300 A017531 A859540 A707127 A107127 A107423 A858548 N59539
40			H68098 158736 D57007 D65697 C00687 D61839 D65661 4M72137 AB71002 D65677 EECH8830 D57972 A568286 A361055 A561071 A262222A A456886 D57139 D5794 D6784 A6204 D67332 D5795 A876503 A876503 R34809 N6758 D58358 A188394 AA14796 A169640 A363166 H40638 AA578137 AW950265 AA300943 A1128999 H46594 AA917355 N57820 AA32094 H51969 H2573 A
	101545	24607_1	BE246154 M31210 NM_001400 AA193392 NM_016537 AF233365 AF022137 H27787 AA370448 F05373 T27666 W21494 AA036907 AI249966 N93476 F01623 AA304390 AA308808
45	109456	180633_1	AW956580 AA886381 AI147670 AI090115 AI168683 AA232545 H99504 AA374707 AA380875 AW139567 AI735132 BE439385 AW629780 N28322 AA232789 AA232790 N73285
	103036	17145_1	M15999 X59527 MM_002421 M16567 X00231 M15999 X039354 AA188634 AA852324 AA187507 AA081149 AA186524 AA187264 AA187361 AA388155 AA186973 AA374217 U70015 AA081230 AA188049 AA186393 W56827 AA852602 AA157468 AA02024 AA186754 AA188084 AA025616 AA304334 AAVA76462 BE43394 M2767642 0A.165673 T18504
50			AA18621 W49496 AW004698 AA083575 AA372890 AW683590 AA132297 W47465 AA185376 AA157260 AW003999 AA037890 A858000 AR59010 AR79309 AA525273 AW041680 AW17552 BE-6399350 AA157416 AW1775966 AB003497 AA081006 AA4100529 AA181048 C02231 T27821 W23596 AW594502 AA471402 AW691289 AW601289 AW601289 AW191603 AW6901523 AW691222 AW6910542 AW601601 AA511431 AW46417 AA1916501 AA525628 D34407 W147810 AA181880
55	133200	28960_1	W49597 WEZTHA AA188269 A852891 AMCARGA AA60866 AA168662 AWK01303 AA162803 AA162803 AA161802 AA162805 AA13182 NA9510 WAT7343 A1885755 AM75956 A1618026 AA162802 AVK01303 AA162803 AA163802 AA161807 AA081202 AA162803 COE085 AA085924 A800044 AA16782 AA161069 AA167752 AA163121 AA163331 AA067263 AA852603 AA168269 AK562609 AWK49628 AA167340 CO2091 AA514695 AA067276 AA360768 AA167270 AA16726 AA16726 AA16726
60	100200	2000_1	AADSTAT NYZUS AADSZIS AADSZIS AWOUNGS AASZIAD TESCSO AWOSSIO ABBROZO AWOZSIGA AWOZSI
65			AND22003 AIS6Z704 H19344 R61511 AI080204 H16566 AA432246 AI767980 T16688 AI84342 AI217475 AI767095 Z38E51 AI359566 AI361437 AID41000 R07033 H16608 H19084 R12674 R61567 N98368 EE221199 Z42320 AA094554 R07078 AVINSOUS88 AA418090 R41262
70	132837	256666_1	AA37082 AA364110 AW59554 AW371737 AW382088 AW604716 AW60473 AA47827 XW371674 AA423137 EBG03231 T93507 W72803 A0806976 AA487977 A24562 EBG43944 Ay204068 R51635 AW2094 T10082 W65553 AJ886215 AW162164 AA700716 AH27443 R15824 AI537587 AA953110 D58024 AI520811 AA659570 A463280 W76329 AW20365 AW02268
70	102898	24023_1	AWX23950 AWX22503 MM, 002250 (20255 M13918 BE070866 AW239485 AW996127 BE273894 BE272590 BE410252 R29975 T11786 T11787 AA301462 AA301165 AW960950 BE272819 AA386086 T39391 AA285030 AA370580 D08585 T39668 AA156213 W24142 AA34323 AW7960FA AA151197 AA378112 R94787 AA302834 H95027 R86701 AA311677 H55697 AW7516950 W26235
75			AL046458 AA471198 AA301952 R46287 R82694 H03186 AA187706 R32562 R27094 R25947 R25320 AW949809 H13505 H79049 R32403 H11213 R39710 H49765 H21142 H21006 AA417664 W52075 N56771 AA284240 N98556 N30907

5			ANTOTISS AVINGUYTE LASMIST HE MESSE ANGERIER DANTOTE ANATOTES ANTONIOR ANGERS (1925) T56588 ANATOTI MISSE PROPER TOSES ANGERS ANGERTE ANGERS ANGERS ANGERS ANGERS (1925) T56588 AIZTVETE ANTOTIS HISTORIA MISSES ANGERS ANG
10			AT 152/E AW193228 AB7776 A SDOMBA 7426059 AW008383 R006468 R26757 R32/04 AA716590 W32222 AW77764 AUZ70161 R016408 AUZ7504 A SAM504 A AJ05624 W327464 A J046256 AW005688 AW7671600 SEI (62593 H410070 AA578313 AW074697 An161224 AA861947 TZ9451 D20041 T50618 AA418731 A/282500 AW081407 AA804560 AA72685A Z62553 AB500257
15	102915 134416	2903_2 30694_1	2007S/30 MM, 002455 BEZT1570 ADSSSER ANDRIGHES A BAZISERY A BAZISTS A ARBST 155 A ABST 146 A A7TCSSOS C 002220 N88264 MM, 00260 A7TCSSOS 0 A7TCSSOS BAZISTS A BAZISTS A BAZISTS A ARBST 155 A A8TCSSOS C 002220 AA32560 BEXISTS I AAMSTOS AA23566 A LAGESTS A ARBST 146 A ARBST 155 A ARBST 147 C 1
20			AVITSTRE ANTBISS ANNOBOTES ANASOTTA ABROSSO AVISDTOSS ACTAMOS ANASTHOST ARCTISSO AGESTOS AGESTO ANASTRETO ALZTOSOS NESSAT NAGOS AVISTETI NEGOSO VESSOS ANAGOSOS FEBETIA AGESTOS NESSAS AAZISTEZ WASSET ARBOTSOS VIPICIE A ALDTIOSS ANAGOSIS NAGOSIS ATAPESTO ALGESTOS ANDSTOS ANDSTOS ANDSTOS ANASTRETOS ANDSTOS ANDSTOS ANASTRETOS ANDSTOS ANDSTOS ANASTRETOS ANDSTOS
25			A4 189229 AW169205 F27926 R72066 F27320 A455697 AUT/STEA AU888584 AD94267 AZ4266 A405630 T393200 A4688278 A405730 A82442 A407541 A3056046 A1051680 A1051690 A411887 A411286 AV27929 A4187509 A157562 A4174006 H05297 A8256177 M6880 H28353 A4075400 F22000 W79542 A059304 A440261 A417441 A4076996 W74531 AU51747 A4187175 A886880 A4936071 A05705 T22564 W30227 AW27365 AU51360 AW170143 AW2267979 A405005 A402520 D8464965 A4325802 A2402261 A4770364 A43596 A415596 A45596 A
30	105178	7792_1	AA313225 AV990347 AF22348 NML 016913 AA186345 AA186508 AA081195 AA147972 AA346943 AV961667 AA18722 AA187207 AV371052 AV446751 AV746803 AV391606 AV071047 AV371057 AV371058 AVX522895 AV371052 AV371056 BED16950 AV6858 AA247876 GV3859 GOIS BF 11938 AV38151 AV3835 F32385 F35069 BH15346 AA2229 06 AA22314 H17056 F08498 2/35076 A069582 AV455108 GV484036 IR 15216 AX299152 AV1103579 VX12539 AA22310 AA23175 AA157197 AA157176 AV371371 AV352731 AV45392 AV655108 AA42361 R15216 AX299152 AV1103579 VX12539 AA22310 AA15715 AA157197 AA157176 AV371371 AV371371 AV59592 AV655089 AV65508 AV65089 AV65080 AV5508 AV65080 AV6508 AV65080 AV65
35			A1 100:27 AA496388 AA05597T A008903 AM014957 AW050208 AW333871 AW131066 D82683 D79715 A18935550 A1336773 IA507076 AA71468 AW060228 D79784 D46147 Ø2728 D16184 A086527 A127353 D161815 D83043 A415346 A128080 A1510828 AA028980 C16943 C16913 AW75741 AW51308 A1804764 AA44089 A1256958 AW103452 AW578078 A27446 C16948 A169470 FW172 A417423 AW052628 A181538 AA081030 A61380 A2156165 AW068499
40	105263	178672 2	AGRECTH 1 ARRORS HITTAGE GERIZORA KRIZZZY AARROZORA ALT STOP REGREZ AW1681 15. AA/20200 RESORD AARRORS AW771716 AA166662 C16504 H15722 AR21181 AA165888 H1706 AA16150 AA10594 AA36942 P128533 AW125047 RHIGGE H14668 AA89941 (D68270 221151 D68168 AD83271 AA645377 D58044 AB34322 AW179425 F00066 H14930 AA890493 176274 AW1688623 AW7840 AW368623 AW1686239 AW568633 AW368414 AW788413 AW388607 AW368453 SW188666 AW3688623 AW7840 AW368623 AW1686239 AW368633 AW368414 AW788413 AW388607 AW368453 AW368667 AW368463 AW368667 AW368665 AW368667 AW36867 AW36867 AW368667 AW36867 AW368667 AW36867 AW3687 AW3687 AW36867 AW3687
45			AVI388480 AVI388591 AVI388511 AVI388511 AVI388451 AVI388570 AVI388464 ABB4383 AVIZ37145 ABG2891 ABB64041 AVI386513 AVIX85351 AVIA965138 AVIA965141 ABS4155 ABF2818 BAB24430 ABF28167 KB5025 ABG3871 AVI378431 AVI378212 ADI15391 AVI352126 NB9396 ABS2317 AVI197115 AVIS7859 AVI797855 AVI7964 AVI2968615 TIGS95 HU5989 AVI7169 AVICE 14 AZCZYGZA ABGS986 RSB073 ADIOT45 T32864 ABT69640 AVIZ3705 TIGT974 AVI38615 TIGS95 HU59894
50	105330 104764 104865 106124	182497_1 90967_1 102037_1 54542_1	AMSSIBES RESZES RISTER AMOZISE A ADDRES ADDRES DASSTET AMOZISE 7 REGENT ARETTED ABSSIBE AREZHTA AMOZISEL AMOZISEL AREZHTA AMOZISEL AMOZISELA AMOZISEL AMOZISELA AMOZISELA AMOZISEL AMOZISELA A
55	100124	01012	R3226 AND 20070 ANHS 1054 ANY ZOM 1 ABERS A RESEAU A A R2386 A A RECARS A RESEAU SA A RESEAU A RESEAU A RACE A RESEAU A
60	107385	6976_1	EIGERIEG ANSI 198 ANDERSC ANGEST ANSIGNT ANTITYTE A INTOTOT ANSSODE REZON A ANGESIS ANSER AZ ANDEZISEA ANGEST ZERO ANGEST ANGEST ANSIGNT ANTITYTE A INTOTOT ANSSODE REZON A ANGESISE ANSER AZ ANDEZISEA ANGEST ZURTS AN ANGESTS ANDEZISEA ANGESTS AN ANGESTS ANAFSTS ANGEST ANDEZISEA ANGEST AZ ANTITYTE ANGEST ANGESTS ANGE
65			AW664384 H52423 W63317 EC378774 EIC391156 AA340138 A4 173095 AW513108 A4027672 A44145029 A A19726 WA1791 AAD7500 EIC362307 EIC36200 A4759735 AA65173 H40571 H67114 AW151257 A545173 A165688 A1 WA067370 A451180 A4622014 AW51308 A857810 AW162267 A1655586 A665266 A4024565 A1617450 A677330 AW052403 A472537 A086987 AW513086 W64526 A1460106 A166696 A166696 A166696 A167450 AW162304 AW162
70			AAD48629 ALT 18589 ARTIOLEZ ARSHKEZ HARDOUT ARTICUS AFTER THE THE ARTICUS ARTI
75	101192	15367_1	AB11228 AW131922 AA862897 AA902519 C31732 AW759045 ALD44660 BEZATZSS AW0000022 ALM3131 Ax158244 MM (00416 L20853 AL138570 WY7073 AW1516906 BE388271 BE409829 W46972 BE23596 BE256697 ALD7010 ALM1058 AX68000 AL039590 AA988740 VY26002 AA369344 AA035235 W27631 AW034836 AW854914 R93390 AA978039 AY646690 T35874 N95824 AA369874 AW845378 AA368267 R08256

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109001 146370_3 AM382743: NHS-09502 AM39893 AM39843 AW263540 AA723689 AA909334 AA156120 AA157141 AA156125 AW409866 W19499 AA157223 AM887438

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TABLE 6:

Pkey: Unique Eos probeset identifier number Exemplar Accession number, Genbank accession number 5 ExAccn:

Extragate recessors managed in the Company of the C summed over 5 experiments.

10 AUC2: AUC1/90th percentile of Al for aorta, aortic valve, vein, and artery.

	Pkey	Ex.Accn	UnigenelD	UnigeneTitle	AUC1	AUC2
15	314941	AA515902	Hs.130650	ESTs	1038	9
	327414			predicted exon	303.2	30.3
		AF026944	Hs.293797		429.2	42.9
		AI246482	Hs.249989		677.4	10.3
				KIAA0716 gene product	395.2	39.5
20				ESTs, Weakly similar to S59501 interfero	324	32.4
		N50617	Hs.80506		394.8	39.5
	326230			predicted exon	357.2	35.7
		AA628517	Hs.118502		433.6	12
	313665	AW751201	Hs.120932	ESTs	-83	0.5
25		Al380792	Hs.135104		348.2	34.8
		AL040178		ESTs, Weakly similar to The KIAA0149 gen	-49.2	0.5
		AA084248		G protein-coupled receptor 39	-1309	0.2
		AA632012			-247.8	1
		AI821409		ESTs, Highly similar to AF116865 1 hedge	-1025.8	1
30	319795	AB037821		protocadherin 10	203.6	5.2
	313350	AW591949	Hs.57958	ETL protein	183.8	18.4
	326759			predicted exon	1654.4	1.2
	300318	AW444502	Hs.256982	ESTs, Highly similar to AF116865 1 hedge	-346	1
	313978	AI870175	Hs.13957	ESTs	576.6	2.3
35		AI077477	Hs.307912	EST	56.4	0.4
	310272	AF216389	Hs.148932	semaphorin Rs, short form	-127.6	0
		BE547674			-102.6	0
	321325	AE033100	Hs.300646	KIAA protein (similar to moușe paladin)	1080.6	4.8
				protocadherin 12	1270.8	5.3
40	302378	AL109712	Hs.296508	Homo sapiens mRNA full length insert cDN	915.8	15.8
	315060	AA551104	Hs.189048	ESTs, Moderately similar to ALUC_HUMAN I	1236.8	4.9
		AW337575	Hs.201591		522.6	4.7
	337214			predicted exon	269	26.9
		AW023595	Hs.232048		796.4	20.2
45		AA582081		gb:nn32h08.s1 NCI_CGAP_Gas1 Homo sapir	ens	316.4 10.5
		AA644669	Hs.193042		349.6	7.6
		AW192334		ESTs	638.6	63.9
		AA972965			360.8	36.1
60				RNA binding motif protein, X chromosome	700.2 274.2	6.6
50		T90309	Hs.269651		238.2	7.5 23.8
		F11802	Hs.6818	ESTs	230.2	23.2
		H75391	Hs.255748		581.6	8.2
	326198	Harana	11. 004504	predicted exon	281.6	9.7
55		H25899	Hs.201591		-213	0.3
22		AW072215			285	0.5
		W87874	Hs.25277	hypothetical protein FLJ21065	26.6	0.3
		BE301700	HS.233950	hypothetical protein FLJ20401 predicted exon	1494.2	34.7
	338316	R44557	Hs.23748	ESTs	975.8	1.8
60		NM_00603		lipase, endothelial	201.2	0.9
00	331261	BE530076	He 103306	Homo saplens mRNA; cDNA DKFZp434B042		478.61.3
		X17033		integrin, alpha 2 (CD49B, alpha 2 subuni	356.2	1.7
	325544	X17000	110.21 1500	predicted exon	1014.6	9.4
	328700			predicted exon	627.4	62.7
65		AW248508	He 279727	Homo sapiens cDNA FLJ14035 fis, clone HE		5.7
00	336034	,,,,E	TIOIZI OI ZI	predicted exon	782.6	78.3
		AA938198	He 148123		746.4	13.8
		AW341683	110.140120	gb:hd13d01.x1 Soares_NFL_T_GBC_S1 Hor		134.8 13.5
		R39288	Hs.6702	ESTs	137	13.7
70		H06350		Human DNA sequence from clone RP5-850E		14.6 0.5
, ,	338033			predicted exon	540.6	14
		Y00272	Hs.184572	cell division cycle 2, G1 to S and G2 to	-494.8	ï
		BE568452		protein regulator of cytokinesis 1	-600	1
	338158			predicted exon	311.2	31.1
75	327036			predicted exon	351.8	35.2
				•		

	302655	AJ227892	Hs 146274	ESTs	180.2	18
	327568	ANLLIGOL	THE TOLLT	predicted exon	229	22.9
	324801	AW770553		sterol O-acyltransferase (acyl-Coenzyme	161.2	16.1
~	317850	Al681545	Hs.152982	hypothetical protein FLJ13117	-690	1
5	322818		Hs.293616		126.4	4.5
	324626	A1685464	Hs.292638		170.2	17
	317224 310955	X73608 Al476732	Hs.93029 Hs.263912	sparc/osteonectin, cwcv and kazal-like d ESTs	-80 466.8	0 46.7
		R38772		KIAA1106 protein	277	27.7
10	338388	1100172	110.11.0010	predicted exon	267.6	26.8
	338442			predicted exon	256	25.6
		AW247252	Hs.75514	nucleoside phosphorylase	1247.8	24.2
	338645			predicted exon	206	20.6
15		N58907	Hs.162430	ESTs	204.8 203.6	20.5
13	330305	BE169746	ms,12004	hypothetical protein DKFZp761D081 predicted exon	199.8	20.4
	308248	Al560919		gb:tq41g10.x1 NCI_CGAP_Ut1 Homo sapiens		199.4 19.9
	308886	Al833240		gb:at76d10.x1 Barstead colon HPLRB7 Homo	198.2	19.8
	315622	Al796144	Hs.258188	Homo sapiens cDNA FLJ11674 fis, done HE		19.1
20	323675	R43240		tumor differentially expressed 1	189.2	18.9
	312164	T91980	Hs.221074		187.6	18.8
	300378 317478	Z45270 Al343569		hypothetical protein FLJ22672 Homo sapiens mRNA for WDC146, complete	271.6	18.7 187 18.7
		AW452344			c 184.2	18.4
25		Al873346	Hs.214505		182.8	18.3
	334834	, 4010010	1101211100	predicted exon	178.8	17.9
		D62892		gb:HUM337C07B Ciontech human aorta poly/	4	177.2 17.7
		AL121460	Hs.272673	hypothetical protein FLJ20508	316.4	17.6
20	328548			predicted exon	174.6	17.5
30		AA884000 Al188183	Hs.8173 Hs.144078	hypothetical protein FLJ10803	172.4 326	17.2 17.2
	314299	AW382682		ESTs	170.8	17.1
	317702	AW173339		ESTS	169.8	17
	316094	AW975920		ESTs	169.4	16.9
35	323706	AA377578		hypothetical protein FLJ20596	169.2	16.9
	325843			predicted exon	321.4	16.9
	316012	AA764950		ESTs	1047.2	16.9
	309687 323329	AW236154 AL134744	Hs.77385 Hs.10852	myosin,lightpolypeptide6,alkali,smoothmu ESTs	168.2 168	16.8 16.8
40	312853	W05086		ESTS	167.4	16.7
70		Al422023	Hs.161338		298.6	16.6
		AW977642			165.6	16.6
	338728			predicted exon	165.4	16.5
	316609		Hs.122062	ESTs	165	16.5
45		AA888220		gb:oj15h01.s1 NCI_CGAP_Kid5 Homo saplen	S	164.6 16.5
	312642	AW052128		gb:wx26c02.x1 NCI_CGAP_Kid11 Homo sapi predicted exon	en 163.6	164 16.4 16.4
	317058	AI217713	Hs.147586		161.8	16.2
	311137		Hs.196042	ESTs	582.2	16.2
50	310178	Al936450	Hs.147482	ESTs ·	161.2	16.1
	320745	H51696	Hs.89278	hypothetical protein FLJ11186	161	16.1
		AW014637	Hs.130212	ESTs	160	16
	309871	AW300366		gb:xs63b05.x1 NCl_CGAP_Kid11 Homo sapie	en	159.8 16
55	302038 332237	AC004076 N52883	Hs.129709 Hs.102676	Homo saplens chromosome 19, cosmid R302	159	159 15.9 15.9
55	312362	AW015994	115. 102010	gb:UI-H-Bi0p-abh-g-09-0-UI.s1 NCL_CGAP_S		15.9
	331558	N62401	Hs.48531	EST	158.6	15.9
	316215	AI684535	Hs.200811		158.4	15.8
	336059			predicted exon	157.4	15.7
60		AJ245245			155.8	15.6
	328418	AK000149	Hs.29493	predicted exon	153.8 153.6	15.4 15.4
	304229 331606	AW273285		hypothetical protein FLJ20142 ESTs	153.0	15.3
	338962	MV1213200	N3.30002		664.4	15.3
65	317959	AI204202	Hs.130264		152.6	15.3
	336228			predicted exon	152.4	15.2
	313534	AW072916		zinc finger protein 131 (clone pHZ-10)	152.2	15.2
	317404	AI806867	Hs.126594	ESTs	152.2	15.2
70		Al469911	Hs.26498	hypothetical protein FLJ21657	152 151.4	15.2 15.1
70		AI247425 N29696	Hs.152182 Hs.44076	EST	151.4	15.1
	338118			predicted exon	151.2	15.1
	329863			predicted exon	150.6	15.1
		AW452886		ESTs	149.6	15
75	317039		Hs.126153		149.6	15
	331138	R63816	Hs.28445	ESTs	149.6	15

	316561	Al917222	Hs.121655		149.4	14.9
	328695			predicted exon	149.2	14.9
	302282	BE396283	Hs.173987	eukaryotic translation initiation factor	148.4	14.8
	318781	F11802	Hs.6818	ESTs	148.2	14.8
5	323709	AW297246	Hs 288546	Homo sapiens cDNA FLJ14190 fls, clone NT	148	14.8
	310790		Hs.248865	ESTS	147.8	14.8
	316833		Hs.124367		147.8	14.8
	323176	NM_00735			229	14.8
				pleckstrin homology-like domain, family		
10	324188		Hs.252709		147.6	14.8
10	317441		Hs.196583		147.4	14.7
	317584	AI825890	Hs.220513		146.8	14.7
	321798	Al308206	Hs.181959		146.8	14.7
	304363	AA206045		gb:zq77f05.s1 Stratagene hNT neuron (937	146.6	14.7
	313952	F20956		gb:HSPD05390 HM3 Homo sapiens cDNA ck	one	146.6 14.7
15	301909	AI702609	Hs.15713	ESTs	263.8	14.7
	309196	Al904895	Hs.9614	nucleophosmin (nucleolar phosphoprotein	146.2	14.6
	321860	N47474	Hs.212631		146.2	14.6
	330187	1444	11012 12001	predicted exon	146	14.6
	323042	AA463571	Hs.172550	polypyrimidine tract binding protein (he	145.6	14.6
20	313636	AA262397	Hs.201366	ESTs	145.2	14.5
20				UDP-N-acetylglucosamine:a-1,3-D-mannosid		
	302437	AB024729				14.5
	318197	Al473096	Hs.133403		144.8	14.5
		M16951		gb:Human Ig mu-chain mRNA VDJ4-region, 5		14.5
~ -	322357	AI734258	Hs.245367			144.614.5
25	300391	Al927371	Hs.288839	hypothetical protein FLJ12178	144.4	14.4
	326077			predicted exon	144.4	14.4
	302004	Y18264	Hs.123094	sal (Drosophila)-like 1	144	14.4
	320668	AA805663		Homo sapiens cDNA: FLJ23077 fis, done L.	144	14.4
	331212		Hs.226410		144	14.4
30	311268	AI969727	Hs.231859		143.2	14.3
	305159	AA659166	He 275668	EST, Weaklysimilarto EF1D_HUMANELONGA	TIONE	143 14.3
	304510	AA457391	He 110122	nbosomalproteinL13a	142.8	14.3
	320852	AA772920	Hs.303527	ESTs	142.8	14.3
	330854		Hs.122139		142.8	14.3
35	318275			ESTs	142.6	
22		AVV44990Z	ns. 190 125	basic-helix-loop-helix-PAS protein		14.3
	314992	AI824879	Hs.211286	ESTs, Weakly similar to 1207289A reverse	142.2	14.2
	322631	AA001697	Hs.293565	ESTs, Weakly similar to putative p150 [H	142.2	14.2
	332283	R40855		EST	142	14.2
	302894	AA719572	Hs.274441			141.2 14.1
40	301808	R35391	Hs.252831	reticulon 3	141	14.1
	318608	Al204491	Hs.151502	ESTs	141	14.1
	316499	AW292947	Hs.122872	ESTs	140.8	14.1
	317011	Al248760	Hs.150276	ESTs	140.8	14.1
	321840	N45600	Hs.46534	Homo saplens mRNA; cDNA DKFZp434P071	4 (f	140.8 14.1
45	327365			predicted exon	140.8	14.1
	331264	AA278898	Hs.225979	hypothetical protein similar to small G	140.8	14.1
	324545	AWI501944	He 127243	Homo saplens mRNA for KIAA1724 protein,	140.4	14
	312986	AA211586		gb:zn56d05.s1 Stratagene muscle 937209 H	140.2	14
		AA825814	Hs.149065	ESTs	140.2	14
50	330723		Hs.31082	hypothetical protein FLJ10525	140.2	14
50	304876	AA595765	115.0 1002	qb:ni28q06.s1 NCI_CGAP_AA1 Homo sapien		139.8 14
	311379			ESTs	139.8	14
			Hs.146840		139.8	14
	324137	AA393127	Hs.222762	ESIS	139.8	14
55	328262			predicted exon	139.6	14
	322349	AK001279	Hs.180171		139.4	13.9
	323504	AA280223	Hs.130865	ESTs	139.4	13.9
	304261	AA059387		gb:zf66d01.s1 Soares retina N2b4HR Homo	139.2	13.9
	310489	AW451493	Hs.235516	hypothetical protein PRO2955	139.2	13.9
60	335946			predicted exon	139.2	13.9
	318155	AI041546	Hs.132133	ESTs	138.8	13.9
	313796	AI797169	Hs.208486	ESTs	138.6	13.9
	333977			predicted exon	138.6	13.9
	324845	AW969635	Hs.283718		138.2	13.8
65	331139	R65706	1,010,001.10	gb:yi16g12.s1 Soares placenta Nb2HP Homo		13.8
00	331131	R54797		gb:yg87b07.s1 Soares infant brain 1NIB H	669.6	13.8
	321250	H58539	Hs.151692	ESTs	138	13.8
		AA668782				137.8 13.8
	312498			ESTs, Weakly similar to ALU1_HUMAN ALU S	407.0	
70	331252	W52470	Hs.34578	alpha2,3-sialyltransferase	137.8	13.8
70	337407			predicted exon	137.8	13.8
	303973	AW512014		gb:xx68a03.x1 NCI_CGAP_Lym12 Homo sap		137.4 13.7
	314582	AA412258	Hs.188817	ESTs	137.4	13.7
	327373			predicted exon	137.2	13.7
7.5	323367	AA234591	Hs.304123		136.6	13.7
75			Hs.120260		136.4	13.6
	315231	AA705809	Hs.119922	ESTs	136.2	13.6

	318592	T39310	Hs.1139	cold shock domain protein A	136.2	13.6
	320906	AW969703	Hs.293332	ESTs	136.2	13.6
	328937			predicted exon	136.2	13.8
	329073			predicted exon	136.2	13.6
5		AV659082	Hs.134228	ESTs	136	13.6
,	318231					
	311992	AL360200	Hs.114145		135.8	13.6
	316497	AA766457	Hs.136849		135.8	13.6
	317677	AA968594	Hs.127868	ESTs	135.8	13.6
	321680	W02848	Hs.93704	ESTs	135.8	13.6
10	326080	1102010	110.007.01	predicted exon	135.8	13.6
10			11 470040			
	330938			KIAA1106 protein	135.8	13.6
	306573	AL134878		ribosomal protein, large P2	135.6	13.6
	307383	A1223207	Hs.147888	EST	135.6	13.6
	311114	AW449382	Hs.195297	ESTs	135.6	13.6
15	320579	R15138		Horno sapiens clone 25052 mRNA sequence		13.5
10	301328	AA884104		ESTs	134.8	13.5
	312063	N58198	Hs.182898		134.8	13.5
	323036	H09604	Hs.13268	ESTs	134.6	13.5
	332776	AF241850	Hs.151428	ret finger protein 2	134.4	13.4
20	332494	AA282330	Hs.145668		134.2	13.4
20	334376	A4202330	115.140000	predicted exon	134.2	13.4
	313264	N93416	Hs.118228	ESTs	133.6	13.4
	313669	AA351109	Hs.5437	Tax1 (human T-cell leukemia virus type I	133.2	13.3
	312083	T87398	Hs.205816	ESTs	132.6	13.3
25	319354	AA993807	Hs.167367	ESTe	132.6	13.3
20	307414	Al242108	110.107007	gb:qh92a02.x1 Soares_NFL_T_GBC_S1 Hon		132.2 13.2
	040774		11: 004100			
	312771	AA018515		Apg12 (autophagy 12, S. cerevislae)-like	131.8	13.2
	313004	Al274963		ESTs	131.2	13.1
	300995	AW510641	Hs.258018	ESTs	220.6	13
30	319323	F12650	Hs.13287	ESTs	125.4	12.5
50	329451	1 12000	113.10207	predicted exon	123.4	12.3
						12.2
	337603			predicted exon	572	
	312480	R68651	Hs.144997	ESTs	121.4	12.1
	324934	AW452051	Hs.147546	ESTs	119.4	11.9
35	320723	BE178025	Hs.7942	hypothetical protein FLJ20080	117	11.7
55	318188	Al792586	110.7012	gb:gi74f02.y5 NCI_CGAP_Ov26 Homo sapler		116.6 11.7
			Hs.283955		112.8	11.3
	320873	AF238869				
	331005	BE003191	Hs.119555	ESIS	112.6	11.3
	304969	AA614406		gb:np46f05.s1 NCI_CGAP_Br11 Homo sapier		112.4 11.2
40	319799	Al139253	Hs.227767	zinc finger protein 41	111.2	11.1
	302610	AA347945	Hs.256024	ESTs	111	11.1
	309485		Hs.108124	ribosomalproteinS4,X-linked	111	11.1
	311880		Hs.258247		110.2	11
	313981		Hs.128148		110.2	11
45	322442	W49701	Hs.29667	ESTs	109.4	10.9
	315099	AA806536	Hs.291841	ESTs	109	10.9
	304793	AA583264		ribosomalproteinl.12	108.8	10.9
	330815	AA019211		KIAA1238 protein	108.8	10.9
	304044	T81656	HS.252259	ribosomal protein S3	714.8	10.8
50	325222			predicted exon	135	10.8
	325889			predicted exon	814.6	10.8
	321447	AW891130	Hs 38173	ESTs	107.8	10.8
	302990		Hs.180182		106.2	10.6
		AI476803	110.100102	gb:tj77e12.x1 Soares_NSF_F8_9W_OT_PA_	0.0	270.6 10.6
	308106			gb.y/reiz.xi ouales_Nor_ro_sw_Oi_rA_	100	
55	310536	Al301041	Hs.150174	ESTs	106	10.6
	315257	AW157431	Hs.248941		233	10.6
	318787	Z42313	Hs.22657	ESTs	105.8	10.6
		Al927226	Hs.175610		105.2	10.5
	326788	MOLITEZO	113.113010	predicted exon	104.4	10.4
C0						
60	312234		Hs.206934	ESTs	104	10.4
	314482	AW085525	Hs.134182	ESTs	234	10.4
	323597	Al185693	Hs.135119	ESTs	102.4	10.2
	302623	AW836724	He 194110	hypothetical protein PRO2730	162.4	10.2
		AI791531	Hs.129993	EOTs	101	10.1
10	323594			E019		
65	324315	N55761	Hs.194718	zinc finger protein 265	100.2	10
	314217	AA256465	Hs.188725	ESTs	99.2	9.9
	320932	AA554913	Hs.162297	ESTs	98.2	9.8
	327876			predicted exon	98.2	9.8
	319736	R17424	Hs.6650	vacuolar protein sorting 45B (yeast homo	98	9.8
70		11/1424	116.0000			
70	327747			predicted exon	97.6	9.8
	327844			predicted exon	97.4	9.7
	318200	Al061192	Hs.166517	ESTs	97.2	9.7
	329414			predicted exon	97.2	9.7
	318296	AI089667	Hs.270713		121.4	9.7
75			110.2/0/13	about 2000 of Passes fold book 55-15 MORE	1206	9.7
13	307010	AI140014		gb:qa68f09.x1 Soares_fetal_heart_NbHH19W	250	
	319792	Al138635	Hs.22968	ESTs	385.4	9.6

				of these			
	305671	AA811688	Hs.82113	dUTPpyrophosphatase	96	9.6	
	329440			predicted exon	93.8	9.4	
	310381	AI263059	Hs.145594	ESTs	93.4	9.3	
	318824	F06771	Hs.27226	ESTs	93.4	9.3	
5	328957	100//1	110.21220	predicted exon	92.2	9.2	
,	318804	7.00.10			92.2		
		Z42549	Hs.160893	ESTs		9.2	
	330836	AA055611		ESTs, Moderately similar to ALU4_HUMAN A		9.2	
	324592	AW752437	Hs.325708	ESTs	91.8	9.2	
	311820	AW274545	Hs 254333	ESTs	91.4	9.1	
10	321614	H86161	110111011000	gb:ys94b01.r1 Soares retina N2b5HR Homo	91	9.1	
10		100 101		gu.ysa-ou i.i i adales letha Nadank nomo			
	330306			predicted exon	91	9.1	
	303096	AL080276	Hs.268562	regulator of G-protein signalling 17	90	9	
	313275	AI027604	Hs.159650	ESTs	110.4	8.8	
	302593	H54855	Hs.36958	ESTs	88	8.8	
15	321421	BE465115	Hs.171688	ESTs	86.2	8.6	
13					456.4		
	330832	Al133530	Hs.62930	ESTs		8.6	
	311847	AW301807		ESTs	86	8.6	
	322036	BE002723	Hs.301905	Homo sapiens cDNA FLJ14080 fis, clone HE	145.8	8.6	
	328688			predicted exon	85.6	8.6	
20	325251			predicted exon	85.4	8.5	
20							
	329088			predicted exon	85.4	8.5	
	322524	W79027	Hs.271762	ESTs	84	8.4	
	337953			predicted exon	451	8.3	
	323529	AA284397	He 201485	Homo sapiens clone FLC0664 PRO2866 mRt		82.6 8.	3
25	307041	Al144243	110.201700	gb:qb85b12.x1 Soares_fetal_heart_NbHH19V	u ,	306.88	
23					'		~
	318285	A1332454		ESTs	81.4	8.1	
	312021	AA759263	Hs.14041	ESTs	81	8.1	
	329350			predicted exon	81	8.1	
	326169			predicted exon	80.4	8	
30	338038			predicted exon	1024.2	7.9	
30							
		A1214510	Hs.146304	ESIS	77.4	7.7	
	312542	D60076		gb:HUM084E10A Clontech human fetal brain	76.8	7.7	
	320992	AB026891	Hs.225972	solute carrier family 7, (cationic amino	76	7.6	
	318596	AI470235	Hs.172698	EST	150.6	7.5	
35	315650	AA649042		ESTs	73.4	7.3	
33							
	324328	AA447276		ESTs	210.4	7.1	
	332622	R10674	Hs.128856	CSR1 protein	70.2	7	
	328229			predicted exon	69.4	6.9	
	319110	T75260	Hs.98321	hypothetical protein FLJ14103		6.9	
40	316133		Hs.125562	FOT-	308.6	6.9	
40		A1187742	ns.120002	E518			
	303992	AW515800		gb:hd88g01.x1 NCI_CGAP_GC6 Homo sapie	ns	67.8 6	ď
	322675	AA017656	Hs.146580	enolase 2, (gamma, neuronal)	377.2	6.7	
	325753			predicted exon	105.2	6.6	
	312539	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	92.2	6.4	
45	302592	AA294921		v-ral simian leukemia viral oncogene hom	361.6	6.3	
43							
	314578	AA410183	HS.13/4/5	ESTs	201.6	6.1	
	335986			predicted exon	108.6	6	
	321478	AW402593	Hs.123253	hypothetical protein FLJ22009	528	6	
	305192	AA666019		gb:ag44a04.s1 Jia bone marrow stroma Hom	58.6	5.9	
50	304275	AA070605		gb:zm53h09,s1 Stratagene fibroblast (937	78.6	5.6	
50				gb.ziiioaioa,a i olialagelie ilbioolaai (aar			
	302779	AJ235667		gb:Homo sapiens mRNA for immunoglobulin	278.8	5.5	
	301976	T97905	Hs.77256	enhancer of zeste (Drosophila) homolog 2	479.2	5.4	
	316021	AW293399	Hs.144904	nuclear receptor co-repressor 1	792.4	5.3	
	320802	BE336699	Hs.185055	BENE protein	2423.8	5.3	
55	317282	AI733112	Hs.176101	ESTs	523.2	5.1	
55					578	5.1	
	316827	Al380429		ESTs			
	303190	BE280787	Hs.16079	hypothetical protein FLJ10233	223	5.1	
	315587	AI268399	Hs.140489	ESTs	136.2	5	
	333122			predicted exon	399	5	
60	310214	AI220072	Hs.165893		234.4	4.9	
00	320089	D43945	Hs.113274		68	4.9	
	309328	AWU24348	HS.233191	EST, Weakly similar to A27217 glucose tr	258.8	4.8	
	318971	Z44067	Hs.10957	ESTs	376.6	4.8	
	327220			predicted exon	47.4	4.7	
65	315757	AW014605	He 170979	ESTs	177.4	4.7	
00							
	320730	R68869	Hs.151072	ESTs	205.2	4.6	
	313339	AI682536	Hs.163495	Homo sapiens cDNA FLJ13608 fis, clone PL	260	4.5	
	318634	T49598	Hs.156832	ESTs	475.2	4.5	
	320955	AW820035	Hs.278679	a disintegrin and metallioproteinase doma	388.6	4.4	
70	306605	AI000497	Hs.119500	ribosomalprotein,largeP2	.81.6	4.4	
, 0			118.113000	The second process of	.01.0	102.44	
	309349	AW051913		gb:wx24a09.x1 NCI_CGAP_Kid11 Homo sap	en		.5
	306004	AA889992	Hs.2186	eukaryotictranslationelongationfactor1ga	451.2	4.2	
	330020			predicted exon	61.2	4.1	
	302308	AW327279	Hs 91379	ribosomal protein L26	342	3.9	
75		AW979268	110.01010	gb:EST391378 MAGE resequences, MAGP I-		56.4 3	8
13					400.4		
	315131	Al753709	Hs.152484	ESTs	130.4	3.7	

		AI493591	Hs.78146	platelet/endothelial cell adhesion molec	3179.6	3.6	
	333585			predicted exon	175.4	3.5	
	312911	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H	219	3.5	
	322966	AA633669	Hs.235920	Homo sapiens cell recognition molecule C	350.2	3.4	
5		R71072	Hs.191269	ESTs	322.8	3	
	318988	Z44203	Hs.26418	ESTs	25	2.5	
	332363	Al123705	Hs.106932	ESTs	773.4	2.5	
	324181	AI025476	Hs.131628	ESTs	634.8	2.4	
	311717	AW205369	Hs.312830	ESTs	54.2	2.4	
10	321342	AA127984	Hs.222024	transcription factor BMAL2	23.4	2.3	
	308852	A1829848	Hs.182937	peptidylprolytisomeraseA(cyclophilinA)	92	2.3	
	331466	AA373210	Hs.43047	Homo sapiens cDNA FLJ13585 fis, clone PL	494	2.3	
	320279	AB033062	Hs 134970	DKFZP434N178 protein	76.2	2.2	
	322221			nucleosome assembly protein 1-like 1	253.2	2.1	
15	302925	AL137449	Hs.126666	homeo box B4	136.6	2.1	
		AB041035	Hs.93847	NADPH oxidase 4	720	1.8	
		AA514416	Hs.152320		27	1.8	
	312695		Hs.200242		303.8	1.6	
	320223	W35132	Hs.267442		189	1.5	
20		AW247977		translocase of inner mitochondrial membr	14.4	1.4	
20	331039	AW378685		Mitochondrial Acyl-CoA Thioesterase	529.8	1.4	
	333123	A11310000	113.10020	predicted exon	396.2	1.4	
	328455			predicted exon	91.8	1.3	
	334458			predicted exon	406.4	1.3	
25	313478	4.4.4.0000	11- 400775	ESTs	413.4	1.1	
23		AA643008 AW338564	No. 192770		-30.8	1	
	309899			annexinA2 Homo sapiens cDNA FLJ12981 fis, clone NT	50.0	1	
	311735	AW294416		nonio sapieris con A PLU 1250 I ils, cione N	-73.6	1	
	312953	NM_00199		coagulation factor II (thrombin) recepto ESTs	-/3.0 -43.8	i	
30	313055	AW367295		ESTs. Weakly similar to ALU4 HUMAN ALU		-63 1	
30	313291	Al267970	Hs.150614				
	315059		Hs.271106		-67	1	
	322284	AI792140	Hs.49265	ESTs	-395.2	1	
	322450	AL121278		ESTs	-1.6		
25		AW975183			4.4	1	
35		AW970939	Hs.291039	ES18	-282.8		
	333610			predicted exon	-152.6	1	
	335093			predicted exon	-23.2	1	
	339403			predicted exon	-331.2	1	
40	302820	X04588	Hs.85844	neurotrophic tyrosine kinase, receptor,	591.2	1	
40	302270	R56151	Hs.93589	Homo saplens mRNA; cDNA DKFZp564B116		276.61	
	323755	AW300094	Hs.136252		135	0.9	
	326946			predicted exon	727.4	0.9	
	315343	BE144306		ESTs, Weakly similar to P4HA_HUMAN PRO		122.8 0.9	,
4.0	311168	AK001270	Hs.196086	hypothetical protein FLJ10408	304	0.9	
45	329732			predicted exon	109.2	0.9	
	321415	BE621807	Hs.3337	transmembrane 4 superfamily member 1	414.8	0.7	
	333121			predicted exon	87.8	0.7	
	333120			predicted exon	379.8	0.7	
~ ^	330392	AW797956	Hs.75748	proteasome (prosome, macropain) subunit,	589.2	0.7	
50	314711		Hs.126058	ESTs	-87	0.6	
	330865	BE409857	Hs.69499	hypothetical protein	347.4	0.6	
	333169			predicted exon	-1182	0.6	
	335095			predicted exon	106.4	0.6	
	335815			predicted exon	-156	0.6	
55	330232			predicted exon	102.6	0.6	
	330823	AA031565		ESTs, Moderately similar to ALU5_HUMAN A		0.5	
	331704	F04225	Hs.66032	ESTs	-14.6	0.5	
	302642			NESH protein	267.6	0.5	
	304484	AA432067	Hs.258373	ESTs	85	0.5	
60	310230	AK000377		homolog of mouse C2PA	-70	0.4	
	301531	AI077462	Hs.134084	ESTs	-195.4	0.4	
	306337	AA954221	Hs.73742	ribosomalprotein,large,P0	-33.4	0.4	
	331327	N46436	Hs.109221		-392	0.4	
	332961			predicted exon	-5.6	0.4	
65	322796	W31178	Hs.154140	Homo sapiens ovary-specific acidic prote	-880.6	0.3	
	328857			predicted exon	55.2	0.3	
	316342	AA743935	Hs.202329	ESTs	43.4	0.3	
	331263	AW780192	Hs.267596	ESTs	-180.4	0.3	
	335987			predicted exon	-134	0.3	
70	311923	T60843	Hs.189679	ESTs	12.2	0.3	
	310522		Hs.244647	ESTs	-187.8	0.3	
	315363	AA759190	Hs.121454	ESTs, Weakly similar to olfactory recept	80	0.3	
				coagulation factor II (thrombin) recepto	-877	0.3	
	302032						
	302032 313140			annexin A2	95.4	0.3	
75		BE265133	Hs.217493 Hs.161359	annexin A2 ESTs	-239	0.3	
75	313140 310860	BE265133	Hs.217493 Hs.161359	annexin A2	-239		

0.3

	328520			predicted exon	-109.2	0.2	
				CD3-epsilon-associated protein; antisens	10	0.2	
		AI866921		Homo sapiens cDNA FLJ12149 fis, clone MA		0.2	
	315065	AK001122	Hs.105859	hypothetical protein FLJ10260	-46.2	0.2	
5	314129	AA228366	Hs.115122	ESTs	-308.8	0.2	
-	335697			predicted exon	-47.2	0.2	
	335989			predicted exon	89	0.2	
		A1AI007042	No torote	hypothetical protein FLJ13465	-205.6	0.2	
	329745	AVV00/343	ns.12/210	predicted exon	103	0.2	
10							
10		AW419069	Hs.209670		-177.8	0.2	
	334616			predicted exon	-936.6	0.2	
		AI821267	Hs.207243	EST	-7.2	0.2	
	320416	AI026984	Hs.293662	ESTs	-18.4	0.2	
	335211			predicted exon	-142	0.2	
15	323629	AA375957	Hs 6682	ESTs	-100	0.1	
		AW452904		gb:Ui-H-Bi3-aly-h-11-0-Ui.s1 NCI_CGAP_Su		0.1	
		AI015862	Un 124702		-250.6	0.1	
	332833	AIUTOBOZ	HS. 13 17 93	predicted exon	-374.2	0.1	
				LIM domain kinase 1	-27.6		
20		NM_00231				0.1	
20		AA004879			-288,2	0.1	
		AV651680			-735.6	0.1	
	330775	AW247020	Hs.250747	SUMO-1 activating enzyme subunit 1	53.6	0.1	
	333168			predicted exon	-1041.8	0.1	
	332079	AI308876	Hs.103849		19.4	0.1	
25		AF161442		Homo sapiens HSPC324 mRNA, partial cds	-123.6	0.1	
23		AI799111	Hs.64341	ESTs	-46.4	0.1	
				DC2 protein	-156.4	0.1	
					-146.6	0.1	
		Al479439	Hs.171532				
20		AA659037	Hs.163780		-304	0.1	
30		AI285970	Hs.183817		-445	0.1	
		R43707	Hs.133159	ESTs, Weakly similar to PIHUSD salivary	-111.8	0.1	
	308677	Al832519		gb:at69h03.x1 Barstead colon HPLRB7 Homo	-149.6	0	
	311275	AI659188	Hs.207144	ESTs	-62.6	0	
	302363	AW163799	Hs.198365	2.3-bisphosphoglycerate mutase	-15	0	
35		AW956580		ESTs	-1059.6	ō	
-				MCT-1 protein	-332.2	ō	
		AA961367	110.102000	qb:or52a05.s1 NCL_CGAP_GC3 Homo saple		21.8	٥
			11. 74000		-97.2	0	٠
		Al292148	Hs.71622	SWI/SNF related, matrix associated, acti	-2222		
40						0	
40		AW262836			-881.6	0	
	332450	AW288085	Hs.11156	hypothetical protein	28.4	0	
	332535	AF167706	Hs.19280	cysteine-rich motor neuron 1	-722	0	
	335990			predicted exon	-421	0	
	330746	AB033888	Hs.8619	SRY (sex determining region Y)-box 18	35.4	0	
45	316820	Al627912	Hs.130783	Forssman synthetase	-373.6	0	
	337429			predicted exon	-257	ō	
		DEC22024	Un 152571	ESTs, Highly similar to IGF-II mRNA-bind	-33	ŏ	
		Al346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	-280	ŏ	
50		AI739435	Hs.39168	ESTs	-3627.6	0	
50		AA531133		hypothetical protein MGC2574	-278.6	0	
		NM_004579		mitogen-activating protein kinase kinase	-244	0	
	332374	X91195	Hs.100623	phospholipase C, beta 3, neighbor pseudo	-1204.2	0	
	333221			predicted exon	-189.6	0	
	335988			predicted exon	-122.6	0	
55		AI984144	Hs.66713	hepatitis delta antigen-interacting prot	-2257.4	ŏ	
		BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	-359.2	ŏ	
		AF131781		hypothetical protein FLJ12442	-874.6	ŏ	
	337113	W. 19 1.01	113.047.33	predicted exon	-24.6	ŏ	
	335149				-191.8	ŏ	
	333149			predicted exon	-131.0	·	

TABLE 6A

5 Table 6A shows the accession numbers for those pleys lacking uniqueneID's for Table 6. The pleys in Table 7 lacking uniqueneID's are presented within Tables 1AA. For each probeset we have lated the gene cluster number from which the objurnatedioties were designed. Gene clusters were compiled using sequences derived from eachine. ESTs and miNNLS. These sequences were clustered based no sequence shrinkly size? Clustering and Alignment Tools (Octoble Twist, Oakfand California). The Gesbank accession numbers for sequences comprising each cluster are listed in the "Accession" column.

10

15

Pkey: Unique Eos probeset identifier number
CAT number: Gene c'uster number
Accession: Genbank accession numbers

```
Pkey CAT Number Accession
```

320925 1525201_1 D62892 D79755 D62760 20 321614 87866 1 H86161 AA054308 AA018955 F20956 AA129374 AA133740 AW819678 313952 136885 1 314648 293660_1 AW979268 AA878419 AA431342 AA431628 302749 458 107 M16951 M16952 M16948 M16949 M16950 312362 764066_1 AW015994 R39898 AW0 312542 1522649_1 D60076 D60259 D61037 AW015994 R39898 AW000978 Al598202 Al521706 25 312642 1005225_1 AW052128 H51439 H51481 312986 171879 1 AA211586 F35799 AA211641 F29720 AW937387 AW937408 329350 c_x_hs 329414 c_y_hs 30 329440 c_y_hs 329451 c_y_hs 329451 c_y_hs 338033 CH22_6528FG_LINK_EM:AC00 338038 CH22_6535FG_LINK_EM:AC00 338116 CH22_6650FG_LINK_EM:AC00 338158 CH22_6700FG_LINK_EM:AC00 35 329732 c14_p2 329745 c14 p2 308106 Al476803 329683 c14_p2 338316 CH22_6944FG__LINK_EM:AC00 40 308248 Al560919 338388 CH22_7034FG_LINK_EM:AC00 338442 CH22_7109FG_LINK_EM:AC00 338645 CH22_7410FG_LINK_EM:AC00 45 338728 CH22 7527FG LINK EM:AC00 308877 Al832519 338962 CH22_7838FG_LINK_DJ32I10 308886 AI833240 333120 CH22_349FG_81_3_LINK_EM:A 333121 CH22_350FG_81_4_LINK_EM:A 333122 CH22_351FG_81_6_LINK_EM:A 50 333123 CH22_352FG_81_7_LINK_EMA 333168 CH22_400FG_94_1_LINK_EMA 333169 CH22_401FG_94_2_LINK_EM:A 55 333221 CH22_458FG_105_1_LINK_EM: 326077 c17_hs 326080 c17_hs 326169 c17 hs 326198 c17 hs 60 326230 c17_hs 333585 CH22_846FG_203_4_LINK_EM: 333610 CH22_871FG_217_5_LINK_EM: 335093 CH22 2423FG 492 3 LINK EM

335095 CH22_2425FG_492_5_LINK_EM 335149 CH22_2484FG_499_5_LINK_EM

326759 c20_hs 333977 CH22_1254FG_309_6_LINK_EM 326788 c20_hs 335211 CH22_2550FG_511_2_LINK_EM

305192 AA666019 303973 AW512014 303992 AW515800 326946 c21_hs 328229 c 6 hs

328262 c 6 hs

65

70

75

172

```
328418 c 7 hs
         328455 c 7 hs
         335697 CH22_3058FG_596_12_LINK_E
         328520 c_7_hs
 5
         328548 c 7 hs
         335815 CH22 3187FG 618 3 LINK EM
         328688 c_7_hs
         328695 c_7_hs
307010 Al140014
         337113 CH22_5058FG_493_1_
10
         307041 Al144243
         328700 c_7_hs
335946 CH22_3324FG_646_20_LINK_D
         335986 CH22_3366FG_654_10_LINK_D
335987 CH22_3367FG_654_11_LINK_D
15
         335988 CH22 3368FG_654_12_LINK_D
         335989 CH22_3369FG_655_2_LINK_DJ
         335990 CH22_3370FG_655_4_LINK_DJ
         337214 CH22 5288FG 613 7_
20
         330020 c16_p2
         305989 AA888220
         326857 c_7_hs
         328937 c_8_hs
         328937 c_8_hs
328957 c_8_hs
330187 c_4_p2
337407 CH22_5607FG_755_1_
337429 CH22_5633FG_762_3_
25
         330232 c_5_p2
         307414 AI242106
30
         330305 c_7_p2
330306 c_7_p2
337603 CH22_5896FG_LINK_C20H12.
         337953 CH22_6395FG__LINK_EM:AC00
         339236 CH22_8181FG_LINK_BA354I1
         339403 CH22_8384FG__LINK_BA232E1
         309349 AW051913
         325222 c10 hs
         325251 c10_hs
                              AI792566 AI053836 AI054127 AI792489 AI288324
         318188 956161_1
40
         309871 AW300366
         325544 c12 hs
         309931 AW341663
332833 CH22_50FG_17_7_LINK_C20H1
         302779 33837_1
                              AJ235667 AJ235666 AJ235664 AJ235665 AJ235668 AJ235669 AJ235670
         302790 34168_1
                              AJ245245 AJ245247 AJ245257 AJ245248 AJ245254 AJ245256 AJ245253 AJ245203 AJ245250 AJ245252 AJ245243 AJ245204
                              AJ245201 AJ245206 AJ245246 AJ245255 AJ245205 AJ245202 AJ245251 AJ245249 AJ245207 AJ245244
         332961 CH22_185FG_48_18_LINK_EM:
         325753 c14 hs
         327036 c21 hs
50
         325843 c18_hs
         325889 c16_hs
         304261 AA059387
         304275 AA070605
         334376 CH22 1670FG 379 8 LINK EM
         327220 c_1_hs
         304363 AA206045
         334458 CH22_1757FG_391_2_LINK_EM
         327365 c_1_hs
         327373 c_2_hs
60
         334616 CH22_1923FG_411_15_LINK_E
         327414 c_2_hs
         327568 c 3 hs
         338034 CH22_3419FG_678_5_LINK_DJ
         336059 CH22 3445FG 684 2 LINK DJ
65
         334834 CH22_2148FG_439_3_LINK_EM
         304782 AA582081
         304876 AA595765
         327747 c_5_hs
336228 CH22_3626FG_730_4_LINK_DA
70
         329073 c_x_hs
         329088 c_x_hs
304969 AA614406
         327844 c_5_hs
         327876 c_6_hs
         306352 AA961367
```

331131 genbank_R54797

R54797

331139 genbank_R65706 R65706 331420 675963_1 AW452904 AW449414 BE467906 AI298565 BE549932 BE326357 F04362

TABLE 6B

Table 6B shows the genomic positioning for those plays backing uniquene ID's and accession numbers in Table 6. The plays in Table 7 leaking uniquentiD's are represented within Tables 1-8C. For each predicted exon, we have listed the genomic sequence source used for prediction. Nucleotide locations of each predicted exon are as its listed. 5

Unique number corresponding to an Eos probeset Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I, et al." refers to the publication Pkey: 10 Ref: entitled "The DNA sequence of human chromosome 22." Dunham L et al., Nature (1999) 402:489-495. Indicates DNA strand from which excris were predicted. Indicates nucleotide positions of predicted excris.

Strand:

Nt_position; 15

15				
	Pkey R	tef	Strand	Nt_position
	332961 D	tunham, I. et.al.	Plus	2521424-2521555
20	333221 D	tunham, I. et.ai.	Plus	3978070-3978187
		tunham, I. et.al.	Plus	6234778-6234894
		lunham, 1. at.al.	Plus	6547007-6547116
		lunham, I. et.al.	Plus	13902218-13902331
0.7		unham, 1. et.ai.	Plus	14353496-14353572
25		unham, l. et.al.	Plus	15176123-15176470
		unham, l. at.al.	Plus	21497441-21497587
		unham, i. et.al.	Plus	21774611-21774680
		tunham, l. et.al.	Plus	25481456-25481649
20		lunham, l. et.al.	Plus	27967791-27967852
30		lunham, l. et.al.	Plus	27971413-27971481
		unham, l. et.al.	Pius	27977912-27978013 27983788-27983860
		iunham, I. at.al. iunham, I. et.al.	Plus Plus	27988532-27988608
		unham, I. et.al.	Plus	29014404-29014590
35		unham, I. et.al.	Plus	6827029-6827125
33		Junham, I. et.al.	Plus	8092128-8092271
		Junham, I. at.al.	Plus	8138219-8138392
		Junham, I. et al.	Pius	17089711-17089988
		Junham, I. et.al.	Plus	19980640-19980698
40		tunham, I. at.al.	Plus	29581892-29582020
		unham, I. at.al.	Minus	1119848-1119705
	333120 D	Junham, I. at.al.	Minus	3307508-3307427
	333121 D	Dunham, I, et.al.	Minus	3308446-3308358
	333122 D	tunham, I. et.al.	Minus	3309596-3309531
45	333123 D	tunham, I. et.al.	Minus	3310817-3310749
		tunham, l. at.al.	Minus	3729896-3729788
		tunham, I. at.al.	Minus	3730864-3730767
		Dunham, I. et.al.	Minus	8722928-8722725
50		Ounham, Letal	Minus	17182681-17182535
50		Dunham, I. at.al.	Minus	21297367-21297214
		Ounham, I. et al.	Minus	21292546-21292381
		Junham, I. at.al.	Minus	26320518-26320421
		Ounham, L. et.al.	Minus	27487203-27487035 29184079-29183969
55		Dunham, I. et al.	Minus Minus	30904602-30904497
23		Dunham, I. et.al. Dunham, I. et.al.	Minus	21233344-21233237
		Junham, Letal	Minus	26095902-26095502
		Junham, I. et.ai.	Minus	31886652-31886567
		Ounham, I. et.al.	Minus	32086238-32086079
60		Ounham, I. et.al.	Minus	1299296-1299194
		Junham, I. et.al.	Minus	10614071-10613814
		Ounham, I. et.al.	Minus	11794465-11794343
	338388 D	Dunham, 1. et.al.	Minus	18662403-18662305
		Ounham, I. et.al.	Minus	24063839-24063775
65	338728 D	Ounham, I. et.al.	Minus	25949039-25948927
	339236 D	Dunham, I. et.al.	Minus	32773355-32773202
		Ounham, I. et.al.	Minus	34050728-34050625
		525287	Minus	22332-22473
70		682448	Minus	411693-411751
70		682452	Plus	171228-171286
		682474	Plus	398512-398621
		065779	Plus	174774-175142
		065783	Plus	161252-161322
75		691797	Plus	196801-196971 223829-223891
13	325889 5	867087	Plus	223029-223691

	325843		Minus	7126-7232
	330020	6671887	Plus	172397-172491
	326198	5867215	Minus	80295-80674
	326230	5867230	Minus	301868-301972
5	326169	5867255	Minus	128321-128388
	326077	6682495	Minus	312108-312168
	326080	6682495	Plus	478644-478847
	326759	6249610	Plus	97216-97311
	326788	6682503	Plus	277132-277335
10	326946	6004446	Minus	116677-116967
	327036	6531965	Plus	319951-320040
	327220	5867525	Minus	65701-65781
	327365	6552412	Minus	118133-118198
	327414	5867750	Plus	102461-102586
15	327373	5867792	Minus	8186-8742
	327568	5867811	Minus	46152-46287
	330187	6706138	Plus	212923-213020
	327747	5867947	Plus	115322-115498
	327844	6249582	Minus	18895-18958
20	330232	6013526	Plus	113655-113830
	328229	5868105	Minus	120936-121053
	327876	5868140	Plus	103882-104034
	328262	6381906	Plus	11867-12027
	328688	5868262	Plus	626030-626094
25	328700	5868264	Plus	764089-764203
	328695	5868264	Plus	318632-318695
	328418	5868409	Minus	258811-258894
	328455	5868431	Plus	385576-385633
	328520	5868477	Plus	1942075-1942246
30	328548	5868487	Plus	72301-72397
	328857	6381927	Minus	80557-81051
	330305	4877982	Minus	52269-52365
	330306	4877982	Plus	96161-96233
	328937	5868500	Minus	1448241-1448333
35	328957	6456773	Plus	219195-219297
	329073	5868596	Plus	37838-37956
	329088	5868608	Plus	116738-116950
	329350	6456785	Plus	98911-98969
	329414	5868874	Plus	942555-942643
40	329440	5868885	Plus	21943-22063
	329451	5868887	Plus'	25974-26048

TABLE 7:

Table 7 depicts Seq ID No., UnigeneID, UnigeneTitle, Pixey, and ExAcon for all of the sequences in Table 8. Seq ID No links the nucleic acid and protein sequence information inTable 8 to Table 7.

Pksy: Unique Eos probeset identifier number
Exercipar Accession number, Genbank accession number
Ultigenerib: Ultigener number
Unigener Title:
Seq.D.No.: Sequence Identification Number found in Table 8

			,		
15	PKey	ExAccn	Unigene ID	Unigene Tiltle	SEQ ID NO
10	101545	BE246154	Hs.154210	endothelial differentiation, sphingolipi	Seq ID 1 & 2
	115819	AA486620	Hs.41135	endomucin-2	Seq ID 3 & 4
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	Seq ID 5 & 6
	102917	AI016712	Hs.287797	integrin, beta 1 (fibronectin receptor,	Seq ID 7 & 8
20	102915	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	Seq ID 9 & 10
	105330	AW338625	Hs.22120	ESTs	Seg ID 11 & 12
	107385	NM_005397	Hs.16426	podocalyxin-like	Seq ID 13 & 14
	102024	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	Seq ID 15 & 16
	102024	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	Seq ID 17 & 18
25	134416	X68264	Hs.211579	melanoma cell adhesion molecule	Seq ID 19 & 20
	103036	M13509	Hs.83169	matrix metalloproteinase 1 (interstitial	Seq ID 21 & 22
	104865	T79340	Hs.22575	B-cell CLL/lymphoma 6, member B (zinc fi	Seq ID 23 & 24
	106124	H93366	Hs.7567	Homo sapiens cDNA: FLJ21962 fis, clone H	Seq ID 25 & 26
	109001	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	Seq ID 27 & 28
30	104764	Al039243	Hs.278585	ESTs	Seq ID 29 & 30
	133200	AB037715	Hs.183639	hypothetical protein FLJ10210	Seq ID 31 & 32
	105263	AW388633	Hs.6682	solute carrier family 7, (cationic amino	Seq ID 33 & 34
	102892	BE440042	Hs.83326	matrix metalloproteinase 3 (stromelysin	Seq ID 35 & 36
	109456	AW956580	Hs.42699	ESTs	Seq ID 37 & 38
35	110906	AA035211	Hs.17404	ESTs	Seq ID 39 & 40
	119073	BE245360	Hs.279477	ESTs	Seq ID 41 & 42
	132050	Al267615	Hs.38022	ESTs	Seq ID 43 & 44
	132490	NM_001290	Hs.4980	LIM domain binding 2	Seq ID 45 & 46
40	102283	AW161552	Hs.83381	guanine nucleotide binding protein 11	Seq ID 47 & 48
40	101714	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	Seq ID 49 & 50 Seq ID 51 & 52
	133975	C18356	Hs.295944	fissue factor pathway inhibitor 2	Seq ID 51 & 52 Seq ID 53 & 54
	106793	H94997	Hs.16450	ESTs ESTs	Seq ID 54 & 55
	118511	N75620 M21305	Hs.43157	gb:Human alpha satellite and satellite 3	Seq ID 56 & 57
45	101447 314941		Hs.130650	go:numan apna saleme and saleme s	Seq ID 58 & 59
43	332466	AA515902 AB018259	Hs.118140	KIAA0716 gene product	Seq ID 60 & 61
	313513	AW298800	Hs.141840	ESTs. Weakly similar to S59501 interfero	Seq ID 62 & 63
	313556	AA628517	Hs.118502	ESTs	Seq ID 64 & 65
	313665	AW751201	Hs.51233	ESTS	Seq ID 66 & 67
50	314372	AL040178	Hs.142003	ESTs	Seg ID 68 & 69
50	429276	AF056085	Hs.198612	G protein-coupled receptor 51	Seg ID 70 & 71
	101345	NM_005795	Hs.152175	calcitonin receptor-like	Seq ID 72 & 73
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecul	Seq ID 74 & 75
	103850	AA187101	Hs.213194	hypothetical protein MGC10895	Seq ID 76 & 77
55	133260	AA403045	Hs.6906	Homo sapiens cDNA: FLJ23197 fis, clone R	Seq ID 78 & 79
	101097	BE245301	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	Seq ID 80 & 81
	104786	AA027167	Hs.10031	KIAA0955 protein	Seq ID 82 & 83
	132173	X89426	Hs.41716	endothelial cell-specific molecule 1	Seq ID 84 & 85
	100420	D86983	Hs.118893	Melanoma associated gene	Seq 1D 86 & 87
60	111018	Al287912	Hs.3628	mitogen-activated protein kinase kinase	Seq ID 88 & 89
	108507	AI554545	Hs.68301	ESTs	Seq ID 90 & 91
	104894	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	Seq ID 92 & 93
	118511	N75620	Hs.43157	ESTs	Seq ID 94 & 95
	125609	AA868063	Hs.104576	carbohydrale (keratan sulfale Gal-6) sul	Seq ID 96 & 97
65	101543	M31166	Hs.2050	pentaxin-related gene, rapidly induced b	Seq ID 98 & 99
	102241	NM_007351	Hs.268107	multimerin	Seq ID 100 & 101
	101560	AW958272	Hs.347326	intercellular adhesion molecule 2	Seq ID 102 & 103
	103280	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	Seq ID 104 & 105
70	105826	AA478756	Hs.194477	E3 ubiquifin ligase SMURF2	Seq ID 106 & 107
70	102804	NM_002318	Hs.83354	lysyl oxidase-like 2	Seq ID 108 & 109
	131647	AA359615	Hs.30089	ESTs	Seq ID 110 & 111
	103095	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and placental growth factor, vascular endoth	Seq ID 112 & 113 Seq iD 114 & 115
	103037	BE018302	Hs.2894 Hs.82733	placental growth factor, vascular endoin nidogen 2	Seg ID 114 & 115 Seg ID 116 & 117
75	100405	AW291587 BE259035	Hs.118400	singed (Drosophila)-like (sea urchin fas	Seq ID 118 & 119
13	102012	DE23303	110.110400	suffer (Northwalaws force morning)	Gug ID TIO OL TIO

	101261	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	Seq ID 120 & 121
	105729	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	Seq ID 122 & 123
	107216	D51069	Hs.211579	melanoma cell adhesion molecule	Seq ID 124 & 125
_	131080	NM_001955	Hs.2271	endothelin 1	Seq ID 126 & 127
5	131486	F06972	Hs.27372	BMX non-receptor tyrosine kinase	Seq ID 128 & 129
	134299	AW580939	Hs.97199	complement component C1q receptor	Seq ID 130 & 131
	134983	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	Seq ID 132 & 133
	115827	AA428000	Hs.283072	actin related protein 2/3 complex, subun	Seq ID 134 & 135
	133614	NM_003003	Hs.75232	SEC14 (S. cerevisiae)-like 1	Seq ID 136 & 137
10	116483	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	Seq ID 138 & 139
	132546	M24283	Hs.168383	intercellular adhesion molecule 1 (CD54)	Seq ID 140 & 141
	133678	AW247252	NA	nucleoside phosphorylase	Seq ID 142 & 143
	130184	H58306	Hs.15165	retingic acid induced 14	Seq ID 144 & 145
	134786	T29618	Hs.89640	TEK tyrosine kinase, endothelial (venous	Seq ID 146 & 147
15	129371	X06828	Hs.110802	von Willebrand factor	Seq ID 148 & 149
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	Seq ID 150 & 151
	322262	AA632012	Hs.188746	ESTs	Seq ID 152 & 153
	312173	Al821409	Hs.304471	EST	Seq ID 154 & 155
	319795	AB037821	Hs.146858	protocadherin 10	Seq ID 156 & 157
20	313978	AI870175	Hs.13957	ESTs	Seq ID 158 & 159
	306840	A1077477	Hs.307912	ESTs	Seq ID 160 & 161
	310272	AF216389	Hs.148932	sema domain, transmembrane domain (TM),	Seq ID 162 & 163
	310272	AF216389	Hs.148932	sema domain, transmembrane domain (TM),	Seq ID 164 & 165
0.5	315044	BE547674	Hs.204169	ESTs, Weakly similar to S65657 alpha-1C-	Seq ID 166 & 167
25	321325	AB033100	Hs.300646	KIAA1274 protein (similar to mouse palad	Seq ID 168 & 169
	321325	AB033100	Hs.300646	KIAA1274 protein (similar to mouse palad	Seq ID 170 & 171
	303251	AF240635	Hs.115897	protocadherin 12	Seq ID 172 & 173
	302378	AL109712	Hs.296506	Homo sapiens mRNA full length insert cDN	Seq ID 174 & 175
20	319267	F11802	Hs.6818	ESTs	Seq ID 176 & 177
30	310442	AW072215	Hs.208470	ESTs	Seq ID 178 & 179
	300469	BE301708	Hs.233955	hypothetical protein FLJ20401	Seq ID 180 & 181
	331237	W87874	Hs.25277	Homo saplens cDNA FLJ10717 fis; clone NT	Seq ID 182 & 183
	330968	R44557	Hs.23748	ESTs	Seq ID 184 & 185
25	301822	X17033	Hs.271986	integrin, alpha 2 (CD49B, alpha 2 subuni	Seq ID 186 & 187
35	422573	AW297985	Hs.295726	Integrin, alpha V (vitronectin receptor	Seq ID 188 & 189
	133061	AI186431	Hs.296638	prostate differentiation factor	Seq ID 190 & 191
	135235	AW298244	Hs.266195	ESTs	Seq ID 192 & 193
	101192	BE247295	Hs.78452	solute carrier family 20 (phosphate tran	Seq ID 194 & 195 Seg ID 196 & 197
40	113195	H83265	Hs.8881	ESTs, Weakly similar to S41044 chromosom	Sea ID 198 & 199
40	101741	NM_003199	Hs.326198	transcription factor 4	Sea ID 200 & 201
	321911	AF026944	Hs.293797	ESTs	Seq ID 202 & 203
	320635	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	Seg ID 204 & 205
	326230	15001500	11-04000	NM_017643:Homo saplens hypothetical prot	Seg ID 204 & 205 Seg ID 206 & 207
45	132968	AF234532	Hs.61638	myosin X	Seg ID 208 & 207
45	135073	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	Seg ID 210 & 211
	108937	AL050107	Hs.24341	transcriptional co-activator with PDZ-bi	Seq ID 212 & 213
	116430	AK001531	Hs.66048	hypothetical protein FLJ10669	Seq ID 212 & 215 Sea ID 214 & 215
	104877	Al138635	Hs.22968	Homo sapiens clone IMAGE:451939, mRNA se	Seq ID 214 & 215 Seq ID 216 & 217
50	122697	AA420683	Hs.98321	hypothetical protein FLJ14103	
50	112522	R68857	Hs.265499	ESTs	Seq ID 218 & 219 Seg ID 220 & 221
	304782	AA582081	11. 405040	gb:nn32h08.s1 NCI_CGAP_Gas1 Homo saplens	Seq ID 220 & 221 Seq ID 222 & 223
	312802	AA844669	Hs.193042	ESTs ESTs	Seg ID 224 & 225
	302680	AW192334	Hs.38218	Phase 2 & 3 Exons	Seg ID 224 & 225 Seg ID 226 & 227
55	326198	NIV 002000	Hs.65370		Seq ID 228 & 229
23	331019	NM_003033	ns.003/0	lipase; endothelial	364 ID 226 & 228

TABLE 8

5 Seq ID NO: 1 DNA SETTENCE
Nucleic Acid Accession #: NM_001400
Coding sequence: 244-2208 [underlined sequences correspond to start and stop codons))

10	1	11	21	31	41	51	
		1	1	1		1	
					CCCGGGCTCT		60
					CTCCAGCCAA		120
1.5					CAGTGAAGGC		180
15					CCTGGGGACA		240
					GCAGCTCGGT		300
					GAAAGCTGAA		360
					TTCTCATCTG		420
20	ATCCTGGAGA	ACATCTTTGT	CTTGCTGACC	ATTTOGAAAA	CCAAGAAATT	CCACCGACCC	480
20					TGGCAGGAGT		540
					CTCCCGCCCA		600
					TCAGTCTCCT		660
					ACGGGAGCAA		720 780
25					TCCTGGGTGG		
23	ATGGGCTGGA	ACTGCATCAG	TGCGCTGTCC	AGCTGCTCCA	CCGTGCTGCC	GCTCTACCAC	840 900
					TTCTGCTCTC		960
					GCCGCCTGAC		1020
					TCATCCTGCT		1020
30	ATCGTCCTGA	GCGTCTTCAT	CGCCTGCTGG	GCACCGCTCT	CGGAGTACTT	CCIGCIGGAI	1140
50					TGACCAACAA		1200
	OCCCCCTTCA	TCCCGGCAC	CHACCCCATC	ALLIACACIC	GCGGAGACTC	WACTOO A A	1260
					GCAAATCGGA		1320
					TGTCTTCTGG		1380
35					GCTCTTTACT		1440
55					CTGCCAGGGA		1500
					TGGTGTCGGG		1560
					GATCAGGTCC		1620
					CCAAAGGTCT		1680
40					TGTCCCCATG		1740
					AGTTTCAAAC		1800
					ACACCCCACC		1860
					CTACCTGAGA		1920
	CTGGGGTTGT	GGAATGATCG	ATCATCTATA	GCAAATAGGC	TATGTTGAGT	ACGTAGGCTG	1980
45	TGGGAAGATG	AAGATGGTTT	GGAGGTGTAA	AACAATGTCC	TTCGCTGAGG	CCAAAGTTTC	2040
	CATGTAAGCG	GGATCCGTTT	TTTGGAATTT	GGTTGAAGTC	ACTITGATIT	CTITAAAAAA	2100
	CATCTTTTCA	ATGAAATGTG	TTACCATTTC	ATATCCATTG	AAGCCGAAAT	CTGCATAAGG	2160
					TGTCCTAGGA		2220
					ACCAAGGGAG		2280
50	AAATGAGTCT	AACAAATATG	ACATCCGTCT	TTCCCACTTT	TGTTGATGTT	TATTTCAGAA	2340
					GTTGTGTTAA		2400
					TATGGATTTT		2460
					TTACTTTAAC		2520
					TGAAGATATG		2580
55					TTCAGTGCAA		2640
						TGTGGATCAT	2700
	TTTGCACATA	GCTTTATCAA	CTTTTAAACA	TTAATAAACT	GATTTTTTTA	AAG	
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00							
		2 Protein :					
	Protein Acc	cession #:	NP_001391				
65	_			24	4.5		
03	1	11			41	51	
		I announce		IMPORT NE CAR	KENSIKLTSV	I TOTAL TOTAL T	
							60 120
					NLLLSGATTY FLLISACWVI		
70					YCRIYSLVRT		180 240
70					GCKVKTCDIL		300
					KRPITAGMEF		360
		TIMSSGNVNS		C. JODOMSKE		nummon	500
	- Mronomark P.D.						

75

5 Seg ID NO: 3 Nucleotide seguence: 10 Nucleic Acid Accession #: NM 016242 Coding sequence: 79-864 (underlined sequences correspond to start and stop codons)) 21 31 15 AAGGCCCTGC CAGCTTGGGA GGGAATTGTC CCTGCCTGCT TCTGGAGAAA GAAGATATTG 60 ACACCATCTA CGGGCACCAT GGAACTGCTT CAAGTGACCA TTCTTTTTCT TCTGCCCAGT 120 180 ATTTGCAGCA GTAACAGCAC AGGTGTTTTA GAGGCAGCTA ATAATTCACT TGTTGTTACT ACAACAAAC CATCTATAAC AACACCAAAC ACAGAATCAT TACAGAAAAA TSTTGTCACA CCAACAACTG GAACAACTCC TAAAGGAACA ATCACCAATG AATTACTTAA AATGTCTCTG 240 20 300 ATGTCAACAG CTACTTTTT AACAAGTAAA GATGAAGGAT TGAAAGCCAC AACCACTGAT 360 GTCAGGAAGA ATGACTCCAT CATTTCAAAC GTAACAGTAA CAAGTGTTAC ACTTCCCAAT 420 GCTGTTTCAA CATTACAAAG TTCCAAACCC AAGACTGAAA CTCAGAGTTC AATTAAAACA 480 ACAGAAATAC CAGGTAGTGT TCTACAACCA GATGCATCAC CTTCTAAAAC TGGTACATTA 540 25 ACCTCAATAC CAGTTACAAT TCCAGAAAAC ACCTCACAGT CTCAAGTAAT AGACACTGAG 600 GGTGGAAAAA ATGCAAGCAC TTCAGCAACC AGCCGGTCTT ATTCCAGTAT TATTTTGCCG 660 GTGGTTATTG CTTTGATTGT AATAACACTT TCAGTATTTG TTCTGGTGGG TTTGTACCGA 720 ATGTGCTGGA AGGCAGATCC GGGCACACCA GAAAATGGAA ATGATCAACC TCAGTCTGAT 780 AAAGAGAGCG TGAAGCTTCT TACCGTTAAG ACAATTTCTC ATGAGTCTGG TGAGCACTCT 840 30 GCACAAGGAA AAACCAAGAA CTGACAGCTT GAGGAATTCT CTCCACACCT AGGCAATAAT 900 TACGCTTAAT CTTCAGCTTC TATGCACCAA GCGTGGAAAA GGAGAAAGTC CTGCAGAATC 960 AATCCCGACT TCCATACCTG CTGCTGG 35 Seq ID NO: 4 Protein sequence: Protein Accession #: NP_057326 40 MELLOVTILE LLPSICSSNS TGVLEARNIS LVVTTTKPSI TTPNTESLQK NVVTPTTGTT PKGTITNELL KMSLMSTATF LTSKDEGLKA TITDVRKNDS IISNVTVTSV TLPNAVSTLQ 120 SSKPKTRYOS SIKTTEIPGS VLOPDASPSK TGTLTSIPVT IPENTSOSOV IDTEGGKNAS 180 TSATSRSYSS IILPVVIALI VITLSVFVLV GLYRMCWKAD PGTPENGNDQ PQSDKESVKL 240 45 TAUKTTSHES GEHSAOGKTK N Seq ID NO. 5 <u>Nicolectide sequences</u>: Nucleic Acid Accession #1 IM_002205 . Coding sequence: 24..3175 [underlined sequences correspond to start and stop codons) 50 21 31 11 CAGGACAGGG AAGAGCGGGC GCTATGGGGA GCCGGACGCC AGAGTCCCCT CTCCACGCCG 55 60 TGCAGCTGCG CTGGGGCCCC CGGCGCCGAC CCCCGCTCGT GCCGCTGCTG TTGCTGCTCG 120 TGCCGCCGCC ACCCAGGGTC GGGGGCTTCA ACTTAGACGC GGAGGCCCCA GCAGTACTCT 180 CGGGGCCCCC GGGCTCCTTC TTCGGATTCT CAGTGGAGTT TTACCGGCCG GGAACAGACG 240 GGGTCAGTGT GCTGGTGGGA GCACCCAAGG CTAATACCAG CCAGCCAGGA GTGCTGCAGG 300 60 GTGGTGCTGT CTACCTCTGT CCTTGGGGTG CCAGCCCCAC ACAGTGCACC CCCATTGAAT 360 TTGACAGCAA AGGCTCTCGG CTCCTGGAGT CCTCACTGTC CAGCTCAGAG GGAGAGGAGC 420 CTGTGGAGTA CAAGTCCTTG CAGTGGTTCG GGGCAACAGT TCGAGCCCAT GGCTCCTCCA 480 TCTTGGCATG CGCTCCACTG TACAGCTGGC GCACAGAGAA GGAGCCACTG AGCGACCCCG 540 TGGGCACCTG CTACCTCTCC ACAGATAACT TCACCCGAAT TCTGGAGTAT GCACCCTGCC 600 65 GCTCAGATTT CAGCTGGGCA GCAGGACAGG GTTACTGCCA AGGAGGCTTC AGTGCCGAGT 660 TCACCAAGAC TGGCCGTGTG GTTTTAGGTG GACCAGGAAG CTATTTCTGG CAAGGCCAGA 720 TCCTGTCTGC CACTCAGGAG CAGATTGCAG AATCTTATTA CCCCGAGTAC CTGATCAACC TGGTTCAGGG GCAGCTGCAG ACTCGCCAGG CCAGTTCCAT CTATGATGAC AGCTACCTAG 840 GATACTCTGT GGCTGTTGGT GAATTCAGTG GTGATGACAC AGAAGACTTT GTTGCTGGTG 900 TGCCCAAAGG GAACCTCACT TACGGCTATG TCACCATCCT TAATGGCTCA GACATTCGAT 960 COCTCTACAA CTTCTCAGGG GAACAGATGG CCTCCTACTT TGGCTATGCA GTGGCCGCCA 1020 CAGACGTCAA TGGGGACGGG CTGGATGACT TGCTGGTGGG GGCACCCCTG CTCATGGATC 1080 GGACCCCTGA CGGGCGGCCT CAGGAGGTGG GCAGGGTCTA CGTCTACCTG CAGCACCCAG 1140 COGCATAGA GCCCACGCC ACCCTTACCC TCACTGGCCA TGATGAGTTT GGCCGATTTG 1200

GCAGCTCCTT GACCCCCCTG GGGGACCTGG ACCAGGATGG CTACAATGAT GTGGCCATCG 1260

GGGCTCCCTT TGGTGGGGAG ACCCAGCAGG GAGTAGTGTT TGTATTTCCT GGGGGCCCAG 1320

CARACTECT T PSICICCICIC CHICAGAGAS GOUGAGACCT GANTSCANAT GANTACCTOR 1 TOTCCECTAS TRECTECTOR GANTSCANA ASSOCIATION TARACAGAGAG COCCUCATOR 1 TOTCCECTAS TRECTECCTOR GANTSCANA ASSOCIATION TARACAGAGAGAGAT TOTCCCCATAGAGAGAGAGAT CANACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGA								
ATCHANTOT GOGGRACHT GOTTOGRICA AGGCTOTOGT ATMAGRGGGG COCCORATOG		GAGGGCTGGG	CTCTAAGCCT	TCCCAGGTTC	TGCAGCCCCT	GTGGGCAGCC	AGCCACACCC	1380
A TOTINATION GOSPICIOTTI GENTIGIACA AGGINTOSTA PIACAGGGGG COCCICATOS I TETCCOGRAS TECCICACET ACCIDITATE COGNICATOR ACCIDIAGA GORGAGOTT TO TETACATOR ACCIDIAGA GORGAGOTT ACCIDIAGA GORGAGOTT ACCIDIAGA GORGAGOTT ACCIDIAGA GORGAGOTT ACCIDIAGA GORGAGOTT ACCIDIAGA GORGAGOTT ACCIDIAGA TO TETACATOR ACCIDIAGA GORGAGOTT ACCIDIAGA GORGAGOTT ACCIDIAGA GORGAGOTT ACCIDIAGA GORGAGOTT ACCIDIAGA ACCIDIAGA GORGAGOTT ACCID		CAGACTTCTT	TGGCTCTGCC	CTTCGAGGAG	GCCGAGACCT	GGATGGCAAT	GGATATCCTG	1440
TETECRICATA TRECTECCT ALCENTRICE COSCENITOT CANCECCAGA GARGEGAGET CANCECCAGA GARGECT CATEGORY CONTROL TRANSCRIPTOR CONTROL CON		ATCTGATTGT	GGGGTCCTTT	GGTGTGGACA	AGGCTGTGGT	ATACAGGGGC	CGCCCCATCG	1500
GARARCAGOT TECHNACTOC AFFORTITCA CASTOGRACT TEAGCTOGRAC TOGRADAGE AGAMAGGAGG GGACCOGGG GGACTOTTCC TEGECTICAGG GGAGGAGACC CTAGACCAGA 1 AGAMACTAGA COMBARTEGG GGACTOTTCC TEGECTICAGG GGAGGAGACC CTAGACCAGA 1 AGAMACTAGA COMBARTEGG GGACTOTTCC TEGECTICAGG GGAGGAGACC CTAGACCAGA 1 AGAMACTAGA COMBARTEGG GGACTOTTCC TEGECTICAGGAGAGACCAGAGAGAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAC								1560
GARARCAGOT TECHNACTOC AFFORTITCA CASTOGRACT TEAGCTOGRAC TOGRADAGE AGAMAGGAGG GGACCOGGG GGACTOTTCC TEGECTICAGG GGAGGAGACC CTAGACCAGA 1 AGAMACTAGA COMBARTEGG GGACTOTTCC TEGECTICAGG GGAGGAGACC CTAGACCAGA 1 AGAMACTAGA COMBARTEGG GGACTOTTCC TEGECTICAGG GGAGGAGACC CTAGACCAGA 1 AGAMACTAGA COMBARTEGG GGACTOTTCC TEGECTICAGGAGAGACCAGAGAGAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAGACACCAC	5	GCAGCTTAGA	GGGGAACCCT	GTGGCCTGCA	TCAACCTTAG	CTTCTGCCTC	AATGCTTCTG	1620
AGANGSBAGG GERACGEGG GENERATECE PROCEEDES GEAGGGCACC CHRACCEGAG A ACCURATECTA COMMANGEG GENERATECE A PRINCIPATION AGAINMENT AND ACCURATECTA CONTROLLAR CON	-	GAAAACACGT	TECTEACTEC	ATTGGTTTCA	CAGTGGAACT	TCAGCTGGAC	TGGCAGAAGC	1680
CCCTIGETCAT COMMATIGN GETCHARGON APTRICAMENTA GRUDIARIA TACCTOMON A ACCIDENCE APTRICAGE APTRICAGE CONTROLLED CONTROLL		AGRAGGGAGG	GGTACGGCGG	GCACTGTTCC	TEGCCTCCAG	GCAGGCAACC	CTGACCCAGA	1740
10 ACCIDENCIAGO CONTROLOGO CANTECIDAD CONTROLOGO CONTR		CCCTGCTCAT	CCAGAATGGG	CCTCGAGAGG	ATTGCAGAGA	GATGAAGATC	TACCTCAGGA	1800
10 ACCCCCAGG COCKETGRA AGOCCACCOGGC TEARSCEARC COTACATAT CARRACAMA I COCKETARAT AGARACAMA ACCCCATAGA AGACTACATA AGACTACATA TO TRADECTOR AGACTACATA TO TRADECTOR AGACTACATA TO TRADECTOR AGACTACATA AGACTACATA TO TRADECTOR AGACTACATA AGACTACATA TO TRADECTOR AGACTACATA TO TRADECTOR AGACTACATA AGACTACA		ACGACTCAGA	ATTTCGAGAC	AAACTCTCGC	CGATTCACAT	CGCTCTCAAC	TTCTCCTTGG	1860
GCCGRATIAG GGAGAGGGC CAGRICTICS TEGRICITICS GABAGGCARA PROTESTORE OF COCCURANCES ACCUMENTS TYTOGGGGAG GABACCATOR GARCINGGG GACCITICAGA GCCGAGAGGA TOGGGTAGA GABACCATOR GACCITICAGA GCCGAGAGGA TOGGGTAGA GABACCATOR GACCITICAGA GACCAGAGGA GABACCATOR GACCITICAGA GACCAGAGGA GACCAGAGGA GACCAGAGA TACCAGGA ACAGAGGA GAGAGCAGA TOGGGTAGA GACCAGAGA GACCAGAGACACAGA GAC	10	ACCCCCAAGC	CCCAGTGGAC	AGCCACGGCC	TCAGGCCAGC	CCTACATTAT	CAGAGCAAGA	1920
CTRACOTROCA GERMANDE THTOGGGNAC AGAACCARDE GRACCARGOT GRACABARDATO CCCCORNACC CARTIFLOR GEOCHAM TOGGRADAD TOGGGNACO CONTROLECA CONTROLECA GRACAGAT GEOCHAMPA TOGGGNACO CONTROLECA CONTROLECA CONTROLECA GRACAGAT GEOCHAMPA TOGGGNACO CONTROLECA CO	10	GCCCCATAGA	CONCARGOOT	CAGATCTTGC	TOGACTOTOG	AGAAGACAAC	ATCTGTGTGC	1980
CCCTGRACCT CACTITICAT GEOGRAPHO TOGGIUMOGO TOGGIUCTATI GROSCICTAMO 2 TTCGGGGTCAC CACCUTACIÓN GAGETGRAS ACTEGRACIA CONTROLAGA. COGRAGACA TOTICAGACCA CATURAGACA GAGETGRAS ACTEGRACIA COGRAGACA COGRAGACA ATTCCCGAGA CACUTAGADA ACACCACAT TORGATICAC GAGCTGRAS GAGACAGAT ACTURCAGA ACCACATAGADA ACACCACAT TORGATICAC GAGCTGRAS GAGACAGAT ACTURCAGA ACCACATAGADA ACACCACAT TORGATICAC ACCACATAGA CACCATAGAT CORRESPONDO CONTROLAGA GAGACAGAT TORGATICAC ACCACATAGA CACCATAGAT TORGACAGAG COCLAGACTO ATMACCAGA GACCATAGAT GACCAGAGAT CACCACAGAT TORGATICAC ACCACATATA CACCAAGAGG COCLAGACAT GATAGACAGA ACCACATATA ACCACAGAGG COCLAGACAT GATAGACAGA ACCACATATA CACCAAGAGG COCLAGACAT GATAGACAGA ACCACATATA CACCAAGAGG COCLAGACAT GATAGACAGA ACCACATATA CACCAAGAGG COCLAGACAT GATAGACAGA ACCACATATA CACCAAGAGG COCLAGACAGA ACCACATATA CACCAAGAGG COCLAGACAGA ACCACATATA CACCAAGAGG COCLAGACAGA ACCACATA CACCACATATA CACCAAGAGGA COCLAGACAGA CACCACATA CACCACATATA CACCAAGAGGA CACCACAGACAGA CACCACACAGA CACCACATA CACCACATAGA TACTACACATAGA CACCACATAGA CACCACACAGA CACCACACACA								2040
TTGGGGTACC GACCCOTTCCA GAGGGTAGAT ACTGGGGACT GOTGGGGACA CCAGGGGACA								2100
15 TOTICCAGOCT GRACTOTICAS TACTITIONOS TRANCORRIS COCICIOROS GRATAGORAS CONCINENTAS GRACTOTICAS PROPERTICAS CONCINENTAS CONCIN		CCCIGNACCI	CACTITUCAL	GCCCAGAATG	ACTCACCACT	CGTCAGACAC	CCAGGGAACT	2160
TEGGORACCO CATURARGEA GEARCCAGTC TETROGOTGS COTTOGOTTA ACASTOCOTO ACTOCOGGA CATURARGEA GEARCCAGTC TETROGOTGS COTTOGOTTA ACASTOCOTO ACACTURE ACADOCACTO COTTOCOTO CONTROLOGO CATURATOR ACADOCACTO CONTROLOGO CATURATOR CONTROLOGO CONTROLOGO CATURATOR	15	TICGGG ICAC	COCCCCCCCC	macrommecocc	MCI CAGGACIA	corcanance	CIVITATIONCO	2220
A TOTOCOGGGA CACHAGAMA ACCACCAGE TREACTICCA GACCACCAGA AMARATOTCA 2 ACADACTECCA AMAGGAGGG GITTCOTTC GGOCTOCOG GAGGAGCAGA CACACCAGAGCAGA CACACCAGAGCAGA CACACCAGAGCAGA CACACCAGAGCAGA CACACCAGAGAGCAGC	13	TCTCCAGCCT	GMGCIGIGAC	COLOGOROUS	TORRICCHORG	CCGCCIGCIG	ACACTOCCCTC	2280
ACADATEGICA MAGIGACITY GITTATCCTTTC GECTTCCOTT GGASSCTCAG GOCCAGGTCA 2 OCCTARAGEG TETTCCAME CTERAGEGA TETTATTCC ATAMAGEGA TESTACTOCA 2 OCCTARAGEGA TETTCCAME CTERAGEGA TETTATTCCA ATAMAGEGA TESTACTICCA 2 AGAGCAGACTA COLORIA GARAGEA GARAGEACTOC GACCTACTTC CACCOTTACT CACCOTTCC TESTACTACTACTACTACTACTACTACTACTACTACTACTACT		TGGGCANCCC	CATGAMGGCA	GGAGCCAGTC	mmca ommoca	CAMCCOCATO	ACAGICCCIC	2340
COCTRANGES TOTCCCARS CONTRIGUES TOTCTTOCC MOTAGEGRAC TRESPRETCO: CRACKING CTCHARAGES GRAGACTOR GENERACES ARCTITICOC MOTAGEGRAC TRESPRETCOC CRACKING CTCHARAGES GRAGACTOR GRACETORT CACCUMPTIC TRANGGERA TORRIGHTO CONTRIGUES TRANGGERA GRACETORT CACCUMPTIC TRANGGERA TORRIGHTO CONTRIGUES TRANGGERA GRACETORT CACCUMPTIC COCCAGNICTOR TORRIGHTO CONTRIGUES TRANGGERA GRACETORT COCCAGNICTOR COCCAGNICTOR CACCUMPTICA ARCCEGNATO CONTRIGUES AGUITECTORT COCCAGNIC CONTRIGUES ARCCIVAGA TRANGGERA		ATCTCCGGGA	CACTAAGAGA	ACCATCUAGI	COOTOTOCA	GAICCICAGC	GOOGLGCECA	2400
20 GARGECTICO CINGALOGRIA GARGACCTOR GARCTICOTET CACCUMENTO TATORAGOGICA COLORAGORI COLORAGORI CATAGORICO GARGACTICOTET CACCUMENTO TATORAGORI COLORAGORI CATAGORICO GONOGICO CATORAGORI CATORAGORI CACCUMENTA GARGACTICA GARGATICA GARGACTICA GARA		ACAACTEGEA	AAGCGACGTG	GTTTCCTTTC	GGCTCTCCGT	DOMESTICAG	macarmagaa	2460
TCAACCAAGG COCCAGGTCC ATTMGCCAGG GTGTGCTGGA ACCAGGTCC CCCAGGGCCC TGGGGCCCAGTC CCCCAAGGCCCAGTC CCCCAAGGCCCAGTC CAGCCAGTCAGTC ACCCCAGTCAGTC ACCCCAGTCAGTC ACCCCAGTCAGTC ACCCCAGTCAGTC CACCCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGT	20	CCCTGAACGG	TGTCTCCAAG	CCTGAGGCAG	CACCONCONCON	AGTANGCGAC	TOGGRATECTE	2520
TOGRAGOTCA GENERICETA TRATOTRACCA GROTTACOGG ACTOARCOG ACCACCANTO 2 ACCCATTAR COCAMAGE CREATURE ATCCAMAGE ATCCAMAGE ATCCAMAGE ACCACATATA COCAMAGE CREATURE ACCACAGA A AACGGGGAA A AACGGGGAA AACGGGGAA AACGGGGAA AACGGGGAA AACGGGGAA AACGGGGAA AACGGGGAA AACGGGAA AACGGGGAA AACGGGGAA AACGGGGAA AACGGGGAA AACGGGGAA AACGGGGAA AACGGGGAA AACGGGGAA AACGGGGAA AACGGGAA AACGGGAA AACGGGAA AACGGGAA AACGGGAA AACGGGAA AACGGAAACGAA AACGGAACGAA AACGGAAACGAA AACGGAAACACAA AACGGAAACAACAA AAACAACAACAAACA	20	GAGACCAGCC	TCAGAAGGAG	GAGGACCTGG	GACCTGCTGT	CCACCATGTC	COCCUPACION COCCU	2520
ACCCOATTIAL CCCIAMAGGG CTGGATGTGG ATCCCCGAGGG TECCGTGGGG CACCAGCAGA A ACCGGGGGGAGAGAC CTCAGGGGG AGUTCTGGTT CCCTGGGGGC CTGGATCCAGGGG AGGCGGAGT GCATTCCAGG AGUTCTGGT CCCCGGGGGG CTGACACAGA GAGAGCCAGA TTAGCCTGCA GTGTGGGCCA GTCTGGGCCA GAGCTGCAGACAGAG GAGACCCAGA TTAGCCTGCA GTGTGGGCCA GAGCTTGTGGGCCAGCAGCAGACAGCCAGACACACACACA		TCAACCAAGG	CCCCAGCTCC	ATTAGCCAGG	GIGIGCIGGA	ACTUAGCIGI	CCCCAGGCIC	2640
25 AAGGGRAGG TOCAGGCGG AGUTCHGUT COTCGGRACC TOAGNICCTS AAATGCCGGG 26 AGGGTAGTG TUTAGGGTG GGUTCHGAG TOGGGGCCT GGACCACAG AGAGCACAG 37 GTCGGATT GCATTCCGA GTCTGGGCCA AGACTTUTT GGAGCGGGG GCCCAGCAGAG 37 GTCGGCATT GCATTCCGA GTCTGGGCCA AGACTTUTT GGAGCGGGG GACCAGCAG 38 GTCGCACTG GTCTACAGAG GCCTGAGAG CCCTGAGAGCCACAG 39 GTCGCACTG GCATCCACTG TGGACATCA GCCTGAGAGCAC CCCTGACGAC CTCGAGCCCA 30 GTCGCCCCC GTCCACCTG TGGACATCA TCCTAGCCAT CCTGATTGC CTCCACCAC 31 AGGGTCTACC CACTCACAG CTCCATCACAG CTCCATCACCAC 32 CAATTCAGA CTCCATCACTC TGAGAACAC TCCAGCCAC CTCTGATTGC CTCCATAGC 34 CACTCAGA CTCCATCAC TGAGAACAC TCCAGCCAC CTCTGATTGC CTCATAGCAC 35 GAGCGCGCCCC CTGAGAGCCAC CTCGATTGC TCCACACCAC 36 GGGCCTGGGCTC TGAGAACAC CTCCAGCCAC CTCTATTGC CTCACACCCA 36 GGGCTCTGGG TACTCATCACACTC TGAGACACCAC CTCCATCACCAC 36 GGGCCTGGGCTC CTGAGACCAC CTCCAGCCCAC CTCCATCACCAC 36 GGGCCTGGCTC CTGAGACCAC CTCCAGCCCCC CTCATCACCAC 36 GGGCCTGGCTC CTGAGACCAC CTCCAGCCCCC CTCATCACCAC 36 GGGCCTGGCCCCC CTGAGCCCC CTCTCATCACCACCAC CTCCATCCACCAC 36 GGGCCACCACCACACACACACACACACACACACACACAC		TGGAAGGTCA	GCAGCTCCTA	TATGTGACCA	GAGTTACGGG	ACTCAACTGC	ACCACCAATC	2700
25 AGGCTGAGTG GTTCAGGCTG GGCTGTGAGC TOGGGCCCCT GCACCACAA GAGAGCCCAA GTTCAGGCTG GTTCAGGCCA AGACTTCTTC GGCAGGGTG GCACCACACA GTTCAGCCCAC GTTCAGGCCA AGACTTCTTC GGCAGGGTG GCACCACCACA TTTCAGCCTGCA GTTGAGGCCA GTCAGCACACA GACCTCACACACACACACACACACACACACACACACACAC		ACCCCATTAA	CCCAAAGGGC	CTGGAGTTGG	ATCCCGAGGG	TTCCCTGCAC	CACCAGCAAA	
GOCCIOCACTO GONAMAGIA GOCCIOCACA GOCCIOCACA AGACTITUCTO GOAGOGGAGA CACCAGCACA TATACACCACA GOTAGACACACA GOCCIACACA ACCORDOCA GOCCIACACA ACCORDOCA GOCCIACACA ACCORDOCA GOCCIACACA ACCORDOCA GOCCIACACA ACCORDOCA GOCCIACACA GOCCIACACACA GOCCIACACA GOCCIACACA GOCCIACACA GOCCIACACACA GOCCIACACACACA GOCCIACACACA GOCCIACACACACA GOCCIACACACACA GOCCIACACACACA GOCCIACACACACACACACACACACACACACACACACACAC	25	AACGGGAAGC	TCCAAGCCGC	AGCTCTGCTT	CCTCGGGACC	TCAGATCCTG	AAATGCCCGG	2760
TITROCUTION GITTAINDRICT GITTAINAMAG COCTIBALBATI GOCCITACORA ATCOTOCTOC 2 GICAGOFTOC COLANABAGI GOTCAGOTTO CACAGOTTO GAANGRACA MAGGACAMA GICAGOTTOCTOC COLATORATORA COLATORA	25	AGGCTGAGTG	TTTCAGGCTG	CGCTGTGAGC	TCGGGCCCCT	GCACCAACAA	GAGAGCCAAA	2820
GGGGGTGGC COMANAGAG GSTGGGTGG COLGGGCTGT GGANTGGGC ÄAGGGGAGAGAG 30 GAGGTATGG GSTCCASTG TGGGGTGTG TGCASTGGTGC CANTGGGCC ÄAGGGGAGAGAG AGAGGTATGG CANCTRACTC CTTACAGAGC TEGGATTCTT CAAGGCTCTC CTTCCASTGCT CACCTGCTC AGAGGTCTACAGCTTCTCAGAGCTTCT CACCTGCTC CACCTGTC CACCTGCTC CACCTGTCCC CACCTGCTC CACCTGTCC CACCTGTCCC CACCTGCTC CACCTGTCCC CACCTGCTC CACCTGCTC CACCTGTCCCC CACCTGCTC CACCTGCTC CACCTGCTC CACCTGCTC CACCTGCTC CACCTGTCCCC CACCTGCTC CACCTGCTC CACCTGTCCCC CACCTGCTC		GTCTGCAGTT	GCATTTCCGA	GTCTGGGCCA	AGACTTTCTT	GCAGCGGGAG	CACCAGCCAT	2880
30 GAGETATOS COTICCACTO TOSATCATCA TOCTACCAT COTOTTOGO CTCCTOCTCO 3 TAGGTCTACT CATCACACA COTACACA TOGATACCAT COTOTTOGO CTCCTATATO 3 GACCOGCCAT GERALAGACT CAGCATACACA TOGATACTACA CAGCACACACACACACACACACACACACACACACAC		TTAGCCTGCA	GTGTGAGGCT	GTGTACAAAG	CCCTGAAGAT	GCCCTACCGA	ATCCTGCCTC	2940
30 TAGGETERAT CALCITACARE CITCACARAGE TEGANITETT CAARGETERE CITCATATO 3 GACOGGCAT GGAATAGAC CITCACARAGE CITCACACAGE CITCAGACAGE CAATTCAGA CITCACACAGE CAATTCAGA CITCACACAGE CAATTCAGA CAATTCAGACAGE CAATTCAGACAGACAGACAGACACAGACAGACAGACAGAC		GGCAGCTGCC	CCARAAAGAG	CGTCAGGTGG	CCACAGCTGT	GCAATGGACC	AAGGCAGAAG	3000
GAGOGGOCAT GARARAGOT CAGOTEMAGO CTCCAGCCAC CTCTRATGCC TEGRITOCTCC ACATTICAGA CTCCATTIC TRADARAGO A GICCOCCAC CICTURITETA CTRARAAGO A GICCOCCAC CICTURITETA CONTRARAGO A GICCOCCAC CICTURITA GICCOCCAC GICCOCCAC A GIACACCAC A ALGORICA CICTURITA GICCOCCAC CICTURITA GICCOCCAC A ALGORICA CA GICCOCCAC A GIACACCAC A ALGORICA CA GICCOCCAC A GICCOCCAC A GIACACCAC A ALGORICA CA GICCOCCAC A GICCOCCAC A GIACACCAC A ALGORICA CA GICCOCCAC A GIACACCAC A ALGORICA CA GICCOCCAC A GIACACCAC GIACACCAC A GIACACCAC A GIACACCAC GIACACCAC A GIACACCAC A GIACACCAC A GIACACCAC A GIACACCAC GIACACCAC A GIACACCAC A GIACACCAC A GIACACCAC GIACACCAC A GIACACCAC GIACACCAC A GIACACCAC A GIACACCAC A GIACACCAC GIACACCAC A GIACACCAC GIACACCAC GIACACCAC A GIACACCAC CICTURICA CONTROL CONTR		GCAGCTATGG	CGTCCCACTG	TGGATCATCA	TCCTAGCCAT	CCTGTTTGGC	CTCCTGCTCC	3060
CARTTCARA CTOCCATTCC TEMARACCA GTOCCOCCAC COTCATTCTA CTGANARGGA 3 GGGGTTCTGGG TACTTCTTA AGGGGGTAGG GGCCAGGGGA AGACCTCATCCCGCCCA CARACCCATAC TEMARGGCCA GAGCCAGGGGG GGCCAGGGGG AGACCCATCAC TEMAGGGCCA GAGCCAGGGG GGCAGGGGG AGACCCACCC TCCCCCCCCAT 3 GAGACCATCAC TAGANACCA TACACCCAC CCCTCTATCAC GAGGGGGAAC CACACCCACCAC 3 GAGACCATCAC CAGACCACAC TACACCCAC TCCACCCACCAC CACACCCAC GACCCACCC	30	TAGGTCTACT	CATCTACATC	CTCTACAAGC	TTGGATTCTT	CAAACGCTCC	CTCCCATATG	3120
GGGGTCTGGG TACTTCTTCA AGGTGCTGAC GGCCLAGGGA AAGCTCCTCT CCCCAGCCCA 3 GAGACTACTACT TRAMGGGCCA GAGCCCAGGG GGTGAGGAGC TOGGGACCCA 3 GAGACTGTGAA GAGCCCTGT TTACACATAC GCTCCTTCATG GATGGGGACA CTCCCCCCAT 3 GGCACTGTGAA GAGCCCTGT TTACACATAC GCTCCTTCATG GATGGGGAAA CTCCAGCCCAG 3 GGCACTGTGAA GAACTGTCC CCTTCTGCCCAG GACCATGCCCAG AAGCACTCCA CAGCCCAG AAGCACCAC AAAGCACCCCAG AAGCACCCCCAG AAGCACCCCCCAG AAGCACCCCCCAG AAGCACCCCCCAG AAGCACCCCCCAG AAGCACCCCCCCAG AAGCACCCCCCAG AAGCACCCCCCCAG AAGCACCCCCCCAG AAGCACCCCCCAG AAGCACCCCCCCC		GCACCGCCAT	GGAAAAAGCT	CAGCTCAAGC	CTCCAGCCAC	CTCTGATGCC	TGAGTCCTCC	3180
3 GARDENTAT TRANSGECCA GARCECAGGGG GGTUAGGAG TOGGGGATCCC TECCOCCCAT 3 GARDENTAG TRANSGECCA GARCECC GARCECC GARCECCAGGGGGACAGCGGGGACAGCGGGGACAGCGGGACAGCGGGACAGCGGGACAGCGGACAGCGGACAGCGGACAGCGGACAGCGGACAGCGGACAGCGGACAGCGGACAGCGGACAGCGGACAGCGGACAGCGGACAGCGACAGCGACAGCGACAGCGACAGCGACAGCGACAGCGACAGCGACAGCGACAGCGACAGCGACAGCAG		CAATTTCAGA	CTCCCATTCC	TGAAGAACCA	GTCCCCCCAC	CCTCATTCTA	CTGAAAAGGA	3240
35 GCACTETIGAA GRACCETTET TYRACATRIC CONCINCATE GARGOGORAA CTCARATCCA 3 GGARGARGAG CCCAGCOTCC CTGABGCOTT TCACATTUTA GARGOGORAA CTCARATCCA 3 GGARGARGAG CCAGCOTCCC CTGABGCOTT TCACATTUTGA GARGATTCCC GARGACACTO 3 GTOCAGCACC CAACCTCACA AGARCATCCA TCAGCATTCC CAACATCCACA AGARGACCA AGARGACCAGA AGARGACCAGA GATCAGACCAGA CACACCAGA GATCAGACCAGA ACATACATATTA GGCCTACCCA GARCCAGATCA GARGACCAGA CACACCAGA CACACCAGA CACACCAGA ACATACCAGA AGARGACCAGA AGARGACCAGA CACACCAGA CACACCACCAGA CACACCAGA CACACCACACACA		GGGGTCTGGG	TACTTCTTGA	AGGTGCTGAC	GGCCAGGGAG	AAGCTCCTCT	CCCCAGCCCA	3300
GGGRACAGGG CCAGCOTCC CTGAAGCCTT TGCATTTYGG AGAGTTTCCT GAACACTG 3 GAAAGTATAC TAGGAAATCC ATTCAAGCTT CTTTGGGCCA GAACACTCCA AAAGGAACTCC 3 TGTCCAGCTC CAACCTGCAA AGACTCTCC TCTGGGCCA GCAGCACCCA AAAGGAACCCC 3 CCAGTAGAAA CACTGCATCT GGGGGTTAA GACCTGCCAG CTGTGGCACA CCCAGCCCC 3 CACACAGCAA CAACACCCTG GGGGTCTAAC TAGCCTGCACA CTCGAGCCTC CAACACCCAACACCACACC		GAGACATACT	TGAAGGGCCA	GAGCCAGGGG	GGTGAGGAGC	TGGGGATCCC	TCCCCCCCAT	3360
GARARITAC TRIGURANTO ATTOCHOST CTTTGGGCCA GRAVISCOCA PAGGACTTCO 3 TOTOCAGGTC CALCOTECA AGRICTACE CTAGGCTTGC CARGARICCA NAGRAGCCA CORTANGA COTGRACTT GGGGAGTTAA GACCTGGGAG CTCTGGACTG CCGATCAGA AGARACCA TAGATGGAG GGCCCAG GGCCCAGCTG CACAGCAGA CARGACCAT AGATTACCAT GGTGCCCCAG GACCGCTG GGACCAGCTG CACAGCGAA TCAGCCCGC GGGGCCAGA GCCGACTCC AGAGGGGATA GACACTGAAC CCACACCAG CAGACCCAG GCTGGACTT TAGATCTGAA CAGAGGGATA GACACTGAAC AGTCACCCC GATTCCAGG ACTATATTTG GGCCTGCTCC AGACCTGAAC CTGGAGGCC AGACCAGC GACCCAGG ACCACAGTA TACATCTGAT TACACCAGG CACCAGGAGCAG AGACCACCT GACCAGCAG CACCAGCAGCAG GACCAGGAGCAGCAG AGACCACCAG CACCAGCACCAGCACCAGCAGCAGCAGCAGCAGCAGCACAGCAG	35	G CACTGTGAA	GGACCCTTGT	TTACACATAC	CCTCTTCATG	GATGGGGGAA	CTCAGATCCA	3420
TOTCOAGCTC CAACCTRICAA AGARCTOTICC TOAGCCTTTGC CAGAGATICCA AAAGAAGCCC 3 CCARTAGAAA CCTGGAACTT GGGGAGTTAA GACCTGGAGG TCCTGGGAGGA CCCACCCCT 3 GCGGGCCAAC AAAGAACACAC TAACTATICAT GGTGCCCCAG GACCAGCTG GGACAGACTC CAACCAGGA GACCAGCCCAG CAGACCAGACT TAACTGGAA CACCAGACTC GGACAGACTC CCAACCCCG GATCAGGA CATATATTTG GGCCTGCTCC AGACCTGAATC CTGGGGCCC 3 AGTCTACCCCT GATTTGGGA AAACCAGCAC TCCTGCAGGACT CACCAGATCA GACCTGAATC AAACAGACCT GATCAGG ACCACAGAC ACAGCCCTC CCTGTTCCCC AGACAGAAGC AAACCACCTT CTCTGGCCAAC CCTGCCCAAC GACCAGCCCC CCTGTTCCCC AGAGAAAGGG ACACAGCCTC CCTGTTCCCC AGACAGAAAGGA CACCACCTC CCTGTTCCCC AGACACAGAC CCTGCCCCACCTC CCTGAGGACC CCTGCACCCC ACACAGAAAGGA AAACAGACCTC CCTGATCCCC AGACACAGAC CCTGCCCCACCTC CCTGATCCCC AGACACAGACCACACACACACACACACACACACAC		GGGACAGAGG	CCCAGCCTCC	CTGAAGCCTT	TGCATTTTGG	AGAGTTTCCT	GAAACAACTG	3480
40 ССЯТАВЛЯ ССИБОЛЬТ БОЯВЛЯТЬЯ ВОССТВОЕЛЯ СТОТЯВЛЬКЯ СОСОССОТО З ОТВЯБЕСЛЯЕ ВАВЛЯКИЕТ ЛАНТЯТОВТИ ОТВОТОСКИЕ ВОСОСВОТО З САСМОВЯТЬ БЛІТОТИВЕ ВОТВОТЕТЬ ВОСОСВЕТО ВОВОВЕТЬ ВОВО		GAAAGATAAC	TAGGAAATCC	ATTCACAGTT	CTTTGGGCCA	GACATGCCAC	AAGGACTTCC	3540
40 ССЯТАВЛЯ ССИБОЛЬТ БОЯВЛЯТЬЯ ВОССТВОЕЛЯ СТОТЯВЛЬКЯ СОСОССОТО З ОТВЯБЕСЛЯЕ ВАВЛЯКИЕТ ЛАНТЯТОВТИ ОТВОТОСКИЕ ВОСОСВОТО З САСМОВЯТЬ БЛІТОТИВЕ ВОТВОТЕТЬ ВОСОСВЕТО ВОВОВЕТЬ ВОВО		TGTCCAGCTC	CAACCTGCAA	AGATCTGTCC	TCAGCCTTGC	CAGAGATCCA	AAAGAAGCCC	3600
40 GTGGGCCHAC ARAGACACH TALTHYGCAT GGTSCCCCAG GACGGCTCA GGACGAGTCA GACGAGTCA CACGAGTCA GACGAGTCA CACGAGTCA GACGAGTCA CACGAGTCA CACGAGAGTCA CACGAGTCA CACGAGTCA CACGAGTCA CACGAGTCA CACGAGTCA CACGAGTCACGAGTCA CACGAGTCA CACGAGTCA CACGAGTCA CACGAGTCA CACGAGTCA CACGAGTCA CACGAGTCA CACGAGTCA CACGAGTCA CACGAGAGTCA CACGAGTCA CACGAGTC		CCAGTAAGAA	CCTGGAACTT	GGGGAGTTAA	GACCTGGCAG	CTCTGGACAG	CCCCACCCTG	3660
CACAGGRATA GATECTIGGC CAGGGCCARA GCCCAGCTCC ANGGGGGATAT AGRACTCARA 3 T0393GCARA TCAAGCCCAG GGTCCAGACT TACATCCATA TCAATCCAGA CCCAGACTCA GACATTGGCA 3 CCCAATCCAGG CAGATCCAGG ACTATATTTG GGCCTGCTCC AGACCTGATAC CTGGGGGCCC 3 AGTTCACCCCT GATTTGGGG AGACCTGAGG TTTCCAGGGG COTGAGGGGC CATATTGGC AACAGACTCT GCAGGACTCAG CAGCCCAGA ACAGCCCTC CCTGTTCCCT AGAGAAAGGC AACAGCACT TCCTGGGCCT GGGAATTTAC CAGAGACACGAG GACTTATTTA CAGACCAGG GACTTATTA CAGACCAGG GACTTATTA CAGACCAGG GACTTATTA CAGACCAGG GACTTATTA CAGACCAGG ACTTAGAAAAA AAAAA	40	GTGGGCCAAC	AAAGAACACT	AACTATGCAT	GGTGCCCCAG	GACCAGCTCA	GGACAGATGC	3720
T0999CCAGA TCCAGCCT09 G9TCTGGAGT TOATCT09GAA CCCAGACTCA GACKTT09CA 3 CCAATCCAGG CAGATCAGA CATATATTO GOCCTOCTAGACA GACKTT09CA 3 ACTCAGCCOG CAGATCAGA CATATATTO GOCCTOCTAGGA CCTGAAGGGG CCATATAGGGA AACTCAGACAGA ACTGAGCCCA CTGAAGGGG CCATATAGGA AACAGCCCTC CCTGATCGCA CTGAGCCAGA CTGACCAGA CTGACCAGA CTGACCAGA CCATACTCATATATA AACTCTGTTC CAAGTGCAAC CCTTCCCTCA CCTGGACCAC ACCACCAG ACTTATATA AAACTCTGTTC CAAGTGCAAT AAATCTGACC CAGTGCCCC ACTGACCAGA ACTAGAAAAA AAAA		CACAAGGATA	GATGCTGGCC	CAGGGCCAGA	GCCCAGCTCC	AAGGGGAATC	AGAACTCAAA	3780
СОАРССИЯ САВАТССКИЙ АСТАТАТТТЯ ОВСЕТОЕТСЕ АВАССТВАТА СТОЯВЛЯССТ 45 АВТЕЛЬССТЕ БАТТИВЕЙ АВАССИВИИ ТЕТСОСИЯВ СОТЕЙЬЯВИЯ СОКТИТИВОВ 45 АВАСИВАТСТВ ОВСЕТОВНО ТОТОВЕТОВНО ТЕТСОВНОВ СОСТЕЙЬЯВИЯ СОКТИТИВОВ 45 АВАСИВСТВ ТОТОВОЕТСЯ ОБДЕТОВНО ТЕТСОВСТВЕ СОСТЕЙТЕТСЯ ВАВАВАНИЯ 46 АВАССИСТВЕТСТ ТОТОВОЕТСЯ ОБДЕТОВНЕ ОБТЕТОВЕТСЯ ОБДЕТОВНО ВОСТЕЙТЕТСЯ ОБТЕТОВНО В ВЕТСОВНО В ОБТЕТОВНО В ОБТЕТОВ		TGGGGCCAGA	TOTAGOCTIGG	GGTCTGGAGT	TGATCTGGAA	CCCAGACTCA	GACATTGGCA	3840
45 ACCAGNIC GANTINGGAG ARECEGGAN TITICOGGGA COTGANGGGG CCNTANGGC ACCAGNIC GAGGAGCC CONTROL CONGROUND CONTROL CANGEROTE CONTROL CONTROL CANGEROTE CONTROL CONTR		CCAATCCAGG	CAGATCCAGG	ACTATATTG	GGCCTGCTCC	AGACCTGATC	CTGGAGGCCC	3900
45 AACAGATOTG GRACOTOAGC CTOGGCAGAC ACAGGCCCTC COTOTTCCCC RAGAGAAGGG 4 GAGCCACCTG TCCTGGGCCT GCAGAATTG GGTTCTGCCT GCCAGCCTGC CTGAGGCCCA CCCTCATCTC TCTGCCCAC CCTTCCCTCA CCTTGCCACC AGCACCCAG GACTRITTTA AACTCTGTTG GRAGTGCAAT AAATCTGACC CAGTGCCCCC ACTGACCAGA ACTAGAAAAA AAAA		AGTTCACCCT	CATTTACCAC	ANGCCAGGAA	TTTCCCAGGA	CCTGAAGGGG	CCATGATGGC	3960
GAGCCCACTS TOCTGGGCT GAGGATTTS GGTTCTGCCT GCOAGCTGCA CTGATGCTGC CCCCACACTC CCTGCCACC CCTGCCCTCA CCTGGGACC AGACGACCAG GACTACTTC AACTCTGTTG CAAGTGCAAT AAATCTGACC CAGTGCCCCC ACTGACCAGA ACTAGAAAAA AAAA	45	AACAGATCTG	GAACCTCAGC	CTGGCCAGAC	ACAGGCCCTC	CCTGTTCCCC	AGAGAAAGGG	4020
CCCTCATCTC TCTGCCCAAC CCTTCCCTCA CCTTGGCACC AGACACCAG GACTTATTA 4 AACTCTGTTG CAAGTGCAAT AAATCTGACC CAGTGCCCCC ACTGACCAGA ACTAGAAAAA AAAA		GAGCCCACTG	TOCTGGGCCT	GCAGAATTTG	GGTTCTGCCT	GCCAGCTGCA	CTGATGCTGC	4080
AACTCTGTTG CAAGTGCAAT AAATCTGACC CAGTGCCCCC ACTGACCAGA ACTAGAAAAA 4		CCCTCATCTC	TOTOCCAAC	CCTTCCCTCA	CCTTGGCACC	AGACACCCAG	GACTTATTTA	4140
AAAA		27CdCdGdda	CARGTGCAAT	ABATCTGACC	CAGTGCCCCC	ACTGACCAGA	ACTAGAAAAA	4200
50			CHOIGGARI					
50	50							
	50							

Seq ID NO: 6 Protein sequence: Protein Accession #: NP_002196.1

55	1	11	21	31	41	51	
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	GFSVEFYRPG	TDGVSVLVGA	PKANTSQPGV	LQGGAVYLCP	WGASPTQCTP	IEFDSKGSRL	120
				SSILACAPLY			180
60	DNFTRILEYA	PCRSDFSWAA	GQGYCQGGFS	AEFTKTGRVV	LGGPGSYFWQ	GQILSATQEQ	240
	TAESYYPEYL	INLVQGQLQT	ROASSIYDDS	YLGYSVAVGE	PSGDDTEDFV	AGVPKGNLTY	300
				AATDVNGDGL			360
	EVGRVYVYLQ	HPAGIEPTPT	LTLTGHDEFG	RFGSSLTPLG	DLDQDGYNDV	AIGAPFGGET	420
				HTPDFFGSAL			480
65				RSCSLEGNPV			540
	GFTVELQLDW	QKQKGGVRRA	LFLASRQATL	TOTLLIQUOA	REDCREMKIY	LRNESEFRDK	600
				SKSRIEDKAQ			660
				AELRVTAPPE			720
	FAVNQSRLLV	CDLGNPMKAG	ASLWGGLRFT	VPHLRDTKKT	IQFDFQILSK	NLNNSQSDVV	780
70	SFRLSVEAQA	QVTLNGVSKP	EAVLFPVSDW	HPRDQPQKEB	DLGPAVHHVY	ELINQGPSSI	840
	SQGVLELSCP	QALEGQQLLY	VTRVTGLNCT	TNHPINPKGL	ELDPEGSLIHH	QQKREAPSRS	900
	SASSGPQILK	CPEAECFRLR	CELGPLHQQE	SQSLQLHFRV	WAKTFLOREH	Obertocky	960
				AEGSYGVPLW	IIILAILFGL	PFFCFFIAIF	1020
	YKLGFFKRSL	PYGTAMEKAQ	LKPPATSDA				
75							

Seq ID NO: 7 <u>Nucleotide sequence:</u> Nucleic Acid Accession #: NM_ NM 002211 104..2500 (underlined sequences correspond to start and stop codons) Coding sequence: 5 11 21 31 41 GTCCGCCAAA ACCTGCGCGG ATAGGGAAGA ACAGCACCCC GGCGCCGATT GCCGTACCAA ACAAGCCTAA CGTCCGCTGG GCCCCGGACG CCGCGCGGAA AAGATGAATT TACAACCAAT 120 TTTCTGGATT GGACTGATCA GTTCAGTTTG CTGTGTGTTT GCTCAAACAG ATGAAAATAG ATGTTTAAAA GCAAATGCCA AATCATGTGG AGAATGTATA CAAGCAGGGC CAAATTGTGG 240 GTGGTGCACA AATTCAACAT TTTTACAGGA AGGAATGCCT ACTTCTGCAC GATGTGATGA 300 TTTAGAAGCC TTAAAAAAGA AGGGTTGCCC TCCAGATGAC ATAGAAAATC CCAGAGGCTC 360 CARAGATATA AAGARAATA AAAATGTAAC CARCCGTAGC AAAGGAACAG CAGAGAAGCT 420 15 CAAGCCAGAG GATATTACTC AGATCCAACC ACAGCAGTTG GTTTTGCGAT TAAGATCAGG 480 GGAGCCACAG ACATITACAT TAAAATTCAA GAGAGCTGAA GACTATCCCA TTGACCTCTA 540 CTACCTTATG GACCTGTCTT ATTCAATGAA AGACGATTTG GAGAATGTAA AAAGTCTTGG 600 AACAGATCTG ATGAATGAAA TGAGGAGGAT TACTTCGGAC TTCAGAATTG GATTTGGCTC 660 ATTTGTGGAA AAGACTGTGA TGCCTTACAT TAGCACAACA CCACCTAAGC TCAGGAACCC TTGCACAAGT GAACAGAAACT GCACCACCCC ATTTAGCTAC AAAAATGTGC TCAGTCTTAC 720 20 780 TAATAAAGGA GAAGTATTTA ATGAACTTGT TGGAAAACAG CGCATATCTG GAAATTTGGA 840 TTCTCCAGAA GGTGGTTTCG ATGCCATCAT GCAAGTTGCA GTTTGTGGAT CACTGATTGG 900 CTGGAGGAAT GTTACACGGC TGCTGGTGTT TTCCACAGAT GCCGGGTTTC ACTTTGCTGG AGATGGGAAA CTTGGTGGCA TTGTTTTACC AAATGATGGA CAATGTCACC TGGAAAATAA 1020 25 TATGTACACA ATGAGCCATT ATTATGATTA TCCTTCTATT GCTCACCTTG TCCAGAAACT 1080 GAGTGAAAAT AATATTCAGA CAATTTTTGC AGTTACTGAA GAATTTCAGC CTGTTTACAA 1140 GGAGCTGAAA AACTTGATCC CTAAGTCAGC AGTAGGAACA TTATCTGCAA ATTCTAGCAA 1200 TGTAATTCAG TTGATCATTG ATGCATACAA TTCCCTTTCC TCAGAAGTCA TTTTGGAAAA 1260 CGGCAAATTG TCAGAAGGAG TAACAATAAG TTACAAATCT TACTGCAAGA ACGGGGTGAA 1320 30 TGGAACAGGG GAAAATGGAA GAAAATGTTC CAATATTTCC ATTGGAGATG AGGTTCAATT 1380 TGRAATTAGC ATAACTTCAA ATAAGTGTCC AAAAAAGGAT TCTGACAGCT TTAAAATTAG GCCTCTGGGC TTTACGGAGG AAGTAGAGGT TATTCTTCAG TACATCTGTG AATGTGAATG 1500 CCAAAGCGAA GGCATCCCTG AAAGTCCCAA GTGTCATGAA GGAAATGGGA CATTTGAGTG 1560 TGGCGCGTGC AGGTGCAATG AAGGGCGTGT TGGTAGACAT TGTGAATGCA GCACAGATGA 1620 35 ACTTAACACT GAAGACATGG ATGCTTACTG CAGGAAAGAA AACAGTTCAG AAATCTGCAG 1680 TAACAATGGA GAGTGCGTCT GCGGACAGTG TGTTTGTAGG AAGAGGGATA ATACAAATGA 1740 AATTTATTCT GGCAAATTCT GCGAGTGTGA TAATTTCAAC TGTGATAGAT CCAATGGCTT 1800 AATTTGTGGA GGAAATGGTG TTTGCAAGTG TCGTGTGTGT GAGTGCAACC CCAACTACAC 1860 TGGCAGTGCA TGTGACTGTT CTTTGGATAC TAGTACTTGT GAAGCCAGCA ACGGACAGAT 1920 40 CIGCAATGGC CGGGGCATCT GCGAGTGTGG TGTCTGTAAG TGTACAGATC CGAAGTTTCA 1980 AGGGCAAACG TGTGAGATGT GTCAGACCTG CCTTGGTGTC TGTGCTGAGC ATAAAGAATG 2040 TGTTCAGTGC AGAGCCTTCA ATAAAGGAGA AAAGAAAGAC ACATGCACAC AGGAATGTTC 2100 CTATTTTAAC ATTACCAAGG TAGAAAGTCG GGACAAATTA CCCCAGCCGG TCCAACCTGA 2160 TCCTGTGTCC CATTGTAAGG AGAAGGATGT TGACGACTGT TGGTTCTATT TTACGTATTC 2220 45 AGTGAATGGG AACAACGAGG TCATGGTTCA TGTTGTGGAG AATCCAGAGT GTCCCACTGG 2280 TCCAGACATC ATTCCAATTG TAGCTGGTGT GGTTGCTGGA ATTGTTCTTA TTGGCCTTGC 2340 ATTACTGCTG ATATGGAAGC TTTTAATGAT AATTCATGAC AGAAGGGAGT TTGCTAAATT 2400 TGAAAAGGAG AAAATGAATG CCAAATGGGA CACGGGTGAA AATCCTATTT ATAAGAGTGC 2460 CGTARCARCT GTGGTCARTC CGARGTATGA GGGARARTGA GTACTGCCCG TGCARATCCC ACARCACTGA ATGCARAGTA GCARTTTCCA TAGTCACAGT TAGGTAGCTT TAGGGCARTA 2520 50 2580 TIGCCATGGT TITACTCATG TGCAGGTITT GAAAATGTAC AATATGTATA ATTITTAAAA 2640 TGTTTTATTA TTTTGAAAAT AATGTTGTAA TTCATGCCAG GGACTGACAA AAGACTTGAG 2700 ACAGGATGGT TATTCITGTC AGCTAAGGTC ACATTGTGCC TITTTGACCT TITCTTCCTG GACTATTGAA ATCAAGCTTA TTGGATTAAG TGATATTTCT ATAGCGATTG ARAGGGCAAT 2820 55 AGTTARAGTA ATGAGCATGA TGAGAGTTTC TGTTAATCAT GTATTAAAAC TGATTTTTAG 2880

70 Seq ID NO: 8 Protein sequence: Protein Accession #: NP_002202

GTTTTAACAG TTCA

60

65

21 31 41 11 75 MNLQPIPWIG LISSVCCVFA QTDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLOEGMPT

CTTTACATAT GTCAGTTTGC AGTTATGCAG AATCCAAAGT AAATGTCCTG CTAGCTAGTT

AAGGATTGTT TTAAATCTGT TATTTTGCTA TTTGCCTGTT AGACATGACT GATGACATAT CTGAAAGACA AGTATGTTGA GAGTTGCTGG TGTAAAATAC GTTTGAAATA GTTGATCTAC

AAAGGCCATG GGAAAAATTC AGAGAGTTAG GAAGGAAAAA CCAATAGCTT TAAAACCTGT

AGCGGTCAAT TTGCCTTTTT AATGAACATG TGAAGTTATA CTGTGGCTAT GCAACAGCTC

TCACCTACGC GAGTCTTACT TTGAGTTAGT GCCATAACAG ACCACTGTAT GTTTACTTCT

GTGCCATTTT AAGAGTTACT TAATGTTTGG TAACTTTTAT GCCTTCACTT TACAAATTCA 3180 AGCCTTAGAT AAAAGAACCG AGCAATTITC TGCTAAAAAG TCCTTGATTT AGCACTATTT

ACATACAGGC CATACTITAC AAAGTATITG CIGAATGGGG ACCITITGAG TIGAATITAT 3300 TTTATTATTT TTATTTTGTT TAATGTCTGG TGCTTTCTAT CACCTCTTCT AATCTTTAA 3360 TGTATTTGTT TGCAATTTTG GGGTAAGACT TTTTTATGAG TACTTTTCT TTGAAGTTTT

CACCATTIGA GITGCCCATC ITGITTCACA CIAGTCACAT ICTIGITITA AGIGCCITIA 3600

2940

3060

3120

3240

3420

3480

				Innovement of	ama pret venomi	***************************************	200	
		KKKGCPPDDI					120	
	LRLRSGEPQT	FTLKFKRAED	ABIDPAATWD	LSYSMKDDLE	NVKSLGTDLM	NEMRRITSDF	180	
						VFNELVGKQR	240	
						GGIVLPNDGQ	300	
5	CHLENNMYTM	SHYYDYPSIA	HLVQKLSENN	IQTIFAVTEE	FOPVYKELKN	LIPKSAVGTL	360	
	SANSSNVIQL	IIDAYNSLSS	EVILENGKLS	EGVTISYKSY	CKNGVNGTGE	NGRKCSNISI	420	
		TSNKCPKKDS					480	
						CVCGQCVCRK	540	
	RDNTNEIYSG	KFCECDNFNC	DRSNGLICGG	NGVCKCRVCE	CNFNYTGSAC	DCSLDTSTCE	600	
10		GICECGVCKC					660	
						NEVMVHVVEN	720	
	PECPTGPDII	PIVAGVVAGI	AFIGFFFFF	WKLLMIIHDR	REFAKFEKEK	MNAKWDTGEN	780	
	PIYKSAVTTV	VNPKYEGK						
15		O Washington						

Seq ID NO: 9 Nucleotide Sequence: Nucleic Acid Accession #:NM_002425

Coding sequence: 23..1453 (underlined sequences correspond to start and stop codons)

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	AGTCTGCTCT	GCCTATCCTC	TGAGTGGGGC	AGCAAAAGAG	GAGGACTCCA	ACAAGGATCT	120
	TGCCCAGCAA	TACCTAGAAA	AGTACTACAA	CCTCGAAAAG	GATGTGAAAC	AGTTTAGAAG	180
25	AAAGGACAGT	AATCTCATTG	TAAAAAAAT	CCAAGGAATG	CAGAAGTTCC	TTGGGTTGGA	240
	GGTGACAGGG	AAGCTAGACA	CTGACACTCT	GGAGGTGATG	CGCAAGCCCA	GGTGTGGAGT	300
	TCCTGACGTT	GGTCACTTCA	GCTCCTTTCC	TGGCATGCCG	AAGTGGAGGA	AAACCCACCT	360
	TACATACAGG	ATTGTGAATT	ATACACCAGA	TTTGCCAAGA	GATGCTGTTG	ATTCTGCCAT	420
	TGAGAAAGCT	CTGAAAGTCT	GGGAAGAGGT	GACTCCACTC	ACATTCTCCA	GGCTGTATGA	480
30	AGGAGAGGCT	GATATAATGA	TCTCTTTCGC	AGTTAAAGAA	CATGGAGACT	TTTACTCTTT	540
	TGATGGCCCA	GGACACAGTT	TGGCTCATGC	CTACCCACCT	GGACCTGGGC	TTTATGGAGA	600
	TATTCACTTT	GATGATGATG	AAAAATGGAC	AGAAGATGCA	TCAGGCACCA	ATTTATTCCT	660
	CGTTGCTGCT	CATGAACTTG	GCCACTCCCT	GGGGCTCTTT	CACTCAGCCA	ACACTGAAGC	720
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Seq ID NO: 10 Protein sequence: 55 Protein Accession #: NP 002416

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70

Seq ID NO: 11 <u>Mucleotide sequence:</u> Nucleic Acid Accession #: XM_058189 Coding sequence: 169.774 (underlined sequences correspond to start and stop codons)

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2100

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						CCATTTCAGT	
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		14 Protein					
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(22							
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Coding sequence: 150..1631 (underlined sequences correspond to start and stop codons)

Seq ID NO: 15 Nucleotide sequence: Nucleic Acid Accession #: NM_004105

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Seq ID NO: 16 Protein sequence: Protein Accession #: NP 004096

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Seq ID NO: 17 Nucleotide sequence: Nucleic Acid Accession #: NM 018894

75 Coding sequence: 27..1967 (underlined sequences correspond to start and stop codons)

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Seq ID NO: 20 Protein sequence: Protein Accession #: NP_006491

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Seq ID NO: 21 Nucleotide sequence:

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Coding sequence: 72..1481 (underlined sequences correspond to start and stop codons)

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Seq ID NO: 22 Protein sequence: Protein Accession #: NP_002412

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	LAHAFQPGPG	IGGDAHFDED	ERWINNFREY	NLHRVAAHEL	GHSLGLSHST	DIGALMYPSY	240
			GRSQNPVQPI				300
			WPQLPNGLEA				360
55			LSEENTGKTY			YPKMIAHDFP	420
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60 Seq ID NO: 23 <u>Mucleotide sequence</u>: Mucleic Acid Accession #: FGENESH predicted ORF Coding sequence: 141-1580 (underlined sequences correspond to start and stop codons)

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Seq ID NO: 24 Protein sequence:
55 Protein Accession #: FGENESH predicted

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70 Seq ID NO: 25 <u>Nucleotide sequence</u>: Nucleic Acid Accession #: U21551

Nucleic Acid Accession #: UZ1551 Coding sequence: 1..1155 (underlined sequences correspond to start and stop codons)

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Seq ID NO: 28 <u>Protein sequence:</u> Protein Accession #: XP 039209

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Seq ID NO: 29 <u>Nucleotide sequence:</u> Nucleic Acid Accession #: NM 024756

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30 Seq ID NO: 36 Protein sequence: Protein Accession #: NP 002413

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		ession #:					
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Coding sequence: 57.764 (underlined sequences correspond to start and stop codons)

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••			LGDAAQEPTG		DYGPCRALLL	RYYYDRYTQS	60	
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	TGATCCTTCA ACTITITIAA GTATAAAAGA TCACAGATTG GGAAAAAAT GAATATAAA CACTTGGATG AGACTTAGAC	CGTARARTGA TTATCACGGT ARTGARTTTT TATTTTTGGC TACCAACTAT ATGCTGCCTT CACTTTTART TARATARGACC TTTATCCTTA	TTCTATTATG ACACTATTGT TTTAAAACAA ATTTCTAGGC TAACTATGTT GGTGCTAATA GAAAGGGAGG AGCTCTTTAC TTGTTGTTAGT	ACTGCCTTTG TTACTTTTCA TCTAGCCATC AAGTATCAGC AAATAAGTAT TTGTATGTAT AACGGAAGGA CCCTTATTTT TGTTGTTAAT	CATGTAGTAA TCTGTAAATG ATCAAGGTGC CAATAAGTAT TCAGTTTCAT TTAAATGATC CAATATTCCAG GGATATGCCT ATTCGTGCT	TATGACAAAG TTTTATTGTT TATAAGAGTT GTTAGTGATA GTGATCTCTG ATCTGACTCA TTCTACACAAAAT TTTTTGGAAAG TCAGCCCACG	120 180 240 300 360 420 480 540	
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45	TGATCCTTCA ACTITITIAA GTATAAAGA TCACAGATTG GGAAAAAAT GAAATATAAA CACTTGGATG AGACTTAGAC GTGCCTTGGT TATTGGGAAA TTACCAGTAG CTGGAGAAAT	CGTAAAATGA TTATCACGGT AATGAATTTT TATTTTTGGC TACCAACTAT AATGATGCGCTT CACTTTAAT AAATAGACC TTTAATCCTTA CTCTCCACAA GTGAGATCCT AAAGACCAG	TTCTATTATG ACACTATTGT TTTAAAACAA ATTTCTAGGC TAACTATGTT GGTGCTAATA GAAAGGGAGG AGCTCTTTAC TTGTTAGT TCAAATGGAG CTCACCATTT GATGCACAGA	ACTGCCTTTG TTACTTTCA TCTAGCCATC AAGTATCAGC AAATAGTAT TTGTATGTAT AACGGAAGGA CCTTATTTT TGTTGTTAAT GATCCCCAA TGCCAAGATA ATGGCATGA	CATGTAGTAA TCTGTAAATG ATCAAGGTGC CAATAAGTAT TCAGTTTCAT TTAAATGATC CAATTTCCAG GGATATGCT ATTCGTGCT GCAGCTTCAT CCTTAAAATG CCTTCAGCTC	TATGACAAAG TTTTATTGTT TATAAGAGTT GTTAGTGATA GTGATACTCTG GTGACAGAAT TTTTTGGAAG TCAGCCCACG TACAGAGTGA ACATCCAAGT ACAGGACACA GAAAACATCG	120 180 240 300 360 420 480 540 600 660 720	
45	TGATCCTTCA ACTITITADA GTATAAAGA TCACAGATTG GGAAAAAAT GAATATAAA GACTTAGAC GTGCCTTGGT TATTGGGATA TTACCAGTAG CTGAAGAAAT CTGCAGTAG CTGCAGTAG CTGCAGTAG CTGCAGTAG	CGTAAAATGA TTATCACGGT AATGAATTTT TATTTTTGGC TACCAACTAT ATGCTGCCTT CACTITTAAT AAATAGACC TTTATCCTA CTCCACAA GTGAGATCCT TAAGAACAG TCAGAACCAG TGACTTCTC TGACTCTTTT	TTCTATTATG ACACTATTGT TTTAAAACAA ATTTCTAGGCTAATGTT GGTGCTAATTAT GGTGCTAATTAT GGTGCTAATTAT TCAAATGGAG AGCTCTTTAC TTCTTAGTTAG TCAAATGGAG CTCACCATTT TCAGCACAGA OTTCTGAATC TCAGGCCATG GTGAAGGAAAT	ACTECCTTTE TTACTTTCA TCTAGCCATE AAGTATCAGC AMATAAGTAT TTATATTAT TTATTATTAT TGTTTTATAT TGCCCCAA TGCCAAGATA ATGGCATTA ATCACGATTA ACCGATTA ACCGATTA ACCGATTA ACCGATTA ACCGATTA ACCGATTA ACCGATTA	CATGTAGTAA CATGTAGTAA TCTGTAAATG ATCAAGGTGC CAATAAGTAT TCAAGTTCAT TTAAATGATC CAATTTCCAG GGATATGCCT GCACGTTCAT CCTTAAAATG CCTCCAGCTCAT CCTTTTGCAT CCTCCCGGTT CTCCCCGGTT CTCCCCGGTT CTCCCCGGTT CTCCCCGGTT CTCCCCGGTT CTCCCCGGTT	TATGACAAAG TTTTATTGTT TATAAGAGTT GTTAGTGATA GTGATCTG ATCTGACTCA TCTGACTCA TTTTTTGGAAG TCAGCCCACG TCAGCCCACG ACATCCAAGT ACATCCAAGT ACATCCAAGT TTTTTGGAAGACAC GAAAACATCG CTTTGACCCC CTTTGAGCCT	120 180 240 300 360 420 480 540 600 660 720 780 840 900	
45	TGATCCTTCA ACTITITIAA GTATAAAGA TCACAGATTO GGAAAAAAAT CACTTGGATO AGACTTAGAC GTGCCTTGGT TATTGGGAAA TTACCAGTAG CTGGAGAAA GCTGGGAAA GCTGGGGAAA TCTGGGAAA TCTGGGAAA TCTGGGAAA TTCCGATAAT TTCCGATTAG	CGTAAAATGA TTATCACGGT AATGAATTT TATTTTGGC TACCAACTAT ATGCTGCCTT CACTTTTAAT ATGCTGCCTT CACTTTAAT CTTATCCTTA CTCTACCACAA GTGAGATCCT AAAGACACAG TCAGAACCAG TGACTTCTCT GGACGTTTCTT CGTATAATTC	TTCTATTATG ACACTATTGT TTAAAACAA ATTTCTAGGC ATTTCTAGGC GTAACTATTGT GGAAGGGAGG CTCAACTATTA CAAAGGAAGT CTCAACCATT GATGCACAGA GTCTGACAGA GTTCTGACAGA GTCAGAGAAAAAAAAAA	ACTGCCTTTG TTACTTTCA TCTAGCCATC AAGTATCAGC AAGTATCAGC AAGTATCAGC ACTGATTTT TGTTATGTAT TGTTGTTATTTTT TGTTGTTATTTTTTGTTCATA ATGGCAAGAATA ATGAGCATCA ATCACCGATTG AGCCTAACAY GAACTOTGGA TACTCTTTC	CATGTAGTAA TCTGTAGATG ATCAAGGGG CAATAAGTAT TCAAGTTCAT TTAAATGAT TCAAGTTCCA GGATATGCT ATTGGTGCT GCAGGTCAGCC CCTTTAGATG CCTTCAGGTC CCTTTTGGAT CCTGCAGGTC CTTGCAAAATG CTTCCAAAATG CTAAAATGGA	TATGACAAAG TTTTATTGTT TATAAGAGTT GTTAGTGATA GTGATCTCT ATCTGACTCA TCTGACTCA TCTACAGAAT TTTTTTGGAAG TCAAGCCACG ACATCCAAGT ACAAGCACAC GAAAACATCG TTCATGCCCG CTTTGAGTCT GTGCTGAAGC	120 180 240 300 360 420 480 540 600 660 720 780 840 900	
45	TGATCCTTCA ACTATCATAAA ACTATCATAAA ACTATCATAAA ACACTTGGATG GGAAAAAAAT GAATATAAA CACTTGGATG TATTGGAAA TTACCAGTAG CTGGAGAAAT CTGGAGAAAT CTGGAGAAAT CTGGAGAAAT CTGGAGTAG CTGCAGTAG CTGCAGTAG CTGCAGTAC CTGCAGTAC CTGCAGTAC CTGCAGTAC CTGCAGTAC CTGCAGTAC CTGCAGTAC CTGCAGTAC CTGCAGTAC CTGCAGTCTTT	CGTAAAATGA TTATCACGGT AATGAATTTT TATTTTTGGC TACCAACTAT AAGCACTAT AAATAAGACC TTATACTTTAAT CTCTCCACAA GTGAGATCCT TAAAGACAG TCAGAACCAG TGAGATCTT TCATTCTTCT GGACGTTTGT TCATTAATTC CTGCCCCTCC	TTCTATTATO ACACTATTOT TTTAANACAA ATTTCTAGTT GGTGCTAATA GGTGCTAATTA GGTGCTAATA GAAAGGAGG AGCNCTTTAC TTGTATGTT CAAATGAG CTCACCATTT CTGAATCACCATTT CTAGAATC GTGAAGAATC ACACGATTT GTGAAGAAT ACTTTTTTTT AGGTGATGAAAA ACTTTTTTTTT	ACTGCCTTTG TTACTTTCA TCTAGCCATC AAGTATCAGC AAATAGTAT TTGTATTAT TAGTATTAT TGTTGTTAAT GATCCCCCAA TGCCAAGATA ATCAGCATGA ATCAGCATGA ATCAGCATGA ACACAGATTG GAACTTCTTC AGGGAAGCCT AGGAAGCATGA ACACAGGATGA ACACATGTGGA TACTTCTTC AGGGAAGCCT	CATGTAGTAA CATGTAGTAA TCTGTAAATG ATCAAGGTGC CAATAAGTAT TCAGTTTCAT TTAAATGATC GGATATGCCT GCAGCTTCAT CCTTCAAATG CCTTCAGCT CCTTTTGCAT CCTGCAGCT GTACAAAATG GAAAATGGAA TTGCCAATGG	TATGACAAAG TTTTATTGTT TATAAGAGTT TATAAGAGTT GTAGTGATA GTGATCACTG ATCTGACTCA TCGCACAGAAT TTTTTGGATG TCAGCCCACG TACAGAGTG ACATCCAAGT TACAGAGTG ACAGCACAC GAAAACATCG GAAAACATCG GTTCTGAGTCT GTCTGAGTCT GTCTGAAGC CCCATGGAAGA	120 180 240 300 360 420 480 540 600 660 720 780 840 900 960 1020	
45	TGATCCTTCA ACTITITADA GTATARARGA TCACAGATTG GGAAAAAAT GAATATAGA CACTIGGATG AGACTTAGAC TGCCTTGGT TATTGGGAA TTACCAGTAG CTGCAGTAG CTGCAGTAGT CTGCAGTAAT TTCCCATTAGT TCCCATTAGT CAGGCTTTT ACACTIGGTT ACACTIGGTT CAGGTTCTTC CAGGTTCTTC	CSTABARTSA TTATCACGGT AATGARTTT TATTTTTGGC TACCACTAT AAGATATAT TATTTTTGGC TACCACACTAT AAATAAGACC TTATACCTA CTTCACACA GTGAGATCCT AAAGACCAG TGAGAACCAG TGAGTTCTCT GGACGTTTGT TCATTABTTC CTGCCCTCC TGAGAACCCAG CAACTCCCAACTCCCAACTCCAAA	TTCTATTATO ACACTATTOT TTTABAACAA ATTICTAGT GTACTATOT GAAAGGAGG AGCTCTTAC TCGTGCTTTAC TCACCACTT TCACCACT TCACCACT TCACCACT TCACCCACT TCACCCACT TCACCCACT TCACCCACT TCACCCACT TCACCCACT TCACCCACT TCACCCACT TCACCCACT ACTICTTTOT AACCTGATGA TCCACCCACT CAACCCACT CAACCCACT CAACCCCCTC	ACTGCCTTTG TTACTTTCA TCTAGCCATC AAGTATCAGC AAATAAGTAT TTGTATGTAT TAGTATTTAT TGTTGTTAAT ATGCCAAGATA ATGCGCAAGATA ATGCGCAAGATA ATGCGCATGAAGATCA TCCCCCAA TCCCAAGATTA ATGGCATGA TCCCCCAA TCCCACAGATTA ATGGCATGA TCCCCCAA TCCCACAGATTA ATGGCATGA TACTCCTCCAAGACCCA AGGGAAGCCCA AGGGCTCCAAGACCCC CAAAGACCCAA AGGGCTCCCAG	CATGTAGTAA TCTGTAAATG ATCAAGGTGC CAATATGAT TCAGTTTCAT TTAAATGAT TCAGTTTCCAG GGATATGCCT ATTCGTTGCT GCAGGTTCAT CCTTCAAATG CCTTCAGCT CCTTCAGCT CCTGCAAATG GTAAATGGA TTGCCAAATG GTAAATGGA TTGCCAATGGA TTGCCATGG AGAGATTAGG	TATGACAAAG TTTTATTGTT TATTAAGAGTT TATTAAGAGTT TATTAAGAGTT GTTAGTACTCA TGCACAGAAT TTTTTTGGAAG TCAGCCCACG TACAGAGTGA ACATCCAAGT ACAGAGTACA GAAAACATCG GAAAACATCG GAAAACATCG GTTCATGAGCC CTTTGAGTCT GTGCTGAAGC CCCATGGAAG AAAAGCCTOG AATTCAAGTATA	120 180 240 300 360 480 540 660 720 780 840 900 960 1020 1080	
45 50 55	TGATCCTTCA ACTITITITAA GTATARAGA TCACAGATTG GGAAAAAAT GAARTATAAA CACTTGGAT AGACTTAGAC GTGCCTTGGT TATTIGGAA TTACCAGTAG CTGGAGAAAT TCCGATTGC TCGAGTAAT TCCGATTGC CATGGCTTAT CACTTGGTTATGC CATGGTTATTCC CATGGTTATTCC TGAATAAATG	GSTABARTGA TTATCACGGT AATGARTTTT TATTTTTGGC TACCAACTAT ATGCGGCCT CACTTTAAA TCTCCACAA TTATCCTTA CTCTCCACAA TGAGACACAG TTATCCTTA TCAGAACCAG TGAGAACCAG TGAGATTCCT TGAGAACCAG TGACTTCCT CTGCCCTCC CTGAGAAACC CAACTCCAAA TTATCTCC	TTCTATTATO ACACTATTGT TTTABAACAA ATTTCTAGGC TAACTATGT GGTGCTAATA GAAGGGAGG AGCTCTTTAG TCTAGTTAG TCTAGTTAG TCTAGTTAG TCTAGTTAG TCTAGTTAG TCTAGTTAG TCTAGTTAG TCTAGTAGAT CTGTGTAAT CTGTGTAAT CTGTGAAT TCAGGCCATT TCAGGCCATT TGCCCACTTC CAGCCTTTC CAGCCCTTC TATTAATGT TTATTAATGT	ACTGCCTTTG TTACTTTCA TCTAGCCATC AAGTATCAGC AAATACTAC AAGTATCAGC AAATAGTAT ACGGAAGGA ACTGTATTTT TGTTGTTAAT GATCCCCCAA ATGGCATGA ATGGCATGA ATCGCAGATA AGCGATGA ACACTGTACCA AGGGAAGCCA AGGGAACCAC AGGGATCCCAAA AGTGTCCCAAA AGTGTCCCAAA AGTGTCCCAAA	CATGTAGTAA CATGTAGTAA TCAGAGTGC CAATATCAT TCAGTTTCAT TTAAATGAT TCAGTTTCCAG GGATATGCCT ATTCGTTGCT GCAGGTTCAT CCTTCAAATG CCTTCAGCT CCTTCAGCT CCTGCAGATTGCAAATG GTAAATGGA TTGCCAAATGGA TTGCCAAATG AGAGATTAGG	TATGACAAAG TTTTATTGTT TATAAGAGTT TATAAGAGTT TATAAGAGTT GTAATCACTG TCACAGAAT TTTTTTGGAAG TCAGCCACG TACAGAAT ACATCCAAG ACATCCAAG ACATCCAAG TCATGCACG TTCATGCCCG CTTTGATCT GTTCATGACTC GTTCATGAAG CCCATTGAAG AAAAGCCTOG	120 180 240 300 360 480 540 660 720 780 840 900 960 1020 1080	
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45 50 55 60	TGATCCTTCA ACTITITAA AGATTATAAAGA TCACAGATTA GGAAAAAAT GGAAAAAT GAGTTAGGAT AGACTTAGGAT ATTACGATA TTACCAGTTAG TGAGGAGAAAT TTCCAGTTAG CTGCAGTAAT TCCCATTAC CATGGTTT ACACTTGTT ACACTTGTT TCAGTTAT CAGTATTTCC TGAATAAT TCCAGTTAG CAGTAGTTT CAGTATTCTC TGAATAATTCTC TGAATAATTCTC TGAATAATTCTC TGAATAATCTC CACCACACCC	COTAMANTOA TTATCACGOT AATGAATTT TATTITGC TACCACTAT AATGAATTT TATTITGC TACCACTAT AAATGAACTAT AAATGAACCA TTATCCTTA CTCCCCACA GTGAGATCCT TAAAGCACAG TCAGATCCT GGACCTTTC TGACTCTCC GGACCTTTC TCATCATTC CTGCCCCTCC TCAGGAACCA TTATTCCTC CTGCCCTCC TCAGGAACCA AAAAAAAAAA	TTCTATTATO ACACTATAT TTTAAAACAA ATTTCTTAGC TACATATGT GAAGGGAG AGTGCTATAT GAAGGGAG AGCCATT TCAAATGGAG CTCACCATT GATGGAAC TTCAAATGGAG ATTCTAGAAC TTCAGCCCATT AGCTCTTAC AGCTCTTAC AGCTCTTAC AGCTCTTAC AGCTCATAC TTCAGCCCATT AAGAAAAAAAAAA	ACTGCCTTTG TTACTTTCA TCTAGCCTTT AAGTATCAC AAATAATAT TTGTATGTAT AACGGAAGGA CCCTTAATTTT TGTTGTTATAT AACGGAAGGA ATGCCCAAA TGCAAGATA ATGCAAGATA AAAA AAA	CATGTAGTAA CATGTAGTAA TCAGAGTGC CAATATCAT TCAGTTTCAT TTAAATGAT TCAGTTTCCAG GGATATGCCT ATTCGTTGCT GCAGGTTCAT CCTTCAAATG CCTTCAGCT CCTTCAGCT CCTGCAGATTGCAAATG GTAAATGGA TTGCCAAATGGA TTGCCAAATG AGAGATTAGG	TATGACAAAG TTTTATTGTT TATTAAGAGTT TATTAAGAGTT TATTAAGAGTT GTTAGTACTCA TGCACAGAAT TTTTTTGGAAG TCAGCCCACG TACAGAGTGA ACATCCAAGT ACAGAGTACA GAAAACATCG GAAAACATCG GAAAACATCG GTTCATGAGCC CTTTGAGTCT GTGCTGAAGC CCCATGGAAG AAAAGCCTOG AATTCAAGTATA	120 180 240 300 360 480 540 660 720 780 840 900 960 1020 1080	
45 50 55	TGATCCTTCA ACTITITAA GTATAARAGA TCACAGATTAGAAAAAAA CACTTGGATA AGACTTAGATC AGACTTAGGATA TTACCAGTAG CTGGAGAATTCCCAGTAGT TTCCGAGTAGT TTCCGAGTAGT TTCCGAGTAGT TCCGAGTATTCCAGTATTCCCAGTATTCCCAGTATTCAGTATTCAGTAGTATTCAGTATTCAGTATTCAGTATTCAGAAAAAAAA	COTANANTOA TTATCAGGET AATOAATTT TATTTTTGGC TACCACCTM ATGCAGCTT AAATAAGACC TTTATCCTTA CTGCCCTA GTGAGTTCCTA AAATAAGACC GTGAGTTCT GTGCCTT GTGCCTT GTGCCTT GTGCCTT GTGCTTTGT TCATAATTC CTGCCCCTCC TCATCATCC AAAAAAAAAA	TTCTATTATO ACACTATTAT TTCTATTATO ACACTATTAT TTTAAAACAA ATTICTAGGC TTAACTAGTT GGTGCTAATA GAAGGGGG AGCCCTTAG TTGTTGTTAG TCAATGGGAC ATTCTGAATCAGA ATTCTGAATC TCAATGGGAC TTCTGAATC TCAGGCCATT AGGCTGATC TGTGAGAAA ACTTTTTTATTATATAT AAAAAAAAAA	ACTGCCTTG TTACTTTCA TCHAGCATA AGTATCAC AAGTATCAC AAGTATCAC AAGTATCAC AAGTATCAC AAGTATCAC AAGTATCAC AAGGAAGC CCTTATTTT TGTTGTTAAT GATCGCCATAC ATGGCCATAC AAGGAAGCA AAGGAAGCA AAGGAAGCA AAGGAAGCAAAAA AAGGAAGCAAAAA AAAAA AAAA	CATGTAGTAA CATGTAGTAA TCAGAGTGC CAATATCAT TCAGTTTCAT TTAAATGAT TCAGTTTCCAG GGATATGCCT ATTCGTTGCT GCAGGTTCAT CCTTCAAATG CCTTCAGCT CCTTCAGCT CCTGCAGATTGCAAATG GTAAATGGA TTGCCAAATGGA TTGCCAAATG AGAGATTAGG	TATGACAAAG TTTTATTGTT TATTAAGAGTT TATTAAGAGTT TATTAAGAGTT GTTAGTACTCA TGCACAGAAT TTTTTTGGAAG TCAGCCCACG TACAGAGTGA ACATCCAAGT ACAGAGTACA GAAAACATCG GAAAACATCG GAAAACATCG GTTCATGAGCC CTTTGAGTCT GTGCTGAAGC CCCATGGAAG AAAAGCCTOG AATTCAAGTATA	120 180 240 300 360 480 540 660 720 780 840 900 960 1020 1080	
45 50 55 60	TGATCCTTCA ACTITITAA AGATAAAAAA TATAAAAAA TAATAATAA TAAAAAAAA	CGTAMANTOA TTATCACGGT ANTOATTTATCACGGT ANTOATTTACCACATM ATGCATCATM ATGCATTATAA TAGCACCATM ANATAAGACC TTTATACCTT ANAGACACA TTATACTTC TCACACAA GGGGGTTTTTAT TCATTACATT TCATACATTC TCAGACACAA TTATATCTC TCAGACACAA TTATATCTC TCAGACACAA TTATATCTCC 54 NALGAC 54 NALGAC 54 NALGAC 54 NALGAC 54 NALGAC 56 ANAGACACA TTATATCT TCAGACACAA TTATATCT TCAGACAA TTATA	TTOTATTANO ACACTATAT TTOTATTANO ACACTATAT TTOTATTANO ACACTATAT TTOTANACAC ATTOTAGG ATTOTAGG AGCTOTTAC TTOTTOTTAG AGCACAC ACCACCATTT GATGCACACA ACTOTTTAC TTOTTOTTAG ATTOCACCAC ACTOTTAC ACCACCATTT CARGACCACA ACTOTTTAC TCAGCACTT ACACCACCAT TCAGCACTT ACACCACCAT TCAGCACTT ACACCACCAT TCAGCACTT ACACCACCAC TTATTANATOT AAAAAAAAAAA ACTOTTATAA	ACTGCCTTIG TTACTITICA TTCAGCCATC AGTATCAGC AGTATCAGC AGTATCAGC AGTATCAGC AGTATCAGC AGTATCAGC AGTATCAGC AGTATCAGC ATTGTATTATA TTGTATTATAA ATTGGCAGAGTA ATTGGCAGAGTA ATTGGCAGAGTA ATTGGCATACAY AGGCATACAY AGGAACTAGCA TACTTCTTC CAAAGACCAA AGTGGCCAGG GTTCTGAAAA AAAA	CATOTRAGTAA TCTGTRAATG ATCAGGTGC CAATAGGTAA TCAGGTGCA CAATAGGCA GOATTICCAG GOAGGTCAT CCTGCAGGTCA CCTTGTAGATC CCTGCAGGTC CCTGTAGATG CATAGGTCA CCTGCAGGTC CATAGGTCAA TTGCAGTCA CCTGCAGGTC CATAGATGCAGCT CATAGATGCAGCT CATAGATGCAGCT CATAGATGCAGCT CATAGATGCAGCT CATAGATGCAGCT CATAGATGCAGCT CATAGATGCAGCT CATAGATTAGGA AGGGATTAGG AGAAGTTTAG	TATTOACRAGE TITTATTGTT TATTOACRAGE TITTATTGTT TATTAMAGGTT TATTAMAGGTT TATTAMAGGTT TATTAMAGGTT TATTAGTATA TATTAGTATA TATTAGTATA TATTAGTATA TATTAGTAGT TATTAGTAGT TATTAGTAGT TATTAGTAGT TATTAGTAGT TATTAGTAGT TATTAGTAGT TATTAGT	120 180 240 300 420 480 540 660 720 720 780 840 900 960 1020 1140 1200	codons)
45 50 55 60	TGATCCTTCA ACTITITAA AGATAAAAAA TATAAAAAA TAATAATAA TAAAAAAAA	CGTAMANTOA TTATCACGGT ANTOATTTATCACGGT ANTOATTTACCACATM ATGCATCATM ATGCATTATAA TAGCACCATM ANATAAGACC TTTATACCTT ANAGACACA TTATACTTC TCACACAA GGGGGTTTTTAT TCATTACATT TCATACATTC TCAGACACAA TTATATCTC TCAGACACAA TTATATCTC TCAGACACAA TTATATCTCC 54 NALGAC 54 NALGAC 54 NALGAC 54 NALGAC 54 NALGAC 56 ANAGACACA TTATATCT TCAGACACAA TTATATCT TCAGACAA TTATA	TTOTATTANO ACACTATAT TTOTATTANO ACACTATAT TTOTATTANO ACACTATAT TTOTANACAC ATTOTAGG ATTOTAGG AGCTOTTAC TTOTTOTTAG AGCACAC ACCACCATTT GATGCACACA ACTOTTTAC TTOTTOTTAG ATTOCACCAC ACTOTTAC ACCACCATTT CARGACCACA ACTOTTTAC TCAGCACTT ACACCACCAT TCAGCACTT ACACCACCAT TCAGCACTT ACACCACCAT TCAGCACTT ACACCACCAC TTATTANATOT AAAAAAAAAAA ACTOTTATAA	ACTGCCTTIG TTACTITICA TTCAGCCATC AGTATCAGC AGTATCAGC AGTATCAGC AGTATCAGC AGTATCAGC AGTATCAGC AGTATCAGC AGTATCAGC ATTGTATTATA TTGTATTATAA ATTGGCAGAGTA ATTGGCAGAGTA ATTGGCAGAGTA ATTGGCATACAY AGGCATACAY AGGAACTAGCA TACTTCTTC CAAAGACCAA AGTGGCCAGG GTTCTGAAAA AAAA	CATOTRAGTAA TCTGTRAATG ATCAGGTGC CAATAGGTAA TCAGGTGCA CAATAGGCA GOATTICCAG GOAGGTCAT CCTGCAGGTCA CCTTGTAGATC CCTGCAGGTC CCTGTAGATG CATAGGTCA CCTGCAGGTC CATAGGTCAA TTGCAGTCA CCTGCAGGTC CATAGATGCAGCT CATAGATGCAGCT CATAGATGCAGCT CATAGATGCAGCT CATAGATGCAGCT CATAGATGCAGCT CATAGATGCAGCT CATAGATGCAGCT CATAGATTAGGA AGGGATTAGG AGAAGTTTAG	TATGACAAAG TTTTATTGTT TATTAAGAGTT TATTAAGAGTT TATTAAGAGTT GTTAGTACTCA TGCACAGAAT TTTTTTGGAAG TCAGCCCACG TACAGAGTGA ACATCCAAGT ACAGAGTACA GAAAACATCG GAAAACATCG GAAAACATCG GTTCATGAGCC CTTTGAGTCT GTGCTGAAGC CCCATGGAAG AAAAGCCTOG AATTCAAGTATA	120 180 240 300 420 480 540 660 720 720 780 840 900 960 1020 1140 1200	codons)
45 50 55 60 65	TGATCCTTCA ACTITITAA AGATAAAAAA TATAAAAAA TAATAATAA TAAAAAAAA	COTAMANTOA TTATCAGGOT AATOANTTTTGGC TACCAACTAT ATGCTTTGCAT TATTTTTGGCT TACCACTAT AAGACAC TTTATCCTT AAAGACAC TTATCCTT AAAGACAC TTATCCTT AAGACACAC COGACCTTTCC COGACCACAC TTAGCACTCC CACTCCCAA TTATCCTTC COGACCACAC TTAGCACTCC TACGACACAC TTATCCTCT CACCACAC TTATCCTCT CACCACAC TTATCTCTCA AAAAAAAA	TTCTATTATO ACACTATTAT TTCTATATATA ACACTATTAT TTTAAAACAA ATTTCTAGGC TAACTAGGT GGTGCTAATA GGTGCTAATA GGTGCTAATA GGTGCTAATA GGTGCTAATA GATGGAG TCCAACATTTAC TTGTTGTTAG GATGCACAGA TCTAGCACTAT TCAGCACTAT	ACTGCCTTTG TTACTTTCA TCAGCATC AGTATCACC AGTATCACC AGTATCACC AGTATCACC AGTATCACC AGTATCACC AGTATCACC ATTGTATACTAT ATGGACACAT ATGGACACAT AGTACCCCAA ATGGACATCACA AGTACCCTAACAY AGTACCCTACACAY AGTACCACATC ACTCCTACACAY AGTACCCTACACAY AGTACCCTACACAY AGTACCCTACAY AGTACCCTACACAY AGTACCTCCACA AGTACCTCCACA AGTACCTCCACA AGTACCTCCACA AGTACCTCCACA AGTACACACAAA AAAA A	CATOTAGTAA TCTGTANATG ATCAGGTGGC CAATTAGAGTAT TTGAATGAGT TTGAATGAGT TTGAATGAGT TTGAATGAGT CAATTTCGAG GOGATTGAG CCTTCTGAGATG CCTTCTGAGATG CCTTCTGAGATG CCTTCTGAGATG CATGTAGATG CAATTCGAG CAATTCGAG CATGTAGATTGAG CATGTAGATTGAGAT CATGTAGATTGAG TAGAGTTGAT TATATTATGA EB COTTESPOI	TATGACARAG TITTATTGTT TATARAGGTT GITAGTSATA GGTAGTGTA ACTGAGTCAC TCACCACAC C	120 180 240 300 420 480 540 660 720 720 780 840 900 960 1020 1140 1200	codons)
45 50 55 60	TGATCCTTCA ACTITITAANAGA CTITITAANAGA CTITITAANAGA TGATAANAGA TGATAANAGA TGATGGATO GGAANATAATA CACTIGGATO GGAANATAATA TTATUGGANA TTATUGGATO TTATUGGATO ACTOGATGAT TCCCAGTAAT TCCCAGTAAT TCCCAGTATAC TCCAGTATTCT TGAATTANATT CCAGTATTCT TGAATTANATT CCACCACACCC Seg ID NO Nucleic Ac Coding seq	COTARANTOA TTATCACGOT AATORATTT TATTITTOGC TACCACCTM TATCACTTT TATTITTOGC TACCACCTM TATCACTTA CTCCCCCACA GTAGARTCCT TATACCTTA CTCCCCCACA GTAGARTCCT TATACCTTA CTCCCCCACA GTAGARTCCT TATACCTTA CTCACCTCCC TATACCT GGACCTTTTAT CACACTCCCCA CACACCCAAA TATATCCCA TATACTCCC CACACCCCAAA TATATCCCA TATACATCC TATACATC TATACATCC TATACATC TATACATC TATACATC TATACATC TATACATC TATACATC TATACATC TATACATC TATACATC	TTCTATTATO ACACTATTAT TTCTATTATO ACACTATTAT TTTATAACATATT TTTAAACATATT TTAAACTATTAT ACACTATTAT TOTTACTATATA TTCTTAG TTCAATCAGA TTCTTAGTAG TTCAATCAGA TTCTTAGTAG TTCAATCAGA TTCTTAGTAG TTCAATCAGA TTCTTAGATC TCAAGCCATT AACTTCAATCA AACTTTTATATT AACTTCAATCA TTATTAAATT AAAAAAAA	ACTOCCTITO TTACTITICA TTACTITICA TTACCTAT ANGTATICAC ANGTATICAC ANGTATICAC ANGTATICAC ANGTATICAC ANGTATICAC ANGTATICAC ANGTATICAC ANGTATICAC ANTOCCACA ANGTACACA ANGACCAC ANGCACACA ANGACCAC ANGCACACAC C ANGCACACACAC ANGCACACACAC ANGCACACACACAC ANGCACACACACACAC ANGCACACACACACACACACACACACACACACACACACAC	CATOTAGTAA TCTGTAAATG ATCAGTAGTAA TCTGTAAATG ATCAGTAGTA TTAGATTAT TTAGATTAT TTAGATTAT TTAGATTAT CCTCTAGATTAG CCTCTTTGCAT CCTTTGCAT CCTTTTGCAT CCTTTGCAT CCTTTGCAT CCTTTGCAT CCTTTGCAT CCTTGCAGT TTAGATAGTA AGAGATTAGG AGAGTTAGG	TATORICARAS TITTATUTGIT TATORICARAT TATANAGGIT GATAGUTGIT GATAGUTGAT TOCHOCATA TOCHOCA	120 180 240 300 360 420 480 540 660 6720 780 900 1020 1080 1140 1200	codons)
45 50 55 60 65	TGATCCTTCA ACTITITAAAAGA GTATAAAAGA GTATAAAAGA GTATAAAAGA GTATAAAAGA GTATAAAAGA GTATAGAT GGAAAAAAAA	COTAMANTOA TTATCAGGGT ANTOATTATCAGGGT ANTOATTTGGC TACCAACTAT ANGARGACTA TTATCTTTGGC TTATCTTTTGGC TTATCTTTGGC TTATCCTCACAA ANAGACAGG TCAGCACAA ANAGACAGG TCAGCACTTTGGC TCAGCATTTGGC TCAGCATTTGGC TCAGCATTTGGC TCAGCATTCGGCCTCC TCAGCATCCCAAA TTATCTCTCA ANAAAAAAAA 54 Nuclect dd Accessione	TTCTATTATO ACACTATATO ACACTATATO TTTATANACAT ATTTCTATAGE TAACTATGT TAACTATGT TAACTATGT TAACTATGT TAACTATGT TTGTTGTTAG TCTAGC TTCTAGC TTTTTTATTATT AAAAAAAAAA	ACTOCCTITO TTACTITICA TTACTITICA TTCASCCATE AAGTATCACE AAGTATCACE AAGTATCACE AAGTATCACE AAGTATCACE AAGTATCACE AACGACACE AACGACACE AACACCACACE AACACCACACAC AACACCACACACA	CATOTAGTAA TCTGTAAATG ATCAGGTAGC CAATTAGAGTAT TTGAATGACT TCAGTTCCA TCAGTTCCA GOACTTCAG GOACTTCAG CCATTTCAG CCATTTCAG CCATTTCAG CCATTTCAG CCATTTCAG CCATTCAG CCATTCAG CCATCAG CCATAGC CTTTAGCAT CCTTCAGC CTTTAGCAT CCTTCAGC CTTTAGCAT CCTTCAGC CTTTAGCAT CCTTCAGC CTTTAGCAT CCTTCAGC CTTTAGCAT TCAGCAATGG AAAAGTTAT TATATTATGA 41 GGGGCAACGA	TATORICARAS TITTATTGTT TATORICARAS TITTATTGTT TATORICARAT TATORICARA TOTARICARAT TOCARGARAT TITTTTGGARA TACAGRACIAA TACAGRACIA	120 180 240 300 360 420 480 540 660 660 720 780 900 1020 1020 1140 1200	codons)
45 50 55 60 65	TGATCCTTCA ACTITITAANAGA TCATAANAGA TCATAANAGA TCATCAANAGA TCACCAGTTO GGAAAANAAT GACTTGGTAC GGAAATATTAA CACTTGGTAC TTCCCAGTTAC TTCCCAGTTAC TTCCCAGTTAC TTCCCAGTTAC TTCCCAGTTAC TCCCAGTTAC T	COTAMANTAA TTATCACGGT AATGAATTT TTATTTTTGGC TACCACTAT AATGATTTATC TTATTTTTGGC TTACATACTAA GTGAGATCC TTATACGTTA CTGAGATCC TTATACGTTA CTGAGATCC TTATACGTTA CTGAGATCC TGAGATCC TGAGATC TGAGATCC TGAGATC TGA	TTCANTATO ACACHATATO TTCANTATO ACACHATATO TTTANANCA ATTICTANAGE TAACTATOT TAACTATOT TAACTATOT TAACTATOT TOTTOTTATO TCANTICORA TTCANTICORA TTCANTICORA TTCANTICORA TTCANGCANT AGETCANTA AGETCANTA TAACTATATA TAATTANTO TAAAAAAAAA TTCANGCACTA TTCANGCACTA TTCANGCACTA TTAATTANTO TAAAAAAAAAAA TTCANGCACTA TTAATTANTO TAAAAAAAAAAAAA TTCANGCACTA TTAATTANTO TAAAAAAAAAAA TTCANGCACTA TTAATTANTO TAAAAAAAAAAA TTCANGCACTA TTAATTANTO TAAAAAAAAAAA TTAATTANTO TTAATTANT	ACTOCCTTTC TTACTTTCA TTCAGCCATC AAGTATCACC AAGTATCACC AAGTATCACC AAGTATCACC AAGTATCACC AAGTATCACC AACTGAAAGA TTCTCATTTAA TGCCAAGATA ATGCCAAGATA ATGCCAAGATA ATGCCAAGATA AGCCTAACAC AAGCCAAGATA AAGCCATACAC AGCCAAGATA AAGCCATACAC AGCCAAGATA AAGCCATACAC AGCCAAGATA AAGCCATACAC AGCCAAGATA AAGCCATACAC TCTCTTCTTC AGCCAAGATA AAGAA AAAA AA	CATOTAGTAA TCTGTAAATG ATCAGTGTGC CAATAAGTAA TTGAGTTGCA CAATTTCGC CAATTTCCAC CAATTTCCAC TCTGATTTCCAT CCTCTTTGCAT CCTCTTTGCAT CCTCTTTGCAT CCTCTTGCAT TTGCAT TT	TATORICARAS TITTATUTGIT TATORICARAT GITATORICATA GITATORICATA GITATORICATA GITATORICATA TOCACOGRAT TOCACOGRAT TOCACOCAC TOCACOGRAT ACATOCACA ACATOCACAC GARAACATOC TITORICATOC GITATORICATO TOCACOCACA ACATOCACAC ACAACATOC TITORICATOC GITATORICATOC TOCACACAC ACAACATOC TITORICATOC TOCACACAC ACAACATOC TITORICATOC TOCACACAC ACAACATOC TOCACACAC TOCACACAC TOCACACAC TOCACACAC TOCACACAC TOCACACAC TOCACACACAC TOCACACACAC TOCACACACAC TOCACACACAC TOCACACACACAC TOCACACACACAC TOCACACACACACACAC TOCACACACACACACACACACACACACACACACACACACA	120 180 240 300 300 300 420 480 540 660 720 780 960 1020 1080 1140 1200	eodons)
45 50 55 60 65	TORNICCTICA MICTITITA AND GIATARARAGA TICTACAGANTA GIATARAGA TORNICATAGA GIATARAGA GIACITAGA GICCITAGA GICCITAGA GICCITAGA GICCITAGA GICCITAGA GICCITAGA TICCAGATAG CICAGATAGA CICAGATAG C	COTARANTOA TTATCACGOT ANTOATTOA TTATCACGOT ANTOATTOA TATCATTOA TATCATTAC TATCATTAC TTATCOTTA CATACOTTA TACATTAC	THORANTAMO ACACHATAGO TA TAGANA ANTACTAGO ACTIVATAGO ACTIVATAGO ACTIVATAGO ACTIVATAGO ACTIVATORA ACTIVATAGO ACTIVATORA ACTIVATORA ACTIVATORA ACTIVATORA ACTIVATIVATORA ACTIVATIVATORA ACTIVATORA ACTIV	ACTOGONITO TRACTITO TRACCATO ANGTATICAC ANGTACA ANGTACAC ANA ANA ANA ANA ANA ANA ANA ANA ANA	CATOTAGATAA TCTGTAAATO ATCAGGTAC CARTAAGTAT TCTGTAAATO ATCAGGTAC CARTAGGTAC CARTAGGTAC CATTGCAG GGAGTICAT TTGAATGAT CCTGTAGATAG CCTGCCGGTT GTACAAATAG CCTGCCGGTT GAAAATGAA TTGCCATTGGC AGAATGAA TTGCCATTGG AGAATGAA TTGCCATTGG AGAATGAA TTGCCATTGG AGAATGAA TTGCCATTGG AGAATGAA TTGCCATTGG AGAATGAA TTGCCATTGG AGAATGAA AGAATTAGG AGAATTAGG AGAATTAGG AGAATTAGG AAAATGAACTC TTGTTAGACAAATGAA AAAACTGCTC TGTTTAGACA	TATOMACARAS TITTATTGTT TATOMACATA TATOMACATA TATOMACATA TOTAGORAT	120 180 240 360 360 360 420 480 660 720 960 1020 1140 1200 120 180 600 120 120 180	eodons)
45 50 55 60 65 70	TORNICCTICA MICTITITA AND GIATARARAGA TICTACAGANTA GIATARAGA TORNICATAGA GIATARAGA GIACITAGA GICCITAGA GICCITAGA GICCITAGA GICCITAGA GICCITAGA GICCITAGA TICCAGATAG CICAGATAGA CICAGATAG C	COTARANTOA TTATCACGOT ANTOATTOA TTATCACGOT ANTOATTOA TATCATTOA TATCATTAC TATCATTAC TTATCOTTA CATACOTTA TACATTAC	THORANTAMO ACACHATAGO TA TAGATAGO ACACHATAGO TA TAGATAGO ACACHATAGO ACACHATAG	ACTOGONITO TRACTITO TRACCATO AND TRACTOR TO TRACTOR AND TRACTOR AND TRACTOR AND TRACTOR AND TRACTOR AND TRACTOR TO TRACTOR AND TRACTOR A	CATOTAGATAA TCTGTAAATO ATCAGGTAC CARTAAGTAT TCTGTAAATO ATCAGGTAC CARTAGGTAC CARTAGGTAC CATTGCAG GGAGTICAT TTGAATGAT CCTGTAGATAG CCTGCCGGTT GTACAAATAG CCTGCCGGTT GAAAATGAA TTGCCATTGGC AGAATGAA TTGCCATTGG AGAATGAA TTGCCATTGG AGAATGAA TTGCCATTGG AGAATGAA TTGCCATTGG AGAATGAA TTGCCATTGG AGAATGAA TTGCCATTGG AGAATGAA AGAATTAGG AGAATTAGG AGAATTAGG AGAATTAGG AAAATGAACTC TTGTTAGACAAATGAA AAAACTGCTC TGTTTAGACA	TATORICARAS TITTATUTGIT TATORICARAT GITATORICATA GITATORICATA GITATORICATA GITATORICATA TOCACOGRAT TOCACOGRAT TOCACOCAC TOCACOGRAT ACATOCACA ACATOCACAC GARAACATOC TITORICATOC GITATORICATO TOCACOCACA ACATOCACAC ACAACATOC TITORICATOC GITATORICATOC TOCACACAC ACAACATOC TITORICATOC TOCACACAC ACAACATOC TITORICATOC TOCACACAC ACAACATOC TOCACACAC TOCACACAC TOCACACAC TOCACACAC TOCACACAC TOCACACAC TOCACACACAC TOCACACACAC TOCACACACAC TOCACACACAC TOCACACACACAC TOCACACACACAC TOCACACACACACACAC TOCACACACACACACACACACACACACACACACACACACA	120 180 240 360 360 360 420 480 660 720 960 1020 1140 1200 120 180 600 120 120 180	eodons)

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70
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      ACCARGIGAC AAGIGAGGGC CATCAGAACT GIGAGITCAG TCAGCCICCT GAATCCAGCC
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      CCCCTGAACA GCTGCTGGCA TCCCACCTGC AGCATGTGCA CCTTGATACC AGGGGCAGCA 1320
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	ANAGRACTICS	CCCACATCCA	GAGGCTGATG	CACACCCCTC	AGAAAAAAGGT	TTCCTGGACC	1560
	G1111G1G1CC	LLCCACATGGA	GCCAGTGAAT	moderate a con	ACCUPATION OF	acamanaaam	1620
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      EKEKLEKEKE TIRTELIALR OEKRELKEAI RSSPGAKLKA LEEAVATLEA OCRAKEERRI
                                                                                780
      DLELKLVAVK ERLOQSLAGG PALGLSVSSK PKSGQLSEND TLTSNGALSE RTSLTSSTPG
60
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      Nucleic Acid Accession #: NM 004126.1
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      Coding sequence: 108-129 (underlined sequences correspond to start and stop codons)
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      GGCACGAGCT CGTGCCGGCC TTCAGTTGTT TCGGGACGCG CCGAGCTTCG CCGCTCTTCC
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      AGCGGCTCCG CTGCCAGAGC TAGCCCGAGC CCGGTTCTGG GGCGAAAATG CCTGCCCTTC
                                                                                120
      ACATCHARGA TTTGCCAGAG AAGGAAAAAC TGAAAATGGA AGTTGAGCAG CTTCGCAAAG
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240

300

360

ARGTGAAGIT GCAGAGACAA CAAGTGTCTA AATGTTCTGA AGAAATAAAG AACTATATTG

AAGAACGTTC TGGAGAGGAT CCTCTAGTAA AGGGAATTCC AGAAGACAAG AACCCCTTTA

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TGAAATTAAA AGGAGACTTT CTTAAGCACC ATATAGATAG GGTTATGTAT AAAAGCATAT
      GTGCTACTCA TCTTTGCTCA CTATGCAGTC TTTTTTAAGA GAGCAGAGAG TATCAGATGT
      ACAATTATGG AAATAAGAAC ATTACTTGAG CATGACACTT CITTCAGTAT ATTGCTTGAT
      GCTTCARATA ARGTTTTGTC TT
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Protein Accession #: NP 004117
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      KNPPKEKGSC VIS
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      GGACCCAGGG AGGCGGGGG AGCCAGGCCT GGGCCCCGGG TCCCCAAGAC CCTTGTGCTC
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      GTTGTCGCCG CGGTCCTGCT GTTGGTCTCA GCTGAGTCTG CTCTGATCAC CCAACAAGAC
      CTAGCTCCCC AGCAGAGAGC GGCCCCACAA CAAAAGAGGT CCAGCCCCTC AGAGGGATTG
                                                                             240
      TGTCCACCTG GACACCATAT CTCAGAAGAC GGTAGAGATT GCATCTCCTG CAAATATGGA
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      CAGGACTATA GCACTCACTG GAATGACCTC CTTTTCTGCT TGCGCTGCAC CAGGTGTGAT
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      TCAGGTGAAG TGGAGCTAAG TCCCTGCACC ACGACCAGAA ACACAGTGTG TCAGTGCGAA
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      GAAGGCACCT TCCGGGAAGA AGATTCTCCT GAGATGTGCC GGAAGTGCCG CACAGGGTGT
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      CCCAGAGGGA TGGTCAAGGT CGGTGATTGT ACACCCTGGA GTGACATCGA ATGTGTCCAC
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      ARRIGATION GUATURTURT AGGRETICACA GTIGCAGCCG TRETCTTERT TETEGCTETE
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      AATGTCCTCA ATGAGATCGT GAGTATCTTG CAGCCCACCC AGGTCCCTGA GCAGGAAATG
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      GAAGTCCAGG AGCCAGCAGA GCCAACAGGT GTCAACATGT TGTCCCCCGG GGAGTCAGAG
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      CATCTGCTGG AACCGGCAGA AGCTGAAAGG TCTCAGAGGA GGAGGCTGCT GGTTCCAGCA
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      AATGAAGGTG ATCCCACTGA GACTCTGAGA CAGTGCTTCG ATGACTTTGC AGACTTGGTG
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      CCCTTTGACT CCTGGGAGCC GCTCATGAGG AAGTTGGGCC TCATGGACAA TGAGATAAAG
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40
                                                                           1080
      GTGGCTAAAG CTGAGGCAGC GGGCCACAGG GACACCTTGT ACACGATGCT GATAAAGTGG
      GTCABCABAR CCGGGGGGAGA TGCCTCTGTC CACACCCTGC TGGATGCCTT GGAGACGCTG 1140
      GGAGAGAGAC TTGCCAAGCA GAAGATTGAG GACCACTTGT TGAGCTCTGG AAAGTTCATG 1200
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      Protein Accession #: NP_003833.1
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      MEORGONAPA ASGARKRHGP GPREARGARP GPRVPKTLVL VVAAVLLLVS AESALITOQD
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      SGEVELSPCT TTRNTVCQCE EGTFREEDSP EMCRKCRTGC PRGMVKVGDC TPWSDIECVH
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      KESGIIIGVT VAAVVLIVAV FVCKSLLWKK VLPYLKGICS GGGGDPERVD RSSCRPGAED
                                                                             240
      NULNEIVSII, OPTOVPROEM EVOEPAEPTG VMMLSPGESE HLLEPAEAER SORRRLLVPA
                                                                             300
      NEGDPTETLE OCFDDFADLV PFDSWEPLME KLGLMDNEIK VAKABAAGHE DTLYTMLIKW
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      VNKTGRDASV HTLLDALETL GERLAKOKIE DHLLSSGKFM YLEGNADSAM S
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      Nucleic Acid Accession #: FGENESH predicted ORF
      Coding sequence: 361- 2220 (underlined sequences correspond to start and stop codons)
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      SCTGAGACTT GCGACTGCGC CCCGGACGCC CGTTGCTTCC CGGCCAACGG CGCATGTCTG
      TGCGAACACG GCTTCACTGG GGACCGCTGC ACGGATCGCC TCTGCCCCGGA CGGCTTCTAC
GGTCTCAGCT GCCAGGCCCC CTGCACCTGC GACCGGGAGC ACAGCCTCAG CTGCCACCCG
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70
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      TGCCAGGCTA CCAGCGGCCT CTGTCAGTGC GCGCCGGGTT ACACGGGCCC TCACTGTGCT
                                                                             540
      AGTOTTTGTC CTCCTGACAC CTACGGTGTC AACTGTTCTG CACGCTGCTC ATGTGAAAAT
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      GCCATCGCCT GCTCACCCAT CGACGGCGAG TGCGTCTGCA AGGAAGGTTG GCAGCGTGGT
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      AACTGCTCTG TGCCCTGCCC ACCCGGAACC TGGGGCTTCA GTTGCAATGC CAGCTGCCAG
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      TGTAGCAACA CCTGCACCTG CAAGAATGGG GGCACCTGTC TCCCTGAGAA TGGCAACTGC
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      ATTGGCATTG CAGTGCTGGG GTCCCTTGTG GTAGCCCTGG TGGCACTGTT CATTGGCTAT
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      GGCCCATTCT ACAATAAAGG GCTCATCTCT GAAGAGGAGC TCGGGGCCAG TGTGGCTTCC 1860
      CTGAGCAGTG AGAACCCATA TGCCACCATC CGGGACCTGC CCAGCTTGCC AGGGGGCCCC
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      CGGGAGAGCA GCTACATGGA GATGAAAGGC CCTCCCTCAG GATCTCCCCC CAGGCAGCCT
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      CCTCAGTTCT GGGACAGCCA GAGGCGGCGG CAACCCCAGC CACAGAGAGA CAGTGGCACC
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      TACGAGCAGC CCAGCCCCCT GATCCATGAC CGAGACTCTG TGGGCTCCCA GCCCCCTCTG
      CCTCCGGGCC TACCCCCGGG CCACTATGAC TCACCCAAGA ACAGCCACAT CCCTGGACAT 2160
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2.5
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      Protein Accession #: FGENESH prediction
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      ABTODCAPDA ROFFANGACL CENGFTGDRC TDRLCPDGFY GLSCQAPOTO DREHSLSCHP
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      MNGECSCLPG WAGLHCNESC PQDTHGPGCQ EHCLCLHGGV CQATSGLCQC APGYTGPHCA
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      SLCPPDTYGV NCSARCSCEN AIACSPIDGE CVCKEGWQRG NCSVPCPPGT WGFSCNASCQ
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      CAHEAVCSPO TGACTCTPGW HGAHCOLPCP KGOPGEGCAS RCDCDHSDGC DPVHGRCQCQ
                                                                           300
      AGWMGARCHL SCPEGLWGVN CSNTCTCKNG GTCLPENGNC VCAPGFRGPS CQRSCQPGRY
                                                                           360
      GKRCVPCKCA NHSFCHPSNG TCYCLAGWTG PDCSQRCPLG TFGANCSQPC QCGPGEKCHP
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      ETGACVCPPG HSGAPCRIGI QEPFTVMPTT PVAYNSLGAV IGIAVLGSLV VALVALFIGY
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      RHWOKGKEHH HLAVAYSSGR LDGSEYVMPD VPPSYSHYYS NPSYHTLSQC SPNPPPPNKV
                                                                           540
      PGPLFASLON PERPGGAQGH DNHTTLPADW KHRREPPPGP LDRGSSRLDR SYSYSYSNGP
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      GPFYNKGLIS EEELGASVAS LSSENPYATI RDLPSLPGGP RESSYMEMKG PPSGSPPRQP
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      POFWDSORRR OPOPORDSGT YEOPSPLIND RDSVGSOPPL PPGLPPGHYD SPKMSHIPGH
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      GTOGRACTGG CCATCGAGCA GATCCGCAAC GAGTCACTCC TGCGCCCCTA CTTCCTCGAC
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      CTGCGGCTCT ATGACACGGA GTGCGACAAC GCAAAAGGGT TGAAAGCCTT CTACGATGCA
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      ATRAAATACG GGCCGAACCA CTTGATGGTG TTTGGAGGGG TCTGTCCATC CGTCACATCC
ATCATTGCAG AGTCCCTCCA AGGCTGGAAT CTGGTGCAGC TTTCTTTTGC TGCAACCACG
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      ATTCCGGGCT GGTACGAGCC TTCTTGGTGG GAGCAGGTGC ACACGGAAGC CAACTCATCC
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      CGCTGCCTCC GGAAGAATCT GCTTGCTGCC ATGGAGGGCT ACATTGGCGT GGATTTCGAG
                                                                           960
      CCCCTGAGCT CCAAGCAGAT CAAGACCATC TCAGGAAAGA CTCCACAGCA GTATGAGAGA
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      GAGTACAACA ACAAGCGGTC AGGCGTGGGG CCCAGCAAGT TCCACGGGTA CGCCTACGAT
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      GGCATCTGGG TCATCGCCAA GACACTGCAG AGGGCCATGG AGACACTGCA TGCCAGCAGC
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      COGCACCAGC GGATCCAGGA CTTCAACTAC ACGGACCACA CGCTGGGCAG GATCATCCTC
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1260

1380

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GAGAGAATGG GGACCATTAA ATTTACTCAA TTTCAAGACA GCAGGGAGGT GAAGGTGGGA

GAGTACAACG CTGTGGCCGA CACACTGGAG ATCATCAATG ACACCATCAG GTTCCAAGGA

TOTGAACCAC CAAAAGACAA GACCATCATC CTGGAGCAGC TGCGGAAGAT CTCCCTACCT

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          AACCTTATCA TCCTTGGAGG GATGCTCTCC TATGCTTCCA TATTTCTCTT TGGCCTTGAT 1620
          GGATCCTTTG TCTCTGAAAA GACCTTTGAA ACACTTTGCA CCGTCAGGAC CTGGATTCTC 1680
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          GGAAACTTCA CTGAGAGCAC AGATGGAGGA AAGGCCATTT TAAAAAATCA CCTCGATCAA 2580
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CACGCCTACC TCCCATCCAT CGGAGGCGTG GACGCCAGCT GTGTCAGCCC CTGCGTCAGC 2760
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          CTGTAA
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          MASPERSGOP GRPPPPPPPP ARTILITIES LIEPLAPGAW GWARGAPEPP PSSPPLSING
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         RCLRKNLLAA MEGYIGVDFE PLSSKOIKTI SGKTPOQYER EYNNKRSGVG PSKFHGYAYD
GIWVIAKTLQ RAMETLHASS RHQRIQDFNY TDHTLGRIIL NAMNETNFFG VTGQVVFRNG
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          NOASTSRLEG LOSENHRLRM KITELDKOLE EVIMOLODIP EKTTYIKONH YORLNDILML
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ATCCATCAGA AAAAGTTACA AAGATCTGTG ACCAAGATGG AAACTGGTTT AGACATCCAG
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          TACACAAAAA TCTGTTCTTC TCATTTGTTT GTAACTCTGT TGTAACAATC ATTCACCTCA
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          CYCCAGTGGC CRACAACCAG GCCTTAGTAG CCACAAATCC TGTTAGTTGC AAAGTGTCCC
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      GAGCTACTCT TATCTTGGTG CCATTGCTTG GCATTGAATT TGTGCTGATT CCATGGCGAC 1620
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      AGGGTCTTTT GGTCTCTACC ATTTTCTGCT TCTTTAATGG AGAGGTTCAA GCAATTCTGA 1740
      GARGARACTG GARTCARTAC ARATCCART TTGGRARCAG CTTTTCCARC TCAGRAGCTC
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      TCCCATCTTG ATTGGGGCAG TTGACTTTTT TTTTTTCCCA GAGTGCCGTA GTCCTTTTTG 2460
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      TTCTATATCA TTAGGAAAAC ATCTTAGTTG ATGCTACAAA ACACCTTGTC AACCTCTTCC 2700
      TGTCTTACCA AACAGTGGGA GGGAATTCCT AGCTGTAAAT ATAAATTTTG TCCCTTCCAT
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Seq ID NO: 75 Protein sequence: Protein Accession #: NP_000441

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Seq ID NO: 76 Nucleotide sequence; Nucleic Acid Accession %: NM 031439 Coding sequence: 69.1235 (underlined sequences correspond to start and stop codons)

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Seq ID NO: 81 Protein sequence: Protein Accession #: NP_003458

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20	1	1	1		1		
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	DESCRIPTION OF THE PARTY OF THE	T-DESTRUCTION TO DO	TOTAL DESIGNATION OF THE PARTY	TERTODONER	DIEMINTELL.	NNNQIKRIPS	120
	KIIVKCHRIII	HPWALLAULE	TOTLIDIKENIC	THEFT	· · · · · · · · · · · · · · · · · · ·	more been been	
	GAFEDLENLK	ALAFAKNEIÖ	SIDRQAFKGL	ASLEQLYLHF	NOTELPDDDS	FQHLPKLERL	180
	DE LIMBITITURIT.	TEDOTONIUT.FC	MKRLRLDSNT	TARCINCTICATE.	ADLLETVARS	SULTREGARD	240
C0	PUNMAKTIND	VFGIFMILLED	MUCCHUDON	THEOREMA	, which is a second	Orange and a con-	300
60	YPRRIQGRSV	ATITPEELNC	ERPRITSEPQ	DADVTSGNTV	YFTCRAEGNP	KPELIWLRNN	
	NIET SMKTTLOD	TANTADDOPTM	LONGORTOG	I YOCMAKKUA	GRVKTOEVTT.	RYFGSPARPT	360
	MEDDIMIDEN	THE THE PART OF THE	- Childringo	22207744777	OD THE QUITE	GOOT ITS ONT	
	FVIQPONTEV	LVGESVTLEC	SATGHPPPRI	SWIRGDRIPL	PADEKANILLE	SGGLYIQNVV	420
	CODECEVACE	ATWINTDGVIIA	TARTIVOAND	OFTVTPODDV	VIRGOTVDFO	CEAKGNPPPV	480
	* ADDITION TAKED	OTTO DO THE	Octor D.T. Commit	TITOOTOWN	NUMERICAN	WANT/PRODOS	
	LAWIKGGSQL	PANKKHTATPS	SGTERTEGAN	THINGGARECO	WANTTOPOKA	VAHLTVQPRV	540
65	TPVFASIPSD	TTVEVGANVO	LPCSSOGEPE	PAITWNKDGV	OVTESCKFHI	SPEGFLTIND	600
	Wanaba ares	COM DIMET COS	CALCINITY OF THE	DOMEDNO	WARRETURETA	TVDRAINSTR	660
	THUFDSRPRS	PNDLLALFRY	PRDPYTVEOA	RAGEIFERTL	OLIOEHVOHG	LMVDLNGTSY	720
		TWI TRNIT COC	TAHRRVNNCS	DMCPHOPYDT	HIDOTONINI ON	DMWCACLTAR	780
			THURKANINGS	PECTUCKIKI	uncarciniandu	FAMOROBIAE	
	HYNDLVSPQY	THUTHURDOWC			GTETVTPDEO	FTHMLMOWGO	840
	HYNDLVSPQY	GENTPRGINP	HRLYNGHALP				
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70	ERLLKSVYEN FLDHDLDSTV VCGSGMTSLL SGKPLLPFAT	GFNTPRGINP VALSQARPSD MNSVYPREQI GPPTECMRDE	HRLYNGHALP GQHCSNVCSN NQLTSYIDAS NESPIPCFLA	DPPCFSVMIP NVYGSTEHEA GDHRANEQLG	PNDSRARSGA RSIRDLASHR LTSMHTLWFR	RCMFFVRSSP GLLRQGIVQR EHNRIATELL	900 960 1020
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	FILDESTV FLDHDLDSTV VCGSGMTSLL SGKPLLPFAT KLNPHWDGDT AFATAAFREG	GFNTPRGINP VALSÇARPSD NNSVYPREQI GPPTECMRDE IYYETRKIVG HTUVNPLLYR	HRLYNGHALP GQHCSNVCSN NQLTSYIDAS NESPIPCFLA AEIQHITYQH LDENFOPIAO	DPPCFSVMIP NVYGSTEHEA GDHRANEQLG WLPKILGEVG DHLPLHKAFF	PNDSRARSGA RSIRDLASHR LTSMHTLWFR MRTLGEYHGY SPFRIVNEGG	RCMFFVRSSP GLLRQGIVQR EHNRIATELL DPGINAGIFN IDPLLRGLFG	900 960 1020 1080 1140
70 75	ERLLKSVYEN FLDHDLDSTV VCGSGMTSLL SGKPLLPFAT KLMPHWDGDT AFATAAFRFG VAGKMRVPSO	GFNTPRGINP VALSÇARPSD NNSVYPREQI GPPTECMRDE IYYETRKIVG HTLVNPLLYR LINTELTERL	HRLYNGHALP GQHCSNVCSN NQLTSYIDAS NESPIPCFLA AEIQHITYQH LDENFQPIAQ FSMAHTVALD	DPPCFSVMIP NVYGSTEHEA GDHRANEQLG WLPKILGEVG DHLPLHKAFP LAAINIQRGR	PNDSRARSGA RSIRDLASHR LTSMHTLWFR MRTLGEYHGY SPFRIVNEGG DHGIPPYHDY	RCMFFVRSSP GLLRQGIVQR EHNRIATELL DPGINAGIFN IDPLLRGLFG RVYCNLSAAH	900 960 1020 1080 1140 1200
	ERLLKSVYEN FLDHDLDSTV VCGSGMTSLL SGKPLLPFAT KLMPHWDGDT AFATAAFRFG VAGKMRVPSO	GFNTPRGINP VALSÇARPSD NNSVYPREQI GPPTECMRDE IYYETRKIVG HTLVNPLLYR LINTELTERL	HRLYNGHALP GQHCSNVCSN NQLTSYIDAS NESPIPCFLA AEIQHITYQH LDENFQPIAQ FSMAHTVALD	DPPCFSVMIP NVYGSTEHEA GDHRANEQLG WLPKILGEVG DHLPLHKAFP LAAINIQRGR	PNDSRARSGA RSIRDLASHR LTSMHTLWFR MRTLGEYHGY SPFRIVNEGG DHGIPPYHDY	RCMFFVRSSP GLLRQGIVQR EHNRIATELL DPGINAGIFN	900 960 1020 1080 1140

RDGORLWYEN PGVFSPAQLT QIKQTSLARI LCDMADNITR VQSDVFRVAB FPHCKSSCDB 1320 IPRVDLRYMO DCCEDCRIEG GYMAFSHIFR GRBSLEFSVQ BDKYFKKTPP RIFISVGRQO 1330 EBLENSTSAF STRDLASTN DFFEFVLEMQ KITLDLAFOL KILLSLEST BCVDAGGESH 1440 ANNIKKKEG

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Seq ID NO: 88 <u>DNA sequence</u> Nucleic Acid Accession #: NM_004834.1

Coding sequence: 80-3577 (underlined sequences correspond to start and stop codons)

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						TGAAGAATTA	
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, ,	CIGCACCORG	TTCCTCTTAT	ATACCACTTT	ATCCCCATTC	TTTTTTTTT	TCTTACTCCA	3780
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Seq ID No: 89 Protein sequence: Protein Accession #: NP 004825.1 11 31 41 51 10 MANDSPAKSL VDIDLSSLRD PAGIFELVEV VGNGTYGQVY KGRHVKTGQL AAIKVMDVTE DEREEIKLEI NMLKKYSHHR NIATYYGAFI KKSPPGHDDQ LWLVMEFCGA GSITDLVKNT 120 KONTLKEDWI AYISREILRG LAHLHIHHVI HRDIKGQNVL LTENAEVKLV DEGVSAQLDR 180 TVGRRNTFIG TPYWMAPEVI ACDENPDATY DYRSDLWSCG ITAIEMAEGA PPLCDMHPMR 240 15 ALFLIPRNPP PRLKSKKWSK KFFSFIBGCL VKNYMQRPST EQLLKHPFIR DQPNERQVRI OLKOHIDRIR KKRGEKDETE YEYSGSEEBE EEVPEOEGEP SSIVNVPGBS TLRRDFLRLO 360 QENKERSEAL RRQQLLQEQQ LREQEEYKRQ LLAERQKRIE QQKEQRRRLE EQQRREREAR 420 ROOERBORRR BOEEKRRLEE LERRRKEEEE RRRAEEEKRR VERBOEYIRR OLEEBORHLE 480 VLQQQLLQBQ AMLLHDHRRP HPQHSQQPPP PQQERSKPSF HAPBPKAHYE PADRAREVPV 540 20 RTTSRSPVLS RRDSPLQGSG QQNSQAGQRN STSIEPRLLW ERVEKLVPRP GSGSSSGSSN 600 SGSOPGSHPG SOSGSGERFR VRSSSKSEGS PSORLENAVK KPEDKKEVFR PLKPAGEVDL 660 TALAKELRAV EDVRPPHKVT DYSSSSEESG TTDEEDDDVE QEGADESTSG PEDTRAASSL 720 NLSNGETESV KTMIVHDDVE SEPAMTPSKE GTLIVRQTQS ASSTLQKHKS SSSFTPFIDP 780 RLLQISPSSG TTVTSVVGFS CDGMRPEAIR QDPTRKGSVV NVNPTNTRPQ SDTPEIRKYK 840 25 KRINSEILCA ALWGVNLLVG TESGLMLLDR SGOGKVYPLI NRRRFOOMDV LEGLNVLVTI 900 SGKKDKLRVY YLSWLRNKIL HNDPEVEKKQ GWTTVGDLEG CVHYKVVKYE RIKFLVIALK 960 SSVEVYAWAP KPYHKFMAFK SFGELVHKPL LVDLTVEEGQ RLKVIYGSCA GFHAVDVDSG 1020 SVYDIYLPTH VRKNPHSMIQ CSIKPHAIII LPNTDGMELL VCYEDEGVYV NTYGRITKDV VLOWGEMPTS VAYIRSNOTM GWGEKAIEIR SVETGHLDGV FMHKRAORLK FLCERNDKVF 1140 30 FASVRSGGSS OVYFMTLGRT SLLSW Seq ID NO: 90 DNA sequence Nucleic Acid Accession #: none found Coding sequence: 2-71 (underlined sequences correspond to start and stop codons) 11 21 31 41 40 TTACACTICA ATTCCTTACA COGTATTICA AACAAACAGI TITGCTGAGA GGAGCTITTG 60 TCTCTCCTTA AGAAATGTT TATAAAGCTG AAAGGAAATC AAACAGTAAT CTTAAAAATG AAAACAAAAC AACCCAACAA CCTAGATAAC TACAGTGATC AGGGAGCACA GTTCAACTCC 180 TIGTTATGTT TTAGTCATAT GGCCTACTCA AACAGCTAAA TAACAACACC AGTGGCAGAT 240 ARARATCACC ATTTATCTTT CAGCTATTRA TCTTTTGAAT GRATAAACTG TGACAAACRA 300 45 ATTAACATTT TTGAACATGA AAGGCAACTT CTGCACAATC CTGTATCCAA GCAAACTTTA 360 AATTATCCAC TTAATTATTA CTTAATCTTA AAAAAAATTA GAACCCAGAA CTTTTCAATG 420 AAGCATTIGA AAGTIGAAGI GGAATTIAGG AAAGCCATAA AAATATAAAI ACIGITATCA 480 CAGCACCAGC AAGCCATAAT CTTTATACCT ATCAGTTCTA TTTCTATTAA CAGTAAAAAC 540 ATTRAGCARG ATATRAGACT ACCTGCCCAR GARTICAGTC TTTTTTCATT TTTGTTTTTC 600 50 TCAGTTCTGA GGATGTTAAT CGTCAAATTT TCTTTGGACT GCATTCCTCA CTACTTTTTG 660 CACAATGGTC TCACGTTCTC ACATTTGTTC TCGCGAATAA ATTGATAAAA GGTGTTAAGT 720 TCTGTGAATG TCTTTTTAAT TATGGGCATA ATTGTGCTTG ACTGGATAAA AACTTAAGTC 780 CACCCTTATG TITATAATAA TITCTTGAGA ACAGCAAACT GCATTTACCA TCGTAAAACA 840 ACATCTGACT TACGGGAGCT GCAGGGAAGT GGTGAGACAG TTCGAACGGC TCCTCAGAAA 900 55 TCCAGTGACC CAATTCTAAA GACCATAGCA CCTGCAAGTG ACACAACAAG CAGATTTATT 960 ATACATTTAT TAGCCTTAGC AGGCAATAAA CCAAGAATCA CTTTGAAGAC ACAGCAAAAA 1020 GTGATACACT CCGCAGATCT GAAATAGATG TGTTCTCAGA CAACAAAGTC CCTTCAGAAT 1080 CTICATGITG CATALATGIT ATGALATATIA ATALAAGIT GATTGAGA 60 Seg ID No: 91 Protein seguence: Protein Accession #: none found 31 51 41 65 YTSIPYTVFO THSFARRSFC LSL Seq ID NO: 92 DNA sequence 70 Nucleic Acid Accession #: NM 003706.1 Coding sequence: 310-1935 (underlined sequences correspond to start and stop codons) 31 41

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Seq ID No: 95 Protein sequence: Protein Accession #: CAC06611.1

55 Protein Accession #: CAC06611.

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65 Seq ID NO: 96 <u>DNA sequence</u> Nucleic Acid Accession #: NM_003654.1 Ccding sequence: 367-1602 (underlined sequences correspond to start and stop codons)

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	CCAGCTTGGA	GCAGTCCCTC	TTTGACCTCA	CCCCTTGGAG	AAGCAGCCCC	ATGAAGGTGC	360

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Seq ID No: 97 Protein sequence: Protein Accession #: NP 003645.1

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      CVRKCGLINL TVAAEACRER SHVAIKTVRV PEVNDLRALV EDPRINLKVI OLVRDPRGIL
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      ASRSETFROT YRLWRLWYGT GRKPYNLDVT QLTTVCEDFS NSVSTGLMRP PWLKGKYMLV
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      RYEDLARNPM KKTEEIYGFL GIPLDSHVAR WIQNNTRGDP TLGKHKYGTV RNSAATAEKW
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Seq ID NO: 98 DNA sequence Nucleic Acid Accession #: NM_002852.1

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Coding sequence: 68-1213 (underlined sequences correspond to start and stop codons)

47

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31

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	TATGTACCTT	ATTACAAAAA	AAATGATGAA	AACATATTTA	TACTACAAGG	TGACTTAACA	1680
10	ACTATAAATG	TAGTTTATGT	GTTATAATCG	AATGTCACGT	TTTTGAGAAG	ATAGTCATAT	1740
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15 Seq ID No: 99 Protein sequence: Protein Accession #: NP_002843.1

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			MVSLGRWTHL				300
25	IVPEGGILQI	GQEKNGCCVG	GGFDETLAFS	GRLTGFNIWD	SVLSNEEIRE	TGGAESCHIR	360
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Seq ID NO: 100 <u>DNA sequence</u>
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Coding sequence: 72-3758 [underlined sequences correspond to start and stop ccdoms) 30

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			GTTCTCTTTC				1980
			TATGATATGG				2040
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			AATGAAGTAC				2220
			ATGGAAGATG				2280
			GATAACTATG				2340
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                                                                           720
```

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GCCAGATGGT CATCATAGTC ACGGTGGTGT CGGTGTTGCT GTCCCTGTTC GTGACATCTG
TCCTGCTCTG CTTCATCTTC GGCCAGCACT TGCGCCAGCA GCGGATGGGC ACCTACGGGG 840
TGCGAGGGC TTGGAGGAG CTGCCCCAGG CCTTCCGGCC ATAGCAACCA TGAGTGGCAT
GGCCACCACC ACGGTGGTCA CTGGAACTCA GTGTGACTCC TCAGGGTTGA GGTCCAGCCC
960
TGGCTGAAGG ACTGTGACAG GCAGCAGAGA CTTGGGACAT TGCCTTTTCT AGCCCGAATA 1020
CAAACACCTG GACTT
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Seq ID No: 103 Protein sequence: Protein Accession #: NP 000864.1

10

	1	11	21	31	41	51	
	1	1	1	1	1	1	
						TCNOPEVGGL	60
15						PPRQVILTLQ	120
			PLDSLTLFLF				180
			GNIFHKHSAP		DSQMVIIVTV	VSVLLSLFVT	240
	SVLLCFIFGQ	HLRQQRMGTY	GVRAAWRRLP	QAFRP			

20 Seq ID NO: 104 DNA sequence Nucleic Acid Accession #: NM_001795.2 Coding sequence: 121-2475 (underlined sequences correspond to start and stop codons)

25							
23	1	11	21	31	41	51	
	1	max an a a a a a a		an amon agam	07.000000000	100020000	60
			CACAGAGCTC			TCCTGGGAAG	120
							180
30			TGCTAACCCT			GCTGGCAGTG	240
30			AGATTGGATT				300
							360
			TGTAGGCAAG				420
			ATATGTGGGC GCTGGACCGG				- 480
35			TGGTGAAAAC				540
33			CTGGCCTGTG				600
			GACCTCAGTC				660
			CTCTGTCATG				720
							720
40			TATTATCACA				840
40			GGAAGCGCGA				
			TCTGCAAGAC				900
			GCCTGAAGAC				960
			GCCCCAGAAC				1020 -
40			CATTGAGACA				1080
45			TGAATACATC				1140
			ATACATGAGC				1200
						CCACTTCCAG	1260
			GCCTCTGATT				1320
						GTTCTTCCGA	1380
50						CTACCCCTGG	
						AGGAAAAGAA	1500
			TGAAGTTTTG				1560
			GTGTGAGAAC				1620
			AACACCACGA				1680
55			GGATAATCAC				1740
			TACCAAGGTC				1800
	GGGATGCCAA	GTCGCACGGG	CACCAGCACG	CTGACCGTGG	CCGTGTGCAA	GTGCAACGAG	1860
			CGAGGATATG				1920
	GTGGTAGCCA	TCTTACTCTG	CATCCTCACC	ATCACAGTGA	TCACCCTGCT	CATCTTCCTG	1980
60	CGGCGGCGGC	TCCGGAAGCA	GGCCCGCGCG	CACGGCAAGA	GCGTGCCGGA	GATCCACGAG	2040
	CAGCTGGTCA	CCTACGACGA	GGAGGGCGGC	GGCGAGATGG	ACACCACCAG	CTACGATGTG	2100
			CCGCGGCGGG				2160
	CGGCCTTCCC	TCTATGCGCA	GGTGCAGAAG	CCACCGAGGC	ACCCCCCTGG	GGCACACGGA	2220
	GGGCCCGGGG	AGATGGCAGC	CATGATCGAG	GTGAAGAAGG	ACGAGGCGGA	CCACGACGGC	2280
65	GACGGCCCCC	CCTACGACAC	GCTGCACATC	TACGGCTACG	AGGGCTCCGA	GTCCATAGCC	2340
	GAGTCCCTCA	GCTCCCTGGG	CACCGACTCA	TCCGACTCTG	ACCTGGATTA	CGACTTCCTT	2400
	AACGACTGGG	GACCCAGGTT	TAAGATGCTG	GCTGAGCTGT	ACGGCTCGGA	CCCCCGGGAG	2460
			CGAGGTCACT				2520
			GCACCACAGC				2580
70			CCAGAGACCT				2640
	CCTGAAATAT	CCAGGAATAT	ATGTCAGTGA	TGACTATICT	CAAATGCTGG	CARATCCAGG	2700
			AGACATCCAC				2760
			TCCCCAAGGC				2820
			TCCCTGAACG				2880
75			CCTGGACAGC				2940
			CATCATGCCC				3000

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CCATACTCCA CTCCAAGTGC CCCACCACTC CCCAACCCCT CTCCAGGCCT GTCAAGAGGG 3060
      AGGAAGGGGC CCCATGGCAG CTCCTGACCT TGGGTCCTGA AGTGACCTCA CTGGCCTGCC 3120
      ATGCCAGTAA CTGTGCTGTA CTGAGCACTG AACCACATTC AGGGAAATGG CTTATTAAAC
      TTTGAAGCAA CTGTGAATTC ATTCTGGAGG GGCAGTGGAG ATCAGGAGTG ACAGATCACA
                                                                            3240
      GGGTGAGGGC CACCTCCACA CCCACCCCCT CTGGAGAAGG CCTGGAAGAG CTGAGACCTT
                                                                            3300
      GCTTTGAGAC TCCTCAGCAC CCCTCCAGTT TTGCCTGAGA AGGGGCAGAT GTTCCCGGAG
                                                                            3360
      CAGAAGACGT CTCCCCTTCT CTGCCTCACC TGGTCGCCAA TCCATGCTCT CTTTCTTTTC 3420
      TCTGTCTACT CCTTATCCCT TGGTTTAGAG GAACCCAAGA TGTGGCCTTT AGCAAAACTG
                                                                            3480
      GACAATGTCC AMACCCACTC ATGACTGCAT GACGGAGCCG AGCCATGTGT CTTTACACCT 3540
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      GCCCTGCCCA ACCTCTGTGG TCACCCATGC ATCTTCCACT GGAACGTTTC ACTGCAAACA
      CACCTTGGAG AAGTGGCATC AGTCAACAGA GAGGGGCAGG GAAGGAGACA CCAAGCTCAC 3720
      CCTTCGTCAT GGACCGAGGT TCCCACTCTG GGCAAAGCCC CTCACACTGC AAGGGATTGT 3780 AGATAACACT GACTTGTTTG TTTTAACCAA TAACTAGCTT CTTATAATGA TTTTTTTACT 3840
15
      AATGATACTT ACAAGTTTCT AGCTCTCACA GACATATAGA ATAAGGGTTT TTGCATAATA 3900
      AGCAGGTTGT TATTTAGGTT AACAATATTA ATTCAGGTTT TTTAGTTGGA AAAACAATTC 3960
      CTGTAACCTT CTATITTCTA TAATTGTAGT AATTGCTCTA CAGATAATGT CTATATATTG
                                                                            4020
      GCCAAACTGG TGCATGACAA GTACTGTATT TTTTTATACC TAAATAAAGA AAAATCTTTA 4080
      GCCTGGGCAA CAAAAAA
20
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Seq ID No: 105 Protein sequence: Protein Accession #: NP_001786.1

- 25 1.1 21 31 41 51 MORIMMILAT SGACIGILAV AAVAAAGANP AORDTHSLIP THRROKRDWI WNOMHIDEEK NTSLPHHVGK IKSSVSRKNA KYLLKGEYVG KVFRVDAETG DVFAIERLDR ENISEYHLTA VIVDKDTGEN LETPSSFTIK VHDVNDNWPV FTHRLFNASV PESSAVGTSV ISVTAVDADD PTVGDHASVM YOILKGKEYF AIDNSGRIIT ITKSLDREKO ARYEIVVEAR DAOGLRGDSG 180 30 240 TATVLVTLQD INDNFPFFTQ TKYTFVVPED TRVGTSVGSL FVEDPDEPQN RMTKYSILRG 300 DYQDAFTIET NPAHNEGIIK PMKPLDYEYI QQYSFIVEAT DPTIDLRYMS PPAGNRAQVI 360 INITOVDEPP IFQQPFYHFQ LKENQKKPLI GTVLAMDPDA ARHSIGYSIR RTSDKGQFFR 420 VTKKGDIYNE KELDREVYPW YNLTVEAKEL DSTGTPTGKE SIVQVHIEVL DENDNAPEFA 480 35 KPYQPKVCEN AVHQQLVLQI SAIDKDITPR NVKFKFTLNT ENNFTLTDNH DNTANITVKY 540 GOFDREHTKY HFLPVVISDN GMPSRTGTST LTVAVCKCNE OGEFTFCEDM AAQVGVSIQA 600 VVAILLCILT ITVITLLIFL RRRLRKQARA HGKSVPEIHE QLVTYDEEGG GEMDTTSYDV 660 SVLNSVRRGG AKPPRPALDA RPSLYAQVQK PPRHAPGAHG GPGEMAAMIE VKKDBADHDG 720 DGPPYDTLHI YGYEGSESIA ESLSSLGTDS SDSDVDYDFL NDWGPRFKML AELYGSDPRE 780 40 RIJV
- Seq ID NO: 106 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 1-474 (underlined sequences correspond to start and stop codons)

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	ACAGTACTCT	GTGCAAAAAA	CCTGGTGAAA	AAGGATTTTT	TCCGACTTCC	TGATCCATTT	60
	GCTAAGGTGG	TGGTTGATGG	ATCTGGGCAA	TGCCATTCTA	CAGATACTGT	GAAGAATACG	120
50	CTTGATCCAA	AGTGGAATCA	GCATTATGAC	CTGTATATTG	GAAAGTCTGA	TTCAGTTACG	180
	ATCAGTGTAT	GGAATCACAA	GAAGATCCAT	AAGAAACAAG	GTGCTGGATT	TCTCGGTTGT	240
	GTTCGTCTTC	TTTCCAATGC	CATCAACCGC	CTCAAAGACA	CTGGTTATCA	GAGGTTGGAT	300
	TTATGCAAAC	TCGGGCCAAA	TGACAATGAT	ACAGTTAGAG	GACAGATAGT	AGTAAGTCTT	360
	CAGTCCAGAG	ACCGAATAGG	CACAGGAGGA	CAAGTTGTGG	ACTGCAGTCG	TTTATTTGAT	420
55	AACGATTTAC	CAGACGGAGC	TCATTATTTG	TGGACTTGGA	AAGATAGATG	TTAATGACTG	480
	GAAGGTAAAC	ACCCGGTTAA	AACACTGTAC	ACCAGACAGC	AACATTGTCA	AATGGTTCTG	540
	GAAAGCTGTG	GAGTTTTTTG	ATGAAGAGCG	ACGAGCAAGA	TTGCTTCAGT	TTGTGACAGG	600
	ATCCTCTCGA	GTGCCTCTGC	AGGGCTTCAA	AGCATTGCAA	GGTGCTGCAG	GCCCGAGACT	660
	CTTTACCATA	CACCAGATTG	ATGCCTGCAC	TAACAACCTG	CCGAAAGCCC	ACACTTGCTT	720
60	CAATCGAATA	GACATTCCAC	CCTATGAAAG	CTATGAAAAG	CTATATGAAA	AGCTGCTAAC	780
	AGCCATTGAA	GAAACATGTG	GATTTGCTGT	GGAATGACAA	GCTTCAAGGA	TTTACCCAGG	840
	AC						

65 Seq ID No: 107 Protein sequence:
65 Protein Accession #: none found

1 11 21 31 41 51

70 TVLCARHLVK KDFFRLFDFF AKVVVDGSGQ CHSTDTVRNT LDFKNRQHVD LYIGKSDSVT 6
ISVNNHRKIH KKÇJARFILG VRLLENBAINE LKDTOYORLD LCKLGFROND TVRGQIVVSL 12
QSRDGIGTGG QVVCCSREPD NDLDGARHYL MYKRGY.

Seq ID NO: 108 DNA sequence

75 Nucleic Acid Accession #: NM 002318.1
Coding sequence: 248-2572 (underlined sequences correspond to start and stop codons)

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)						GAGACCAGAG	60
		TGCTCGAGAA					120
						CCTGCTGCTT	180
		CCTGTCCCTC					240
10	GACAGGGATG	GAGAGGCCTC	TGTGCTCCCA	CCTCTGCAGC	TGCCTGGCTA	TGCTGGCCCT	300
10						AGTACTTCCA	360
	GCAACCGGCT	CCTGAGTATC	ACCAGCCCCA	GGCCCCCGCC	AACGTGGCCA	AGATTCAGCT	420
						ACTATGATGG	480
						TCGTCTGCCG	540
15		TATGTGGAGG					600
13		TGGTTAGACA					660 720
		GGCTGGGGCG					780
						AGATAGAGAA ACCGCAAGCG	
		ATGGAGGGCT					900
20		TGGACGGCCA					960
20							1020
		TCCATGGACT					1080
	COGGGGATTC	TCACTGGACC	CCAMCAACAA	TOTAL COTTO	ATCTCCAGCT	maccaccam	1140
						TCCGGAAAGC	1200
25		GAGCAACCCC					1260
23		CTCAAAAATG					1320
						CAGTCACTGG	1380
						GCACAGGCAA	1440
							1500
30						TGCGCCTGAA	1560
50	CGGCGGCCGC	AATCCCTACG	AGGGCCGAGT	GGAGGTGCTG	GTGGAGAGAA	ACGGGTCCCT	1620
						TGGTCTGCCG	1680
						GGCACGGAGA	1740
						AGCTGTCCCT	1800
35	GGCGCACTGC	CGCCACGACG	GGGAGGACGT	GGCCTGCCCC	CAGGGCGGAG	TGCAGTACGG	1860
	GGCCGGAGTT	GCCTGCTCAG	AAACCGCCCC	TGACCTGGTC	CTCAATGCGG	AGATGGTGCA	1920
	GCAGACCACC	TACCTGGAGG	ACCGGCCCAT	GTTCATGCTG	CAGTGTGCCA	TGGAGGAGAA	1980
	CTGCCTCTCG	GCCTCAGCCG	CGCAGACCGA	CCCCACCACG	GGCTACCGCC	GGCTCCTGCG	2040
							2100
40						TCACCCACTA	2160
						GCTTCTGCTT	2220
						ACTTCGGCGA	2280
		ACCATGGGCT					2340
		GACGTGCCCC					2400
45						GCTATGACGG	2460
						AGACGGAAAA	2520
						<u>AA</u> AGAAGCCT	
							2640
60	CTGAGTCTGA	ACGAATGCCA	CGTGCCCTCA	CCCAGCCCGG	CCCCCACCCT	GTCCAGACCC	2700
50		GTCTAAGCTC					2760
		TGGGGCCTGA					2820
		AAGAGCCAGT					2880
		AAGCCACCGA					2940
55	ACACGTGGAC	AAATGCGGGC	TCATCAGCCC	CCCCAGAGAG	GGTCAGGCCG	AACCCCATTT	3000
22		TAGGTCATTT					3060
		ATTATAGTCA					3120 3180
	CAGACTTGGT	GUTTUCCTCT	CCACAACCCC	CACCCCTTGT	TTTTCAAGAT	ACTATTATTA	3180
						ATCTGGGCCC	3340
60	TIGGAAGTAC	AAATCTAAGG GTGGGTTTTT	AAAAACCAAC	CCACIGIGIA	AGTGACTCAT	CTICCIGITIG	3360
00							3420
	GAAAGATTTA		CATCACAGAC	ACTIACACAT	MCTIGAAACT	TOGAATAAAA	3420
	GMAAGATITA	10					
	Com TD No.	109 Protein	. commondo.				
65	sed ID NO:		I sequence:				

65 Protein Accession #: NP_002309.1

	1	11	21	31	41	51	
	Ī	1	1	1	1	1	
70	MERPLCSHLC	SCLAMLALLS	PLSLAQYDSW	PHYPEYFOOP	APEYHOPOAP	ANVAKIQLEL	60
	AGOKRKHSEG	RVEVYYDGQW	GTVCDDDFSI	HAAHVVCREL	GYVEAKSWTA	SSSYGKGEGP	120
		NEATLAACTS					180
		ILSTYRKRTP					240
	TYNTKVYKMF	ASRRKQRYWP	FSMDCTGTEA	HISSCKLGPQ	VSLDPMKNVT	CENGLPAVVS	300
75		GPSRFRKAYK					360
	SUVCRELGEG	SAKEAVTGSR	LGOGIGPIHL	NEIOCTGNEK	SIIDCKFNAE	SOGCNHEEDA	420

```
GVRCNTPAMG LOKKLRINGG RNPYEGRVEV LVERNGSLVW GNVCGONWGI VEAMVVCROL
                                                                            480
      GLGFASNAFO ETWYWHGDVN SNKVVMSGVK CSGTELSLAH CRHDGEDVAC PQGGVQYGAG
                                                                            540
      VACSETAPDL VLNAEMVQQT TYLEDRPMFM LQCAMEENCL SASAAQTDPT TGYRRLLRFS
                                                                            600
      SOIHNINGOSD FRPKNGRHAW INHDCHRHYH SMEVFTHYDL INLINGTEVAE GHKASFCLED
                                                                            660
      TECEGDIOKN YECANFODOG ITMGCWDMYR HDIDCOWVDI TDVPPGDYLF OVVINPNFEV
                                                                            720
      AESDYSNNIM KCRSRYDGHR INMYNCHIGG SFSEETEKKF EHFSGLLNNQ LSPQ
      Seq ID NO: 110 DNA sequence
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      CGGACGCGTG GGTCGACCCA CGCGTCCGCC CACGCGTCCG TATGGACAGA GCCTCCACTG
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15
      GCTGCTGCCT GCCCGCCACA TACCCAGCTG ACATGGGCAC CGCAGGAGCC ATGCAGCTGT
                                                                            120
      CTGGGTGATC CTGGGCTTCC TCCTGTTCCG AGGCCACAAC TCCCAGCCCA CAATGACCCA
                                                                            180
      ACCTCTAGCT CTCAGGGAGG CCTTGGCGGT CTAAGTCTGA CCACAGAGCC AGTTTCTTCC
                                                                            240
      ACCCAGGATA CATCCCTTCC TCAGAGGCTA ACAGGCCAAG CCATCTGTCC AGCACTGGTA
                                                                            300
      CCCAGGCGCA GGTGTCCCCA GCAGTGGAAG AGACGGAGGC ACAAGCAGAG ACACATTTCA
                                                                            360
20
      ACTGTTCCCC CCAATTCAAC CACCATGAGC CTGAGCATGA GGGAAGATGC GACCATCCTG
                                                                            420
      CCAGCCCCAC GTCAGAGACT GTGCTCACTG TGGCTGCATT TGGGATGGAG TCGGGTGGAG
                                                                            480
      GCCCACTCTG GCTAGGGGGC GGCAGGCTGA GAGCTCACCT GTTCAGCAGA GAAGTGGAAC
                                                                            540
      CACTITIGGIC CIGGAGCCIG TCTACCACAG IGTTATCAGC TICATIGICA TCCIGGIGGI
                                                                            600
      GTGGTGATCA TCCTAGTTGG TGTGGTCAGC CTGAGGGTTC AGTGTCGGAA GAGCAAGGAG
                                                                            660
25
      TCTGAAGATC CCAGAACCTG GGAGTACAGG GCGTGTCTGA CAAGCTGGTC ACAGACCATG
                                                                            720
      GCGAGAACGA CAGCATCGCC CATTATCACA TGGAAGACAT CACACGACTT AGGGCAACAC
                                                                            780
      GCACTCAGCA GCGAGCATCA AAGGAGCCTA CGCATGGCCC AGACTGAGAG CAAGCACAAA
                                                                            840
      agac
30
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      Protein Accession #: none found, CAT 73007 3
                             21
                                        31
                                                    41
35
      RTRGSTHASA HASVWTEPPL AAACPPHTQL TWAPQEPCSC LGDPGLPPVP RPQLPAHNDP 60
TSSSQGGLGG LSLTTEPVSS TQDTSLPQRL TGQAICPALV PRRRCPQQWK RRRHKQRHIS 120
      TVPPNSTIMS LSMREDATIL PAPRORLCSL WLHLGWSRVE AHSG
40
      Seg ID NO: 112 DNA seguence
      Nucleic Acid Accession #: NM 005424.1
      Coding sequence: 37-3453 (underlined sequences correspond to start and stop codons)
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                 11
                             21
                                        31
      CGCTCGTCCT GGCTGGCCTG GGTCGGCCTC TGGAGTATGG TCTGGCGGGT GCCCCCTTTC
      TTGCTCCCCA TCCTCTTCTT GGCTTCTCAT GTGGGCGCGG CGGTGGACCT GACGCTGCTG
                                                                            120
      GCCAACCTGC GGCTCACGGA CCCCCAGCGC TTCTTCCTGA CTTGCGTGTC TGGGGAGGCC
                                                                            180
50
      GGGGGGGGA GGGGCTCGGA CGCCTGGGGC CCGCCCCTGC TGCTGGAGAA GGACGACCGT
                                                                            240
      ATCGTGCGCA CCCCGCCCGG GCCACCCCTG CGCCTGGCGC GCAACGGTTC GCACCAGGTC
      ACGCTTCGCG GCTTCTCCAA GCCCTCGGAC CTCGTGGGCG TCTTCTCCTG CGTGGGCGGT
                                                                            360
      GCTGGGGCGC GGCGCACGCG CGTCATCTAC GTGCACAACA GCCCTGGAGC CCACCTGCTT
                                                                            420
      CCAGACAAGG TCACACACAC TGTGAACAAA GGTGACACCG CTGTACTTTC TGCACGTGTG
                                                                            480
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      CACAAGGAGA AGCAGACAGA CGTGATCTGG AAGAGCAACG GATCCTACTT CTACACCCTG
                                                                            540
      GACTGGCATG AAGCCCAGGA TGGGCGGTTC CTGCTGCAGC TCCCAAATGT GCAGCCACCA
                                                                            600
      TCGAGCGGCA TCTACAGTGC CACTTACCTG GAAGCCAGCC CCCTGGGCAG CGCCTTCTTT
                                                                            660
      CGGCTCATCG TGCGGGGTTG TGGGGCTGGG CGCTGGGGGC CAGGCTGTAC CAAGGAGTGC
                                                                            720
      CCAGGTTGCC TACATGGAGG TGTCTGCCAC GACCATGACG GCGAATGTGT ATGCCCCCCT
                                                                            780
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CAGGAGCAGT GCCCAGGCAT ATCAGGCTGC CGGGGCCTCA CCTTCTGCCT CCCAGACCCC
                                                                            840
                                                                            900
      TATGGCTGCT CTTGTGGATC TGGCTGGAGA GGAAGCCAGT GCCAAGAAGC TTGTGCCCCT
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                                                                           1080
65
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      COGATCAACT GTGCAGCTGC AGGGAACCCC TTCCCCGTGC GGGGCAGCAT AGAGCTACGC 1200
      AAGCCAGACG GCACTGTGCT CCTGTCCACC AAGGCCATTG TGGAGCCAGA GAAGACCACA
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      GCTGAGTTCG AGGTGCCCCG CTTGGTTCTT GCGGACAGTG GGTTCTGGGA GTGCCGTGTG
                                                                           1320
      TECRCATCTG GCGGCCAAGA CAGCCGGCGC TTCAAGGTCA ATGTGAAAGT GCCCCCCGTG 1380
70
      CCCCTGGCTG CACCTCGGCT CCTGACCAAG CAGAGCCGCC AGCTTGTGGT CTCCCCGCTG 1440
      GTCTCGTTCT CTGGGGATGG ACCCATCTCC ACTGTCCGCC TGCACTACCG GCCCCAGGAC 1500
      AGTACCATGG ACTGGTCGAC CATTGTGGTG GACCCCAGTG AGAACGTGAC GTTAATGAAC 1560
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75
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      CCCTTGGTGC CCGGGCCACT GGTGGGCGAC GGTTTCCTGC TGCGCCTGTG GGACGGGACA 1800
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      GGCCCGGCCT CGCCCCCTGC ACACGTGCTT CTGCCCCCCA GTGGGCCTCC AGCCCCCCGA
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      CACCTCCACG CCCAGGCCCT CTCAGACTCC GAGATCCAGC TGACATGGAA GCACCCGGAG
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      GCTCTGCCTG GGCCAATATC CAAGTACGTT GTGGAGGTGC AGGTGGCTGG GGGTGCAGGA
                                                                            2100
      GACCCACTGT GGATAGACGT GGACAGGCCT GAGGAGACAA GCACCATCAT CCGTGGCCTC
      AACGCCAGCA CGCGCTACCT CTTCCGCATG CGGGCCAGCA TTCAGGGGCT CGGGGACTGG
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      AGCAACACAG TAGAAGAGTC CACCCTGGGC AACGGGCTGC AGGCTGAGGG CCCAGTCCAA
                                                                            2280
      GAGAGCCGGG CAGCTGAAGA GGGCCTGGAT CAGCAGCTGA TCCTGGCGGT GGTGGGCTCC
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10
      GTGTCTGCCA CCTGCCTCAC CATCCTGGCC GCCCTTTTAA CCCTGGTGTG CATCCGCAGA
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      AGCTGCCTGC ATCGGAGACG CACCTTCACC TACCAGTCAG GCTCGGGCGA GGAGACCATC
                                                                            2460
      CTGCAGTTCA GCTCAGGGAC CTTGACACTT ACCCGGCGGC CAAAACTGCA GCCCGAGCCC
                                                                            2520
      CTGAGCTACC CAGTGCTAGA GTGGGAGGAC ATCACCTTTG AGGACCTCAT CGGGGAGGGG
                                                                           2580
      AACTTCGGCC AGGTCATCCG GGCCATGATC AAGAAGGACG GGCTGAAGAT GAACGCAGCC
                                                                            2640
15
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      GAAGTTCTGT GCAAATTGGG GCATCACCCC AACATCATCA ACCTCCTGGG GGCCTGTAAG
                                                                            2760
      AACCGAGGTT ACTTGTATAT CGCTATTGAA TATGCCCCCT ACGGGAACCT GCTAGATTTT 2820
      CTGCGGAAAA GCCGGGTCCT AGAGACTGAC CCAGCTTTTG CTCGAGAGCA TGGGACAGCC 2880
      TCTACCCTTA GCTCCCGGCA GCTGCTGCGT TTCGCCAGTG ATGCGGCCAA TGGCATGCAG 2940
20
      TACCTGAGTG AGAAGCAGTT CATCCACAGG GACCTGGCTG CCCGGAATGT GCTGGTCGGA 3000
      GAGAACCTAG CCTCCAAGAT TGCAGACTTC GGCCTTTCTC GGGGAGAGGA GGTTTATGTG 3060
      AAGAAGACGA TGGGGCGTCT CCCTGTGCGC TGGATGGCCA TTGAGTCCCT GAACTACAGT 3120
      GTCTATACCA CCAAGAGTGA TGTCTGGTCC TTTGGAGTCC TTCTTTGGGA GATAGTGAGC 3180
      CTTGGAGGTA CACCCTACTG TGGCATGACC TGTGCCGAGC TCTATGAAAA GCTGCCCCAG 3240
GGCTACCGCA TGGAGCAGCC TCGAAACTGT GACGATGAAG TGTACGAGCT GATGCGTCAG 3300
25
      TGCTGGCGGG ACCGTCCCTA TGAGCGACCC CCCTTTGCCC AGATTGCGCT ACAGCTAGGC 3360
      CGCATGCTGG AAGCCAGGAA GGCCTATGTG AACATGTCGC TGTTTGAGAA CTTCACTTAC
                                                                           3420
      GCGGGCATTG ATGCCACAGC TGAGGAGGCC TYAGCTGCCA TCCAGCCAGA ACGTGGCTCT 3440
GCTGGCCGGA GCAAACTCTG CTGTCTAACC TGTGACCAGT CTGACCCTTA CAGCCTCTGA 3540
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      CTTAAGCTGC CTCAAGGAAT TTTTTTAACT TAAGGGAGAA AAAAAGGGAT CTGGGGGATGG 3600
      GGTGGGCTTA GGGGAACTGG GTTCCCATGC TTTGTAGGTG TCTCATAGCT ATCCTGGGCA
                                                                            3660
      TCCTTCTTTC TAGTTCAGCT GCCCCACAGG TGTGTTTCCC ATCCCACTGC TCCCCCAACA
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Seq ID No: 117 Protein sequence: Protein Accession #: NP_031387.1

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Seq ID NO: 118 DNA Sequence
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Coding sequence: 112-1593 (underlined sequences correspond to start and stop codons)

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      CTACTCCTCG GGAGAGATAT TTTCTTATGT TTATTCGGAG AATTTGGAGA AGTGATTGAA
                                                                          700
                                                                          840
      CTTTTCAAGA CATTGGAAAC AAATAGAACA CAATATAATT TACATTAAAA AATAATTTCT
      ACCAAAATGG AAAGGAAATG TICTATGTTG TICAGGCTAG GAGTATATTG GTTCGAAATC
                                                                          900
      CCAGGGAAAA AAATAAAAAT AAAAAATTAA AGGATTGTTG ATAAAA
55
      Seq ID No: 123 Protein sequence:
      Protein Accession #: none found
                            21
                                       31
                                                  41
                                                             51
                 11
      EKLGETPLVP EQDNSVTSIP EIPRWGSQST MSTLQMSLQA ESKATITPSG SVISKFNSTT
      SSATPOAFDS SSAVVFIFVS TAVVVLVILT MTVLGLVKLC FHESPSSOPR KESMGPPGLE
      SDPEPAALGS SSAHCTNINGV KVGDCDLRDR ABGALLAESP LGSSDA
      Seq ID NO: 124 DNA sequence
65
      Nucleic Acid Accession #: NM 006500.1
      Coding sequence: 27-1967 (underlined sequences correspond to start and stop codons)
                            21
                                       31
                                                  41
                 11
70
      ACTIGORICI CGCCCTCCGG CCAAGCAIGG GGCTTCCCAG GCTGGTCTGC GCCTTCTTGC
                                                                          60
      TOGOCCOCCTG CTGCTGCTGT CCTCGCGTCG CGGGTGTGCC CGGAGAGGCT GAGCAGCCTG
                                                                          120
      CGCCTGAGCT GGTGGAGGTG GAAGTGGGCA GCACAGCCCT TCTGAAGTGC GGCCTCTCCC
                                                                          180
      AGTCCCAAGG CAACCTCAGC CATGTCGACT GGTTTTCTGT CCACAAGGAG AAGCGGACGC
                                                                          240
75
      TCATCTTCCG TGTGCGCCAG GGCCAGGGCC AGAGCGAACC TGGGGAGTAC GAGCAGCGGC
                                                                          300
      TCAGCCTCCA GGACAGAGGG GCTACTCTGG CCCTGACTCA AGTCACCCCC CAAGACGAGC
                                                                          360
```

	GCATCTTCTT	GTGCCAGGGC	AAGCGCCCTC	GGTCCCAGGA	GTACCGCATC	CAGCTCCGCG	420
	TCTACAAAGC	TCCGGAGGAG	CCAAACATCC	AGGTCAACCC	CCTGGGCATC	CCTGTGAACA	480
	GTAAGGAGCC	TGAGGAGGTC	GCTACCTGTG	TAGGGAGGAA	CGGGTACCCC	ATTCCTCAAG	540
					GAACCGGGTC		600
5	CGTCCCAGAC	TGTGGAGTCG	ACTGCTTTCT	ACACCTTGCA	GAGTATTCTG	AAGGCACAGC	660
	TGGTTAAAGA	AGACAAAGAT	GCCCAGTTTT	ACTGTGAGCT	CAACTACCGG	CTGCCCAGTG	720
	GGAACCACAT	GAAGGAGTCC	AGGGAAGTCA	CCGTCCCTGT	TTTCTACCCG	ACAGAAAAAG	780
					GGACCGCGTG		840
					CAAGCAGAAC		900
10	GGGAGGCAGA	GGAAGAGACA	ACCAACGACA	ACGGGGTCCT	GGTGCTGGAG	CCTGCCCGGA	960
	AGGAACACAG	TGGGCGCTAT	GAATGTCAGG	CCTGGAACTT	GGACACCATG	ATATCGCTGC	1020
					CGTCCGAGTG		1080
	CCCCTGAGAG	ACAGGAAGGC	AGCAGCCTCA	CCCTGACCTG	TGAGGCAGAG	AGTAGCCAGG	1140
	ACCTCGAGTT	CCACTGGCTG	PGPGFGFGF	CAGACCAGGT	GCTGGAAAGG	GGGCCTGTGC	1200
15	TTCACTTCCA	TGACCTGAAA	CCCCACCCAC	GAGGGGGCTA	TCGCTGCGTG	COCTCHICTIC	1260
10	CCACCATACC	CGGCCTGAAC	CCCACACACAC	TECTCAACCT	GGCCATTTTT	GGCCCCCCTT	1320
	GGATCCCATT	CAACCACACAC	ANGGRATAGOG	TODADAGAGAA	TATGGTGTTG	AATCTCTCTT	1380
	CTCAACCCTC	7.000C1.000C	CCCCCCACCA	TOTOCTGGAA	CGTCAACGGC	ACCCCAACTC	1440
	DAGRAGEGIC	AGGGGCACCCC	CONCERCON	CCACCCTCAA	TGTCCTCGTG	ACCCCCCCARGC	1500
20	TOTTOGRACIA	AGGTGTTCAA	TGCTCGCCCT	CCDACGACCT	GGGCAAAAAC	ACCAGCATCC	1560
20					CTCCAACACA		1620
					CACCTCCACA		1680
	TUAGCACTTU	CACTGCCAGT	CCTCATACCA	TOOTSOOTOT	GATTGTGTGC	AMOORGOMOO	1740
	TGCCGGAGCC	GGAGAGCCGG	GGCGIGGICA	TCGIGGCIGI	GATIGIGIGE	ATCCTGGTCC	1800
25	TGGCGGTGCT	GGGCGCTGTC	CTCTATTTCC	TCTATAAGAA	GGGCAAGCTG	CCGTGCAGGC	
23	GCTCAGGGAA	GCAGGAGATC	ACGCIGCCCC	CGTCTCGTAA	GACCGAACTT	GTAGTTGAAG	1860
					GGGCAGCAGC		1920
					GCATTAGCCC		1980
	CAGCTCCCTT	CCCTGCCTGG	ACCATTCCCA	GCTCCCTGCT	CACTCTTCTC	TCAGCCAAAG	2040
20	CCTCCAAAGG	GACTAGAGAG	AAGCCTCCTG	CTCCCCTCAC	CTGCACACCC	CCTTTCAGAG	2100
30	GGCCACTGGG	TTAGGACCTG	AGGACCTCAC	TTGGCCCTGC	AAGCCGCTTT	TCAGGGACCA	2160
					AAGCAAGGAG		2220
					TTTACACACA		2280
					TCTGAGCTGG		2340
	CAAAGGCTGG	CTTCCACCAT	CCAGGTGCAC	CACTGAAGTG	AGGACACACC	GGAGCCAGGC	2400
35	GCCTGCTCAT	GTTGAAGTGC	GCTGTTCACA	CCCGCTCCGG	AGAGCACCCC	AGCGGCATCC	2460
						GTCTCCTGTG	2520
					CCTTAAAAGA		2580
						GGCGGGCGGA	2640
	TCACAAAGTC	AGGACGAGAC	CATCCTGGCT	AACACGGTGA	AACCCTGTCT	CTACTAAAAA	2700
40	TACAAAAAAA	AATTAGCTAG	GCGTAGTGGT	TGGCACCTAT	AGTCCCAGCT	ACTCGGAAGG	2760
	CTGAAGCAGG	AGAATGGTAT	GAATCCAGGA	GGTGGAGCTT	GCAGTGAGCC	GAGACCGTGC	2820
	CACTGCACTC	CAGCCTGGGC	AACACAGCGA	GACTCCGTCT	CGAGGAAAAA	AAAAGAAAAG	2880
	ACGCGTACCT	GCGGTGAGGA	AGCTGGGCGC	TGTTTTCGAG	TTCAGGTGAA	TTAGCCTCAA	2940
	TCCCCGTGTT	CACTTGCTCC	CATAGCCCTC	TTGATGGATC	ACGTAAAACT	GAAAGGCAGC	3000
45	GGGGAGCAGA	CARAGATGAG	GTCTACACTG	TCCTTCATGG	GGATTAAAGC	TATGGTTATA	3060
	TTAGCACCAA	ACTTCTACAA	ACCAAGCTCA	GGGCCCAAC	CCTAGAAGGG	CCCAAATGAG	3120
	AGAATGGTAC	TTAGGGATGG	AAAACGGGGC	CTGGCTAGAG	CTTCGGGTGT	GTGTGTCTGT	3180
					CAGGTGTGTA		3240
					TATATATATA		3300
50	ABACCTTAAT	TGTCCCAGAA	AATCATACAT	TOCTTTTTTA	TTCTACATGG	GTACCACAGG	3360
					AACCGTTTCC		3420
	ACCIGGGGG	COTOTOTOT	CCTTCTCLCC	ABBTGCCTCA	AGCTCTACCA	CACCAGACAG	3480
					GCACGAAGGG		3540
				TTTCCGTCCA		CCIGGCAGGC	3540
55	TGTTMGCAGG	MOCIMIGICO	CITCCIATOG	TITCCGTCCM	CII		
22							
		125 Proteir					
	Protein Acc	ession #: 1	VP_000491.1				
60	_						
00	1	11	21	31	41	51	
	1	1	1	1	1		
	MGLPRLVCAP	LLAACCCCPR	VAGVEGEABQ	PWEEDARAEA	GSTALLKCGL	agaggniaHV	60
	DWFSVHKEKR	TLIFRVRQGQ	GUSEPGEYEQ	KLSLQDRGAT	LALTQVTPQD	EKIFLCUGKR	120
CE	PRSQEYRIQL	KVYKAPEEPN	TONNERGIEA	NEKEPEEVAT	CVGRNGYPIP	QVIWYKNGRP	180
65	LKEEKNRVHI	QSSQTVESSG	LYTLQSILKA	ÖTAKBDKDYÖ	PYCELNYRLP	SGNHMKESRE	240
					HFSISKQNPS		300
					NYVSDVRVSP		360
					AGGGYRCVAS		420
~~	QLVKLAIFGP	PWMAFKERKV	MAKENWATNT	SCEASGHPRP	TISWNVNGTA	SEQDQDPQRV	480
70					TLTPDSNTTT		540
					FLYKKGKLPC	RRSGKQEITL	600
	PPSRKTELVV	EAKSDKPEE	MGLLQGSSGD	KRAPGDQGEK	YIDLRH		

⁷⁵ Seq ID NO: 126 <u>DNA sequence</u> Nucleic Acid Accession #: NM_001955.1

Coding sequence: 337-975 (underlined sequences correspond to start and stop codons)

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11
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      GGAGCTGTTT ACCCCCACTC TANTAGGGGT TCAATATAAA AAGCCGGCAG AGAGCTGTCC
      AAGTCAGACG CGCCTCTGCA TCTGCGCCAG GCGAACGGGT CCTGCGCCTC CTGCAGTCCC
                                                                             120
      AGCTCTCCAC CACCGCCGCG TGCGCCTGCA GACGCTCCGC TCGCTGCCTT CTCTCCTGGC
                                                                             180
      AGGCGCTGCC TTTTCTCCCC GTTAAAGGC ACTTGGGCTG AAGGATCGCT TTGAGATCTG
                                                                             240
10
      AGGAACCOGC AGCGCTTTGA GGGACCTGAA GCTGTTTTTC TTCGTTTTCC TTTGGGTTCA
      GTTTGAACGG GAGGTTTTTG ATCCCTTTTT TTCAGAATGG ATTATTTGCT CATGATTTTC
TCTCTGCTGT TTGTGGCTTG CCAAGGAGCT CCAGAACAG CAGTCTTAGG CGCTGAGCTC
                                                                             360
                                                                             420
      AGCCCGGTGG GTGAGAACGG CGGCGAGAAA CCCACTCCCA GTCCACCCTG GCGGCTCCGC
                                                                             490
      CGGTCCAAGC GCTGCTCCTG CTCGTCCCTG ATGGATAAAG AGTGTGTCTA CTTCTGCCAC
                                                                             540
15
      CIGGACATCA TITGGGTCAA CACTCCCGAG CACGITGITC CGTATGGACT IGGAAGCCCI
                                                                             600
      AGGTCCAAGA GAGCCTTGGA GAATTTACTT CCCACAAAGG CAACAGACCG TGAGAATAGA
                                                                             660
      TGCCAATGTG CTAGCCAAAA AGACAAGAAG TGCTGGAATT TTTGCCAAGC AGGAAAAGAA
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      CTCAGGGCTG AAGACATTAT GGAGAAAGAC TGGAATAATC ATAAGAAAGG AAAAGACTGT
      TCCAAGCTTG GGAAAAAGTG TATTTATCAG CAGTTAGTGA GAGGAAGAAA AATCAGAAGA
                                                                             840
20
      AGTTCAGAGG AACACCTAAG ACAAACCAGG TCGGAGACCA TGAGAAACAG CGTCAAATCA
                                                                             900
      TOTTTCATG ATCCCAAGCT GAAAGGCAAG CCCTCCAGAG AGCGTTATGT GACCCACAAC
                                                                             960
      CGAGCACATT GGTGACAGAC TTCGGGGCCT GTCTGAAGCC ATAGCCTCCA CGGAGAGCCC
                                                                            1020
      TGTGGCCGAC TCTGCACTCT CCACCCTGGC TGGGATCAGA GCAGGAGCAT CCTCTGCTGG 1080
      TTCCTGACTG GCAAAGGACC AGCGTCCTCG TTCAAAACAT TCCAAGAAAG GTTAAGGAGT 1140
25
      TCCCCCAACC ATCTTCACTG GCTTCCATCA GTGGTAACTG CTTTGGTCTC TTCTTTCATC 1200
      TGGGGATGAC AATGGACCTC TCAGCAGAAA CACACAGTCA CATTCGAATT C
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Seq ID No: 127 Protein sequence: Protein Accession #: NP_001946.1

30

45

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	MDYLLMIPSL	LFVACQGAPE	TAVLGAELSA	VGENGGEKPT	PSPPWRLRRS	KRCSCSSLMD	60
35	KECVYFCHLD	IIWVNTPEHV	VPYGLGSPRS	KRALENLLPT	KATDRENRCQ	CASQKDKKCW	120
	NFCQAGKELR	AEDIMEKDWN	NHKKĠKDCSK	LGKKCIYQQL	VRGRKIRRSS	EEHLROTRSE	180
	TMRNSVKSSF	HDPKLKGKPS	RERYVTHNRA	HW			

40 Seq ID No: 128 <u>DNA sequence</u>
Nucleic Acid Accession #: NM_001721.1
Coding sequence: 34-2061 (underlined sequences correspond to start and stop codons)

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21
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                                                  41
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      CTTCTTCTCA AAAGATCACA GCAAAAGAAG AAAATGTCAC CAAATAATTA CAAAGAACGG
50
      CTTTTTGTTT TGACCAAAAC AAACCTTTCC TACTATGAAT ATGACAAAAT GAAAAGGGGC
                                                                          180
      AGCAGAAAAG GATCCATTGA AATTAAGAAA ATCAGATGTG TGGAGAAAGT AAATCTCGAG
                                                                          240
      GAGCAGACGC CTGTAGAGAG ACAGTACCCA TTTCAGATTG TCTATAAAGA TGGGCTTCTC
                                                                          300
      TATGTCTATG CATCAAATGA AGAGAGCCGA AGTCAGTGGT TGAAAGCATT ACAAAAAGAG
                                                                          360
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55
      TTCCTGTGTT GCCAGCAGAG CTGTAAAGCA GCCCCAGGAT GTACCCTCTG GGAAGCATAT
                                                                          480
      GCTAATCTGC ATACTGCAGT CAATGAAGAG AAACACAGAG TTCCCACCTT CCCAGACAGA
                                                                          540
      GTGCTGRAGA TACCTCGGGC AGTTCCTGTT CTCRAAATGG ATGCACCATC TTCRAGTACC
                                                                          600
      ACTCTAGCCC AATATGACAA CGAATCAAAG AAAAACTATG GCTCCCAGCC ACCATCTTCA
                                                                          660
      AGTACCAGTO TAGCGCAATA TGACAGCAAC TCAAAGAAAA TCTATGGCTC CCAGCCAAAC
                                                                          720
60
      TTCAACATGC AGTATATTCC AAGGGAAGAC TTCCCTGACT GGTGGCAAGT AAGAAAACTG
                                                                          790
      ARRIGTAGUR GURGUNGTGA AGRICTTGUR AGURGTARCU ARRARGARAG ARRIGTGART
                                                                          840
      CACACCACCT CAAAGATTTC ATGGGAATTC CCTGAGTCAA GTTCATCTGA AGAAGAGGAA
                                                                          900
      AACCTGGATG ATTATGACTG GTTTGCTGGT AACATCTCCA GATCACAATC TGAACAGTTA
                                                                          960
      CTCAGACAAA AGGGAAAAGA AGGAGCATTT ATGGTTAGAA ATTCGAGCCA AGTGGGAATG
                                                                         1020
65
      TACACAGTGT CCTTATTTAG TAAGGCTGTG AATGATAAAA AAGGAACTGT CAAACATTAC 1080
      CACGTGCATA CARATGCTGA GAACAAATTA TACCTGGCAG AAAACTACTG TTTTGATTCC
                                                                         1140
      ATTCCARAGO TTATTCATTA TCATCARCAC AATTCAGCAG GCATGATCAC ACGGCTCCGC 1200
      CACCUTGTGT CAACAAAGGC CAACAAGGTC CCCGACTCTG TGTCCCTGGG AAATGGAATC
                                                                         1260
      TOGGAACTGA AAAGAGAAGA GATTACCTTG TTGAAGGAGC TGGGAAGTGG CCAGTTTGGA
                                                                         1320
70
      GTGGTCCAGC TGGGCAAGTG GAAGGGGCAG TATGATGTTG CTGTTAAGAT GATCAAGGAG
                                                                         1380
      GGCTCCATGT CAGAAGATGA ATTCTTTCAG GAGGCCCAGA CTATGATGAA ACTCAGCCAT
                                                                         1440
      CCCAAGCTGG TTAAATTCTA TGGACTGTGT TCAAAGGAAT ACCCCATATA CATAGTGACT
                                                                         1500
      GAATATATAA GCAATGGCTG CTTGCTGAAT TACCTGAGGA GTCACGGAAA AGGACTTGAA 1560
      CUTTCCCAGC TOTTAGAAAT GTGCTACGAT GTCTGTGAAG GCATGGCCTT CTTGGAGAGT
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75
      CACCAATTCA TACACOGGGA CTTGGCTGCT CGTAACTGCT TGGTGGACAG AGATCTCTGT 1680
      GTGARAGTAT CTGACTTTGG AATGACAAGG TATGTTCTTG ATGACCAGTA TGTCAGTTCA 1740
```

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GTCGGAACAA AGTTTCCAGT CAAGTGGTCA GCTCCAGAGG TGTTTCATTA CTTCAAATAC 1800
      AGCAGCAAGT CAGACGTATG GCCATTTGGG ATCCTGATGT GGGAGGTGTT CAGCCTGGGG 1860
      AAGCAGCCCT ATGACTTGTA TGACAACTCC CAGGTGGTTC TGAAGGTCTC CCAGGGCCAC
                                                                               1920
      AGGCTTTACC GGCCCCACCT GGCATCGGAC ACCATCTACC AGATCATGTA CAGCTGCTGG 1980
      CACGACCTTC CACAAAAGC TCCCACATTT CAGCACTCC TGTCTTCCAT TGAACCACTT 2040
CGGGANAAG ACAACCATTG AAGAAGAAT TAGGAGTGCT GATAAGAATG AATATAGATG 2100
      CTGGCCAGCA TTTTCATTCA TTTTAAGGAA AGTAGGAAGG CATAAGTAAT TTTAGCTAGT 2160
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      ATTCCCTIGA AATTTAGATC AAATTAGTAA TTTTGTTTTA TGCTGCTCCT GATATAACAC 2280
10
      TTTCCAGCCT ATAGCAGAAG CACATTTTCA GACTGCAATA TAGAGACTGT GTTCATGTGT 2340
      AAAGACTGAG CAGAACTGAA AAATTACTTA TTGGATATTC ATTCTTTTCT TTATATTGTC 2400
      ATTGTCACAA CAATTAAATA TACTACCAAG TACAGAAATG TGGAAAAAAA AAACCG
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Seq ID No: 129 Protein sequence: 15 Protein Accession #: NP 001712.1

41 51 21 31 20 MDTKSILEEL LLKRSQCKKK MSPNNYKERL FVLTKTNLSY YEYDKMKRGS RKGSIEIKKI RCVEKVNLEE CTPVERCYPF OIVYKDGLLY VYASNEESRS OWLKALOKEI RGNPHLLVKY 120 HSGFFVDGKF LCCQQSCKAA PGCTLWEAYA NLHTAVNEEK HRVPTFPDRV LKIPRAVPVL 180 KMDAPSSSTT LAGYDNESKK NYGSQPPSSS TSLAGYDSNS KKIYGSQFNF NMQYIPREDF 240 PDWWQVRKLK SSSSSEDVAS SNQKERNVNH TTSKISWEFP ESSSSEREEN LDDYDWFAGN 300 ISRSOSEOLL ROKGKEGAFM VRNSSOVGMY TVSLFSKAVN DKKGTVKHYH VHTNAENKLY LAENYCFDSI PKLIHYHQHN SAGMITRLRH PVSTKANKVP DSVSLGNGIW ELKREBITLL 420 KELGSGQFGV VQLGKNKGQY DVAVKMIKEG SMSEDEFFQE AQTMMKLSHP KLVKFYGVCS 480 KEYPIYIVTE YISNGCLLNY LRSHGKGLEP SQLLEMCYDV CBGMAFLESH QFIHRDLAAR 540 NCLVDRDLCV KVSDFGMTRY VLDDQYVSSV GTKFPVKWSA PEVFHYFKYS SKSDVWAFGI 600 30 LMWEVFSLGK QPYDLYDNSQ VVLKVSQGHR LYRPHLASDT IYQIMYSCWH ELPEKRPTFQ 660 OLLSSIEPLR EKDKH

Sec ID NO: 130 DNA secuence Nucleic Acid Accession #: NM_012072.2

35 Coding sequence: 149-2107 (underlined sequences correspond to start and stop codons)

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	TCCCGCAGAG	GGCCACACAG	AGACCGGGAT	GCCACCTCC	ATGGGCCTGC	TGCTGCTGCT	180	
	GCTGCTGCTC	CTGACCCAGC	CCGGGGCGGG	GACGGGAGCT	GACACGGAGG	CGGTGGTCTG	240	
45	CGTGGGGACC	GCCTGCTACA	CGGCCCACTC	GGGCAAGCTG	AGCGCTGCCG	AGGCCCAGAA	300	
	CCACTGCAAC	CAGAACGGGG	GCAACCTGGC	CACTGTGAAG	AGCAAGGAGG	AGGCCCAGCA	360	
	CGTCCAGCGA	GTACTGGCCC	AGCTCCTGAG	GCGGGAGGCA	GCCCTGACGG	CGAGGATGAG	420	
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50	GCTCCGGAAC	TOGTGCATCT	CCAAGCGCTG	TGTGTCTCTG	CTGCTGGACC	TGTCCCAGCC	600	
			CCAAGTGGTC				660	
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55						TCGACTGGGG	900	
			TCAGCCCCAA				960	
			GGGGGGATGG				1020	
			TGACCTGTGC				1080	
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60			CGAGTCAGCT				1200	
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			AGGGCTGCAC				1380	
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65			TCTGCGACAG				1500	
			GGGTGCTGGC				1560	
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			CAACAGCCAG				1680	
			GACCTTCGCT				1740	
70			GTGGGTCCTC				1800	
			CCCAGGAGCC				1860	
			GGCAAAAGCT				1920	
			CCCTGGCTCT				1980	
			AGAAGAAGCC				2040	
75			GGGCCATGGA				2100	
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	CARACRATTC	TARGETTOT	CCTTABAGGC	CCCTTGGAAC	ATGCAGGTAT	TTTCTACGGG	2280
	TCTTTTTTTTTT	mooman name	CA A CONCINCIO	CHARGOCANCO	CACCGTGGGC	ATTTCGTGAC TTCCGGATCA CACTTCCACC TGTTTCTCTT	2240
	TOTTTGATGI	TCCTGMMGTG	GAMGCIGIGI	GIIGGCGIGC	THOMAS 043 3	MITTEGIONE.	2400
5	TCTATAATGA	TIGITACICC	CCCTCCCTTT	TCAAATTCCA	ATGTGACCAA	TTCCGGATCA	2400
J	GGGTGTGAGG	AGGCTGGGGC	TAAGGGGCTC	COUTGAATAT	CTTCTCTGCT	CACTICCACC TGTTTCTCTT GGTTTTTTGG CCATTTCGCC	2460
	ATCTAAGAGG	AAAAGGTGAG	TTGCTCATGC	TGATTAGGAT	TGAAATGATT	TGTTTCTCTT	2520
	CCTAGGATGA	AAACTAAATC	AATTAATTAT	TCAATTAGGT	AAGAAGATCT	GGTTTTTTGG	2580
	TCAAAGGGAA	CATGTTCGGA	CTGGAAACAT	TTCTTTACAT	TTGCATTCCT	CCATTTCGCC	2640
	AGCACAAGTC	TTGCTAAATG	TGATACTGTT	GACATCCTCC	AGAATGGCCA	GAAGTGCAAT	2700
10	TAACCTCTTA	GGTGGCAAGG	AGGCAGGAAG	TGCCTCTTTA	GTTCTTACAT	TTCTAATAGC	2760
						AAGTGCATTA	
	Chaamamaa	TO A CTCACA	THE STREET ACCOUNT	cccmacaaca	AGAGAGGGCCA	GGGATTTGTT	2880
	CAGGIGITIG	TORROTCACA	CAMPOCA A AMO	WA COURT COMM	A COLOR OF CR		2940
	CACAGATACT	IGANIIAAII	CHICCHMIG	TACIGMOGII	MCCACACAC.I	CONCINCOUN	3000
15	TGTGATCAAC	ACTAACAAGG	AAACAAATTC	AAGGACAACC	TGTCTTTGAG		
15						GCCAGTGCTC	3060
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	TGAACGGGAG	ATGATGCACT	GTGTTTTGAA	AGTIGTCATT	TTAAAGCATT	TTAGCACAGT	3180
	TCATAGTCCA	CAGTTGATGC	AGCATCCTGA	GATTTTAAAT	CCTGAAGTGT	GGGTGGCGCA	3240
	CACACCAAGT	AGGGAGCTAG	TCAGGCAGTT	TGCTTAAGGA	ACTITIGATE	TCTGTCTCTT	3300
20	TTCCTTAAAA	TTGGGGGGTAA	GGAGGGAAGG	AAGAGGGAAA	GAGATGACTA	ACTAAAATCA	3360
	THETTACAGE	AAAAACTGCT	CARACCCATT	TARATTATAT	CCTCATTTTA	AAAGTTACAT	3420
	TOTAL DESIGNATION OF THE PARTY	MANAGE COMME	Characteria	mccama cocom	CCTCMITTIN	AAAGTTACAT TCTCTCTCTC	3480
	TOCAMATAT	THETCCCIAI	AGE CE CE CE	PODGE COOL	AGAGACACGG	Caccacacac	3540
	TCTCTCTCAC	ACACACACAC	MUMUMUMUMU	ACACACACAC	MUMUMCACGG	CACCATICIG	
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25	TGAGTATCTC	TGGGAGGCCT	CATGTCTCCT	GTGGGCTTTT	TACCACCACT		3660
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	GGTTTTGCCT	TAGCAATGCA	TCGGTCTCTG	AGGTGACACT	CTGGAGTGGT		3780
	CAAGGTGCAG	GGTTAATACT	CTTGCCAGTT	TTGAAATATA	GATGCTATGG	TTCAGATIGT	3840
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					CCATTTGGCA		4020
	000000000	CECENT COMOL	mamaman naa	WOOGG TOTOT	amaamamaan	GAGCAGCCAT	4080
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	** I GT I I GUC	NA CHOTOLOGO	ACCOMACCOM	CAGAGATCGA	COTTOTOOTC	TGAGTTCTAA	6600
75	MIGITICCCA	ANCIGIONGG	AGGGMAGGCT	CHOMMICGH	CTTTCTTCTC	CTTTGAGCTT	6660
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Seq ID No: 131 Protein sequence: Protein Accession #: NP_036204.1

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Seq ID NO: 132 DNA sequence Nucleic Acid Accession #: NM 000963.1

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Coding sequence: 135-1949 (underlined sequences correspond to start and stop codons)

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25						51	
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Seq ID NO: 136 <u>DNA sequence</u> Nucleic Acid Accession #: NM_003003.1 Coding sequence: 304-2451 (underlined sequences correspond to start and stop codons) 15

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      ARATCAGAAT ATGGGATTTG TTTGCCTTTT ACATTTTGTT TAATTCCTGA TTTTAAAGCC
                                                                             3660
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      TGCTCTATCT GGTACAGGCC CTTATTTTTT CAGCTTTTTA TGGGAAAAGC AGGTTATTTG
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      AGAATCTOTC CAGAACTTGC ATAGGGGATG GCCTCCACGA TAAGGACATG CAACACGTGT
                                                                            3780
      TTCTGTGTGC AGCAGAGGCC GTGTTTTTCA TGCCAAACCC CACGCGGCTG TCAACTGTGT
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      GCGTGGTAGG CATGGAGATC CTGGTTGTGC CGTCTCAGCT CCGCTCTGAA GGCACTGTGT
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      GOGTGCTGCG TGACTGGAGA GCTGTGTGGA GGCCATGTGT GCCCCGTGCA GGGATCAGGA 3960
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      GGGCGGGGGA GGGACCGAGC AGCCCTCTTG CCCGGTCGGG TCAGCCCTAG TGGCTGCCTG
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      CACACTGTAG ACGTCCCAGG GCCTGTGCTG TGATCACCTG CCTTTGGACC ACATTTGTGT
                                                                             4080
      TTGCTCTTAG AGATCGAGCT CCTCAGTGGT ACCTGAAGCC TTTGCTTCCG GAAAGCGCGG 4140
      TAGGGTTCGT AGGTAGGGCT AGTAGGTAGG GTTAGTAGGT AGGGCTAGTA GGTAGGGCTA 4200
      GTAGGTAGGG TTAGTAGGTA GGGTTCGTAG GTAGGGCTGG TAGGTAGGGT TAGTAGGTAG
                                                                            4260
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                                                                            4320
      GGTAGGGCTA GTAGGTAGGG TTAGTAGGTA GGGTTCGTAG GTAGGGCTGG TAGGTAGGGT
                                                                            4380
      TAGTAGGTAG GGCTAGTAGG TAGGGTTCGT AGGTAGGGCT AGTAGGTAGG GTTAGTAGGT
                                                                            4440
      AGGGCTAGTA GGTAGGCTA GTAGGTAGGG TTAGTAGGTA GGGTTCGTAG GTAGGGCTGG
                                                                            4500
      TAGGTAGGGT TAGTAGGTAG GGCTAGTAGG TAGGGCTAGT AGGTAGGCT AGTAGGTAGG
                                                                            4560
20
      GTTAGTAGGT AGGCCTAGTA GGTAGGCCTA GTAGGTAGGG TTAGTAGGTA GGGTTCGTAG 4620
      GTAGGGCTGG TAGGTAGGGT TAGTAGGTAG GGCTAGTAGG TAGGGCTAGT AGGTAGGGCT
                                                                            4680
                                                                            4740
      AGTAGGTAGG GCTAGTAGGT AGGGCTAGTA GGTAGGGCTA GTAGGTAGGG CTAGTAGGTA
      GGGTTGGTAG GTAGGGTTGG TAGGTAGGGT TCGTAGGTAG GGTTAGTAG GGGTCTGTGC 4800
TGCTTCCACC TGGTGCTTC TGTTCCCAAA TCACAAGGGC CTGAAGGTGG TCCTGTCTT 4800
CCCTTTCTCT TCTCCTGTGT CTCAGATGGC GATTTTGGCTA AGAAAATGGT 4920
2.5
      TCACTCAACA GTCCTCATGT GCCCAGAGAT GTTTATAGAA CTGTTTGAAT TGCAGCCATC 4980
      CCCTGCCCC TCCCAGGCTG AAGATCTGTT CTTTTTAAGT TGATTCGGGA GTGGCATTCT
                                                                            5040
      TTTATACCCA AAGACTGTAG TGCATCTTGA AGAGCTCAAA GCACATGACC GCACAAATGC 5100
      TTACAGGGTT TCCTCCCGAG TAATCCAATC TCACTCCCCT TGTAAGGGAA TTCTGGGGCA
                                                                            5160
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      GCTATGGTTT GAGTATGCAG TTTGCATCGT GTTTCTACCT TTAGTACCTT GCCACTCTTT
                                                                            5220
      TAAAACGCTG CTGTCATTTC CCATTTCTTA GTACTAATGA TTCTTTGATT CTCCCTCTAT
                                                                            5280
      TATGTCTTAA TTCACTTCC TTCCTAAATT TGTTATTTGC ATATCAAATT CTGTAAATGT
                                                                             5340
      TTTGTAAACA TATTACCTCA CTTGGTAATA CAATACTGAT AGTCTTTAAA AGATTTTTT 5400
      ATTGTTATCA ATAATAAATG TGAACTATTT AAAG
35
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Seq ID No: 137 Protein sequence: Protein Accession #: NP 002994.1

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	1	1	1		1		
				PLIPMFVGSD			60
				RTLHIBAYNE			120
				QYTSNIKKGK			180
45				AALKEGLSGD			240
				KGKIPKDEHI			300
				WHHHDKDGRP			360
	EALLRYVLSV	NEERLRRCEE	NTKVFGRPIS	SWICLVDLEG	LIMRHLWRPG	VKALLRIIEV	420
				FIDDNTRRKF			480
50				ELENEDLKLW			540
				POPPKKDSLG			600
	LGRDYSMVES	PLICKEGESV	QGSHVTRWPG	FYILOWKFHS	MPACAASSLP	RVDDVLASLQ	660
	VSSHKCKVMY	YTEVIGSEDF	RGSMTSLESS	HSGFSQLSAA	TTSSSQSHSS	SMISR	

55 Seq ID NO: 138 <u>DNA sequence</u> Nucleic Acid Accession #: NM_004181.1 Coding sequence: 22-670 (underlined sequences correspond to start and stop codons)

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                                       31
                                                   47
                                                              51
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      GOTOGOGGC CAGTOGOGCT TOSTOGACCT GCTGGGGCTG GAAGAGGAGT CTCTGGGCTC
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      GGTGCCAGCG CCTGCCTGCG CGCTGCTGCT GCTGTTTCCC CTCACGGCCC AGCATGAGAA
                                                                           180
65
      CTTCAGGAAA AAGCAGATTG AAGAGCTGAA GGGACAAGAA GTTAGTCCTA AAGTGTACTT
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      CATGARGCAG ACCATTGGGA ATTCCTGTGG CACAATCGGA CTTATTCACG CAGTGGCCAA
      TAATCAAGAC AAACTGGGAT TTGAGGATGG ATCAGTTCTG AAACAGTTTC TTTCTGAAAC
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      AGAGAAAATG TCCCCTGAAG ACAGAGCAAA ATGCTTTGAA AAGAATGAGG CCATACAGGC
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      AGCCCATGAT GCCGTGGCAC AGGAAGGCCA ATGTCGGGTA GATGACAAGG TGAATTTCCA
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70
      TTTTATTCTG TTTAACAACG TGGATGGCCA CCTCTATGAA CTTGATGGAC GAATGCCTTT
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                                                                           600
      CAGAGAATTC ACCOAGCGTG AGCAAGGAGA AGTCCGCTTC TCTGCCGTGG CTCTCTGCAA
                                                                           660
      GGCAGCCTAA TGCTCTGTGG GAGGGACTTT GCTGATTTCC CCTCTTCCCT TCAACATGAA
                                                                           720
                                                                           780
      AATATATACC CCCCATGCAG TCTAAAATGC TTCAGTACTT GTGAAACACA GCTGTTCTTC
75
      TGTTCTGCAG ACACGCCTTC CCCTCAGCCA CACCCAGGCA CTTAAGCACA AGCAGAGTGC
                                                                           840
      ACAGCTGTCC ACTGGGCCAT TGTGGTGTGA GCTTCAGATG GTGAAGCATT CTCCCCAGTG
                                                                           900
```

TATGTCTTGT ATCCGATATC TAACGCTTTA AATGGCTACT TTGGTTTCTG TCTGTAAGTT 960 AAGACCTTGG ATGTGGTTAT GTTGTCCTAA AGAATAAATT TTGCTGATAG TAGC

Seq ID No: 139 Protein sequence: Protein Accession #: NP_004172.1

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	MLNKVLSRLG	VAGOWRFVDV	LGLEEESLGS	VPAPACALLL	LFPLTAOHEN	FRKKOIEELK	60
	GQEVSPKVYF	MKOTIGNSCG	TIGLIHAVAN	NODKLGFEDG	SVLKQFLSET	BKMSPEDRAK	120
	CFEKNEAIOA	AHDAVAOEGO	CRVDDKVNFH	FILFNNVDGH	LYELDGRMPF	PVNHGASSED	180
	TLLKDAAKVC	REFTEREQUE	VRFSAVALCK	AA			

15 Seg ID NO: 140 DNA seguence

Seq ID NO: 140 DNA sequence Nucleic Acid Accession #: NM 000201.1 Coding sequence: 58-1656 (underlined sequences correspond to start and stop codons)

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	COCCCC CACC	CGACGCTGAG	Cancerterate in	ACTORCACACTO	GCNACCTCAC	CCTCCCTATC	60
25		GCCCCGGCC					120
		GCAATGCCCA					180
		TGGTGACATG					240
		CTAAAAAGGA					300
		AAGAAGATAG					360
30		CCTTCCTCAC					420
		AGCCAGTGGG					480
		ACCTCACCGT					540
		AGCCCGCTGA					600
		CGTGCCGCAC					660
35		CCCCCTACCA					720
		GGGTCCTAGA					780
		TCTCGGAGGC					840
		ATGGCAACGA					900
		CCCAGCGGCT					960
40		TGACCATCTA					1020
		GGACCGAGGT					1080
		TTCCAGCCCA					1140
		ACGGGCGCAG					1200
		ACCAGACCCG					1260
45		GAAACTGGAC					1320
		CATTGCCCGA					1380
		TGACTGTCAC					1440
	ACTCAAGGGG	AGGTCACCCG	CGAGGTGACC	GTGAATGTGC	TCTCCCCCCC	GTATGAGATT	1500
	GTCATCATCA	CTGTGGTAGC	AGCCGCAGTC	ATAATGGGCA	CTGCAGGCCT	CAGCACGTAC	1560
50	CTCTATAACC	GCCAGCGGAA	GATCAAGAAA	TACAGACTAC	AACAGGCCCA	AAAAGGGACC	1620
	CCCATGAAAC	CGAACACACA	AGCCACGCCT	CCCTGAACCT	ATCCCGGGAC	AGGGCCTCTT	1680
		CCCATATTGG					1740
	CATGCAGCTA	CACCTACCGG	CCCTGGGACG	CCGGAGGACA	GGGCATTGTC	CTCAGTCAGA	1800
		TTTGGGGCCA					1860
55	CTGTAGTCAC	ATGACTAAGC	CAAGAGGAAG	GAGCAAGACT	CAAGACATGA	TTGATGGATG	1920
	TTAAAGTCTA	GCCTGATGAG	AGGGGAAGTG	GTGGGGGAGA	CATAGCCCCA	CCATGAGGAC	1980
	ATACAACTGG	GAAATACTGA	AACTTGCTGC	CTATTGGGTA	TGCTGAGGCC	CACAGACTTA	2040
	CAGAAGAAGT	GGCCCTCCAT	AGACATGTGT	AGCATCAAAA	CACAAAGGCC	CACACTTCCT	2100
	GACGGATGCC	AGCTTGGGCA	CTGCTGTCTA	CTGACCCCAA	CCCTTGATGA	TATGTATTTA	2160
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		CTCACGGAGC					2280
		ACACTGCAGG					2340
		CCTGCCTTTC					2400
		AATGGTTCAC					2460
65		TGACACCTTT					2520
		CTCAGCGGTC					2580
		CTTGTCCTGT					2640
		ATCAGGGTCC					2700
		TTGGAAGGGT					2760
70		CCCAGGCTGG					2820
	TTTGGGCTCA	AGTGATCCTC	CCACCTCAGC	CTCCTGAGTA	GCTGGGACCA	TAGGCTCACA	2880
	ACACCACACC	TGGCAAATTT	GATTTTTTT	TTTTTTTTCA	GAGACGGGGT	CTCGCAACAT	2940
	TGCCCAGACT	TCCTTTGTGT	TAGTTAATAA	AGCTTTCTCA	ACTGCC		

⁷⁵ Seq ID No: 141 Protein sequence: Protein Accession #: NP_000192.1

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11
      MLQFVRAGAR AWLRPTGSQG LSSLAEBAAR ATENPEQVAS EGLPEPVLRK VELPVPTHRR
      PVQAWVESLR GFEQERVGLA DLHPDVFATA PRIDIIHQVA MWQKNFKRIS YAKTKTRAEV
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      RGGGGKPLAA ERHWAGPAWQ HPLSALARRR CCPWPPGPTS YYYMLPMKVR ALGLKVALTV
                                                                              180
      KLAODDLHIM DSLELPTGDP OYLTELAHYR RWGDSVLLVD LTHEEMPQSI VEATSRLKTF
                                                                              240
      NLIPAVGLNV HSMLKHQTLV LTLPTVAFLE DKLLWQDSRY RPLYPFSLPY SDFPRPLPHA
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      Nucleic Acid Accession #: NM 000270.1
      Coding sequence: 110-979 (underlined sequences correspond to start and stop codons)
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                                                                              120
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      ATACACCTAT GAAGATTATA AGAACACTGC AGAATGGCTT CTGTCTCATA CTAAGCACCG
      ACCTCAAGTT GCAATAATCT GTGGTTCTGG ATTAGGAGGT CTGACTGATA AATTAACTCA
                                                                              240
      GGCCCAGATC TITGACTACA GIGAAATCCC CAACTITCCT CGAAGTACAG IGCCAGGICA
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      TGCTGGCCGA CTGGTGTTTG GGTTCCTGAA TGGCAGGGCC TGTGTGATGA TGCAGGGCAG
                                                                              360
      GTTCCACATG TATGAAGGGT ACCCACTCTG GAAGGTGACA TTCCCAGTGA GGGTTITCCA
                                                                              420
25
      CCTTCTGGGT GTGGACACCC TGGTAGTCAC CAATGCAGCA GGAGGGCTGA ACCCCAAGTT
                                                                              480
      TGAGGTTGGA GATATCATGC TGATCCGTGA CCATATCAAC CTACCTGGTT TCAGTGGTCA
                                                                              540
      GAACCCTCTC AGAGGGCCCA ATGATGAAAG GTTTGGAGAT CGTTTCCCTG CCATGTCTGA
                                                                              600
      TGCCTACGAC CGCACTATGA GGCAGAGGGC TCTCAGTACC TGGAAACAAA TGGGGGAGCA
                                                                              660
      ACGTGAGCTA CACGAAGGCA CCTATGTGAT GGTGGCAGGC CCCAGCTTTG AGACTGTGGC
                                                                              720
30
      AGAATGTCGT GTGCTGCAGA AGCTGGGAGC AGACGCTGTT GGCATGAGTA CAGTACCAGA
                                                                              780
      AGTTATOGTT GCACGGCACT GTGGACTTCG AGTCTTTGGC TTCTCACTCA TCACTAACAA
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      GGTCATCATG GATTATGAAA GCCTGGAGAA GGCCAACCAT GAAGAAGTCT TAGCAGCTGG
                                                                              900
      CAAACAAGCT GCACAGAAAT TGGAACAGTT TGTCTCCATT CTTATGGCCA GCATTCCACT
      CCCTGACAAA GCCAGTTGAC CTGCCTTGGA GTGGTCTGGC ATCTCCCACA CAAGACCCAA 1020
GTAGCTGCTA CCTTCTTTGG CCCCTTGCTG GAGTCATGTG CCTCTGTCCT TAGGTTGTAG 1080
35
      CAGAAAGGAA AAGATECTG TCCTTCACCT TTCCCACTTT CTTCTACCAG ACCCTTCTGG 1140
      TGCCAGATCC TCTTCTCAAA GCTGGGATTA CAGGTGTGAG CATAGTGAGA CCTTGGCGCT 1200
ACAAAATAAA GCTGTTCTCA TTCTGTGTCT TTCTTACACA GAGACTGGAGA CCCGGTGCCCT 1260
ACCACACATC TGTGGGAGATG CCCAGGATT GACTGGGGC TTAGAAACTT GCATAGCAGC 1230
40
      TGCTACTAGC TCTTTGAGAT AATACATTCC GAGGGGCTCA GTTCTGCCTT ATCTAAATCA 1380
      CCAGAGACCA AACAAGGACT AATCCAATAC CTCTTGGA
      Seq ID No: 143 Protein sequence:
      Protein Accession #: NP 000261.1
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      VPGHAGRLVF GFLNGRACVM MQGRFHMYEG YPLWKVTPPV RVPHLLGVDT LVVTNAAGGL
                                                                              120
      NPKFEVGDIM LIRDHINLPG FSGQNPLRGP NDERFGDRFP AMSDAYDRTM RQRALSTWKQ
                                                                             180
      MCEQRELQEC TYVMVAGPSF ETVAECRVLQ KLGADAVGMS TVPEVIVARH CGLRVFGFSL
                                                                             240
      ITHKVIMDYE SLEKANHEEV LAAGKQAAQK LEQFVSILMA SIPLPDKAS
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      Nucleic Acid Accession #: NM 015577.1
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                                         31
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      CCCCTCTCA AAACTCTCCT CTAGACCTTT GCAAGGCTGA ATGCACTAAA CATGAAGAGC
                                                                              120
      TTGAAAGCGA AGTTCAGGAA GAGTGACACC AATGAGTGGA ACAAGAATGA TGACCGGCTA
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65
      CTGCAGGCCG TGGAGAATGG AGATGCGGAG AAGGTGGCCT CACTGCTCGG CAAGAAGGGG
                                                                              240
      GCCAGTGCCA CCAAACACGA CAGTGAGGGC AAGACCGCTT TCCATCTTGC TGCTGCAAAA
                                                                              300
      GGACACCTCG AATGCCTCAG GGTCATGATT ACACATGGTG TGGATGTGAC AGCCCAAGAT
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      ACTACCEGAC ACAGCECCTT ACATCTCECA ECCAAGAACA ECCACCATGA ATECATCAGE
                                                                              420
      AGGCTGCTTC AGTCTAAATG CCCAGCCGAA AGTGTCGACA GCTCTGGGAA AACAGCTTTA
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70
       CATTATGCAG CGGCTCAGGG CTGCCTTCAA GCTGTGCAGA TTCTCTGCGA ACACAAGAGC
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      TTAATTAAAA AGGGTGCAGA CCTAAACCTT GTAGATTCTC TTGGATACAA TGCCTTACAT
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75
      TATTCCAAAC TCTCAGAAAA TGCAGGAATT CAAAGCCTTC TATTATCAAA AATCTCTCAG
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      CATCCTGATT TARACACCCC AACAAAACCA AAGCAGCATG ACCAAGTCTC TARAATAAGC
                                                                              900
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	TCAGAAAGAA	GTGGAACTCC	AAAAACACGC	AAAGCTCCAC	CACCTCCTAT	CAGTCCTACC	960
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						AGAAAACAAA	
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	AAGGAGTTAC	ARGATARATT	ACAGGCCAAA	TCACCCAAGG	PGGCGGFFGC	AGACCTAAGC	1260
	TTTCACTCAT	ACCATECCAC	CCADACTGAC	TOTALOGUETOS	CCCTGGGAAA	ACCTGGTGAA	1320
	ACCTUTUTO	CAGACTCCAA	ATCATCTCCA	TCTCTCTTTAA	TACATTCTTT	AGGTAAATCC	1380
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10						ATCCCGAAGG	
10						CCTCAGCCAG	
	DEAGNACION	ANDCTONO	CARATACGAG	GAGGCTATGA	ADGRAGETCET	TAGTGTGCAG	1620
	AAGCACACGA	AACTCCCTCT	TOTAL	GNAAGCATOG	ATTATOMOTOC	ACATTTCCAC	1680
	CACCINCACCC	MCTCGGICI	CCADATTAAT	CECCENTREC	ACCONTOTOCA	GAATGCATTA	1740
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13	CACATACCES	CACTOATTA	COCACCTOTO	GRAGAGTIAG	ACCADATCEA	AAGTTCATAT	1860
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						ACAGGAAGCC	
						ACTCAATAAA	
20						GGATTACAGG	
20						GCATGAGAAA	
	ANGAGGIOUNT	CTCTAGAGGA	TGTCACAGCT	GAMINIMICC	ATAMAGCAGA	GCATGAGAAA	2100
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	TCTCAGTATT	CAAAAGTGTT	GAATGAGTTG	ACCCAGCTCA	AACAACTGGT	GGATGCACAA	2280
25	AAAGAGAACT	CTGTCTCTAT	CACAGAACAT	TTGCAAGTGA	TAACCACGCT	GCGGACTGCA	2340
43	GCAAAAGAGA	TGGAAGAAAA	AATAAGCAAT	CTTAAGGAAC	ACCTTGCAAG	CAAGGAAGTG	2400
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						GAGTGTGTTG	
	GCATCGAAAT	TAAAGGAATC	TGTGAAAGAG	AAAGAGAAGG	TCCATTCAGA	GGTTGTCCAG	2580
20	ATTAGAAGTG	AGGTCTCACA	GGTGAAAAGA	GAAAAGGAAA	ATATTCAGAC	TCTCTTGAAA	2640
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						TTCTTCCCTT	
	TCCAAAGGTT	TCTGAGGACT	TCTCCCAGGA	GAAGACTGCC	CGCCTCAGAA	CTGCTTAGAG	3240
40	ACTTCAAACC	AGCAGAGGTG	AAAGTCCCTG	TCATCCCTTC	AGATTCCAGA	GCTGGGATCA	3300
	GCCATGCCCA	GAGGTCTGGT	CCTGATGCTG	GCAGGGGGC	CCCCTCCTCC	ATCCCTGACT	3360
	GGCTGAGTGG	CTTTATCACC	ACCGAGTGAT	GTGCTGAGGC	CTCCTGCAGT	ATCCCTGACT GAATGCTCCT	3420
	TCCATTCCTG	TACTCGGGCA	GTGCCATTCA	GCACAGGAGA	CCTCTTTTTG	CCTTTGGCTT	3480
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45	CTGCTTAAAA	CCCTTCATCA	TGATATCCTG	TGGATTTAAA	AACTCTAATT	CCATGITITC	3600
	TTCCCATCTG	CCTTATATAT	CTCATCACCC	TGCTTATCAA	TATTCAGTTT	GATGAGCACT	3660
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50	CCANAGAAA	TGCCTCATAG	TTCTTAACCT	CAACTTTTGT	AGAAGTATTT	TTTTCTCTGT	3900
	ΔΤΡΤΤΤΑΤΑ	ттуусстуудта	AAGAWATTTT	CATATCTGAA	CTCCTAAATA	AGTGAAATTA	3960
	CAGTAGATTA	TATTARCARA	ATTTTTTA	GGTAGCCATG	CTTGAGACTT	TTTAAAAATA	4020
						CAGACCTAAT	
						TTGTAGCGCA	
55						CTGACTCTAC	
						CAACTTTGAA	
	CCTABABACC	CTYCATATYCCT	AATATTATOG	TGCATAGCAG	AGGTCTCGGA	TATAAAAAA	4320
	TTCTCTTCAC	TTTACTTCA	COTTANANA	GTTTCTAACA	CCCTTCCAAC	TTCCCTTATG	4380
	COMMENTATION	TITINGTITION	OFCACACION	ATTCCTCCACT	CTCCAAACTA	TTTAACTGAA	4440
60	GCATTANTCT	TGTTGAGGGA	GAGAGACAGA	ATCCIGGACT	CICCADAGIA	AGTGGGTGCT	4540
00	MGTAGGGCCT	GCICIGACAG	OGCCCATGIC	mmccama acc	3 CCTT SUCCETC	GCAAAGCAAA	4550
						AAGCAATTTC	
						AAATACACAA	
65						GACATTITTG	
U.S						TATTACGAGT	
	ACTCTGGTTA	AATATTGAAA	AGTTATATGC	TGTAGTTTTT	AGTATTTTGT	CTTTGTAATT	4860
		ATTGGAGAAA	ATAAACTTGT	TICATTTTGC	AAAAAAAA	АААААААА	4920
	AAAAA						
70							
70	Seq ID No:	145 Protein	sequence:				

V Seq ID No: 145 <u>Protein sequence:</u> Protein Accession #: NP_056392.1

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AAKGHVECLR VMITHGVDVT AQDTTGHSAL HLAAKNSHHE CIRRLLQSKC PARSVDSSGK 120
      TALHYAAAQG CLQAVQILCE HKSPINLKDL DGNIPLLLAV QNGHSEICHF LLDHGADVNS
      RNKSGRTALM LACEIGSSNA VEALIKKGAD LNLVDSLGYN ALHYSKLSEN AGIOSLLLSK
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     ISQDADLKTP TKPKQHDQVS KISSERSGTP KTRKAPPPPI SPTQLSDVSS PRSITSTPLS
                                                                             300
     GKESVFFAEP PFKAEISSIR ENKORLSDST TGADSLLDIS SEADQQDLLS LLQAKVASLT
                                                                             360
      LHNKELQDKL QAKSPKEAEA DLSFDSYHST QTDLGPSLGK PGETSPPDSK SSPSVLIHSL
                                                                             420
      GKSTTDNDVR IQOLQEILQD LQKRLESSEA ERKQLQVELQ SRRAELVCLN NTEISENSSD
                                                                            480
      LSQKLKETQS KYEEAMKEVL SVQKQMKLGL VSPESMDNYS HFHELRVTEE EINVLKQDLQ
                                                                            540
     NALEESERNK EKVRELEEKL VEREKGTVIK PPVEEYEEMK SSYCSVIENM NKEKAFLFEK
                                                                             600
10
     YQEAQEEIMK LKDTLKSQMT QEASDEAEDM KEAMNRMIDE LNKQVSELSQ LYKEAQAELE
DYRRKSLED VTAEYIHKAE HEKLMQLTNV SRAKAEDALS EMKSQYSKVL NELTQLKQLV
                                                                             660
                                                                             720
      DAQKENSVSI TEHLQVITTL RTAAKEMEEK ISNLKEHLAS KEVEVAKLEK QLLEEKAAMT
                                                                            780
      DAMVPRSSYE KLQSSLESEV SVLASKLKES VKEKEKVHSE VVQIRSEVSQ VKREKENIQT
                                                                            840
      LLKSKEGEVN ELLOKFOGAG EELAEMKRYA ESSSKLEEDK DKKINEMSKE VIKLKEALNS
                                                                            900
15
      LSQLSYSTSS SKRQSQQLEA LQQQVKQLQN QLARCKKQHQ EVISVYRMHL LYAVQGQMDE 960
     DVOKVLKOIL TMCKNOSOKK
```

Seq ID NO: 146 DNA sequence

Nucleic Acid Accession #: NM 000459.1

20 Coding sequence: 149-3523 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	ī	ī	ī	Ĭ-	i -	ĭ	
25	CTTCTGTGCT	GTTCCTTCTT	GCCTCTAACT	TGTAAACAAG	ACGTACTAGG	ACGATGCTAA	60
	TGGAAAGTCA	CAAACCGCTG	GGTTTTTGAA	AGGATCCTTG	GGACCTCATG	CACATTTGTG	120
	GARACTGGAT	GGAGAGATTT	GGGGAAGCAT	GGACTCTTTA	GCCAGCTTAG	TTCTCTGTGG	180
	AGTCAGCTTG	CTCCTTTCTG	GAACTGTGGA	AGGTGCCATG	GACTTGATCT	TGATCAATTC	240
	CCTACCTCTT	GTATCTGATG	CTGAAACATC	TCTCACCTGC	ATTGCCTCTG	GGTGGCGCCC	300
30	CCATGAGCCC	ATCACCATAG	GAAGGGACTT	TGAAGCCTTA	ATGAACCAGC	ACCAGGATCC	360
	GCTGGAAGTT	ACTCAAGATG	TGACCAGAGA	ATGGGCTAAA	AAAGTTGTTT	GGAAGAGAGA	420
		AAGATCAATG					480
	CAGGATACGA	ACCATGAAGA	TGCGTCAACA	AGCTTCCTTC	CTACCAGCTA	CTTTAACTAT	540
	GACTGTGGAC	AAGGGAGATA	ACGTGAACAT	ATCTTTCAAA	AAGGTATTGA	TTAAAGAAGA	600
35	AGATGCAGTG	ATTTACAAAA	ATGGTTCCTT	CATCCATTCA	GTGCCCCGGC	ATGAAGTACC	660
	TGATATTCTA	GAAGTACACC	TGCCTCATGC	TCAGCCCCAG	GATGCTGGAG	TGTACTCGGC	720
	CAGGTATATA	'GGAGGAAACC	TCTTCACCTC	GGCCTTCACC	AGGCTGATAG	TCCGGAGATG	780
	TGAAGCCCAG	AAGTGGGGAC	CTGAATGCAA	CCATCTCTGT	ACTGCTTGTA	TGAACAATGG	840
	TGTCTGCCAT	GAAGATACTG	GAGAATGCAT	TTGCCCTCCT	GGGTTTATGG	GAAGGACGTG	900
40	TGAGAAGGCT	TGTGAACTGC	ACACGTTTGG	CAGAACTTGT	AAAGAAAGGT	GCAGTGGACA	960
		AAGTCTTATG					1020
		GGTCTGCAGT					1080
		TGCAGCTGCA					1140
		TGGCAGGGGC					1200
45		TTGCCAGATC					1260
		TGGCCGCTAC					1320
		CCAAAAGACT					1380
		CTCCCCCCTG					1440
		AAGCCCTTCA					1500
50		GACACTGGAC					1560
		CCAATCAAAT					1620
		ATTCAAGTGA					1680
		CTCTGTGTGC					1740
		CGCTTCACAA					1800
55		AGTCAGACCA					1860
		TATGTTGAAG					1920
		GGCAACTTGA					1980
		GCTAGAGTCA					2040
c0		AGTGACATTC					2100
60		GCTGTGATTT					2160
		AAGGTTCAAG					2220
		ATTCAGTATC					2280
		GAGAACAACA					2340
65		TCTCAAGCAC					2400
03		GCTGGAATGA					2460
		GCAAATGTGC					2520
		CAGTTCAACT					2580
		ATTTATCCAG					2640
70		TTTGGCCAAG					2700
70		AAAAGAATGA					2760
	AGAACTGGAA	GTTCTTTGTA	AACTIGGACA	CUATUCAAAC	ATCATCAATC	TCTTAGGAGC	2820 2880
	ATGTGAACAT	CGAGGCTACT	TGTACCTGGC	CATTGAGTAC	GCGCCCCATG	GMAACCTTCT	2940
	GGACTTCCTT	CGCAAGAGCC	GTGTGCTGGA	GAUGGACUCA	GCATTTGCCA	TIGUCAATAG	
75	CACCGCGTCC	ACACTGTCCT TTGAGCCAAA	CCCAGCAGCT	CCTTCACTTC	GUTGUUACG	Chance	3000
		AACTATGTGG					3120
	AGTIGGIGAA	AMCINIGIGG	CHAMMATAGC	AGMITTIGGA	TIGICCCGMG	GICHNORGGT	3120

```
TRACETIANA AMACIANEM GANGECTECE AUTROCCIUM ATGRICATEMA 3180
TRACATUM TRACETACA ACASTRATOR TREGECTATUM GANTIGATUM ATTRACETAM TRACETAM TRACETAM GANTIGATUM TRACETAM ```

Seq ID No: 147 Protein sequence: 20 Protein Accession #: NP 000450.1

|     |             | 11         | 21         | 31         | 41         | 51         |      |
|-----|-------------|------------|------------|------------|------------|------------|------|
|     | î           | 1          | ī          | ĭ          | ī.         | ī          |      |
| 2.5 | MDSIASIATIC | GVSLLLSGTV | RGAMDIJLIN | SLPLVSDAET | SLTCIASGWR | PHEPITIGRD | 60   |
|     |             |            |            | EKASKINGAY |            |            | 120  |
|     |             |            |            | RDAVIYKNGS |            |            | 180  |
|     |             |            |            | CEAOKWGPEC |            |            | 240  |
|     | ICPPGFMGRT  | CEKACELHTF | GRICKERCSG | OEGCKSYVFC | LPDPYGCSCA | TGWKGLQCNE | 300  |
| 30  | ACHPGFYGPD  | CKLRCSCNNG | EMCDRFQGCL | CSPGWQGLQC | EREGIPANTP | KIVDLPDHIE | 360  |
|     | VNSGKFNPIC  | KASGWPLPTN | REMTLVKPDG | TVLHPKDFNH | TDHFSVAIFT | IHRILPPDSG | 420  |
|     |             |            |            | PNVIDTGHNF |            |            | 480  |
|     |             |            |            | TEYELCVQLV |            |            | 540  |
|     |             |            |            | EDDFYVEVER |            |            | 600  |
| 35  |             |            |            | AWTLSDILPP |            |            | 660  |
|     |             |            |            | NATIIQYQLK |            |            | 720  |
|     |             |            |            | ILGSAGNTCL |            |            | 780  |
|     |             |            |            |            |            | GEGNFGQVLK | 840  |
|     |             |            |            | GELEVLCKLG |            |            | 900  |
| 40  |             |            |            | STASTLSSQQ |            |            | 960  |
|     |             |            |            | VYVKKTMGRL |            |            | 1020 |
|     |             |            |            | LPQGYRLEKP |            | MRQCWREKPY | 1080 |
|     | ERPSFAQILV  | SLNRMLEERK | TYVNTTLYEK | FTYAGIDCSA | EEAA       |            |      |

45 Seq ID NO: 148 <u>DNA sequence</u> Nucleic Acid Accession #: NM 000552.2 Coding sequence: 311-8752 (underlined sequences correspond to start and stop codons)

| 50 | 1          | 11<br>     | 21<br>     | 31<br>     | 41<br>     | 51<br>     |      |
|----|------------|------------|------------|------------|------------|------------|------|
|    | AGCTCACAGC | TATTGTGGTG | GGAAAGGGAG | GGTGGTTGGT | GGATGTCACA | GCTTGGGCTT | 60   |
|    | TATCTCCCCC | AGCAGTGGGG | ACTCCACAGC | CCCTGGGCTA | CATAACAGCA | AGACAGTCCG | 120  |
|    | GAGCTGTAGC | AGACCTGATT | GAGCCTTTGC | AGCAGCTGAG | AGCATGGCCT | AGGGTGGGCG | 180  |
| 55 |            |            | AGTTTCCCAG |            |            |            | 240  |
|    | GCAGGGGAAG | GCACCATTGT | CCAGCAGCTG | AGTTTCCCAG | GGACCTTGGA | GATAGCCGCA | 300  |
|    | GCCCTCATTT | ATGATTCCTG | CCAGATTTGC | CGGGGTGCTG | CTTGCTCTGG | CCCTCATTTT | 360  |
|    | GCCAGGGACC | CTTTGTGCAG | AAGGAACTCG | CGGCAGGTCA | TCCACGGCCC | GATGCAGCCT | 420  |
|    | TTTCGGAAGT | GACTTOGTCA | ACACCTTTGA | TGGGAGCATG | TACAGCTTTG | CGGGATACTG | 480  |
| 60 | CAGTTACCTC | CTGGCAGGGG | GCTGCCAGAA | ACCCTCCTTC | TCGATTATTG | GGGACTTCCA | 540  |
|    | GAATGGCAAG | AGAGTGAGCC | TCTCCGTGTA | TCTTGGGGAA | TTTTTTGACA | TCCATTTGTT | 600  |
|    | TGTCAATGGT | ACCGTGACAC | AGGGGGACCA | AAGAGTCTCC | ATGCCCTATG | CCTCCAAAGG | 660  |
|    | GCTGTATCTA | GAAACTGAGG | CTGGGTACTA | CAAGCTGTCC | GGTGAGGCCT | ATGGCTTTGT | 720  |
|    | GGCCAGGATC | GATGGCAGCG | GCAACTTTCA | AGTCCTGCTG | TCAGACAGAT | ACTTCAACAA | 780  |
| 65 | GACCTGCGGG | CTGTGTGGCA | ACTITAACAT | CTTTGCTGAA | GATGACTITA | TGACCCAAGA | 840  |
|    | AGGGACCTTG | ACCTCGGACC | CTTATGACTT | TGCCAACTCA | TGGGCTCTGA | GCAGTGGAGA | 900  |
|    | ACAGTGGTGT | GAACGGGCAT | CTCCTCCCAG | CAGCTCATGC | AACATCTCCT | CTGGGGAAAT | 960  |
|    | GCAGAAGGGC | CTGTGGGAGC | AGTGCCAGCT | TCTGAAGAGC | ACCTCGGTGT | TTGCCCGCTG | 1020 |
|    | CCACCCTCTG | GTGGACCCCG | AGCCTTTTGT | GGCCCTGTGT | GAGAAGACTT | TGTGTGAGTG | 1080 |
| 70 | TGCTGGGGGG | CTGGAGTGCG | CCTGCCCTGC | CCTCCTGGAG | TACGCCCGGA | CCTGTGCCCA | 1140 |
|    | GGAGGGAATG | GTGCTGTACG | GCTGGACCGA | CCACAGCGCG | TGCAGCCCAG | TGTGCCCTGC | 1200 |
|    | TGGTATGGAG | TATAGGCAGT | GTGTGTCCCC | TTGCGCCAGG | ACCTGCCAGA | GCCTGCACAT | 1260 |
|    | CAATGAAATG | TGTCAGGAGC | GATGCGTGGA | TGGCTGCAGC | TGCCCTGAGG | GACAGCTCCT | 1320 |
|    | GGATGAAGGC | CTCTGCGTGG | AGAGCACCGA | GTGTCCCTGC | GTGCATTCCG | GAAAGCGCTA | 1380 |
| 75 | CCCTCCCGGC | ACCTCCCTCT | CTCGAGACTG | CAACACCTGC | ATTTGCCGAA | ACAGCCAGTG | 1440 |
|    | GATCTGCAGC | AATGAAGAAT | GTCCAGGGGA | GTGCCTTGTC | ACTGGTCAAT | CCCACTTCAA | 1500 |

|    | GAGCTTTGAC  | AACAGATACT   | TCACCTTCAG  | TGGGATCTGC  | CAGTACCTGC  | TGGCCCGGGA                             | 1560         |
|----|-------------|--------------|-------------|-------------|-------------|----------------------------------------|--------------|
|    | TTGCCAGGAC  | CACTCCTTCT   | CCATTGTCAT  | TGAGACTGTC  | CAGTGTGCTG  | ATGACCGCGA<br>GCCTTGTGAA<br>CCCTCCTGAA | 1620         |
|    | CGCTGTGTGC  | ACCCGCTCCG   | TCACCGTCCG  | GCTGCCTGGC  | CTGCACAACA  | GCCTTGTGAA                             | 1680         |
|    | ACTGAAGCAT  | GGGGCAGGAG   | TTGCCATGGA  | TGGCCAGGAC  | ATCCAGCTCC  | CCCTCCTGAA                             | 1740         |
| 5  | AGGTGACCTC  | CGCATCCAGC   | ATACAGTGAC  | GGCCTCCGTG  | CGCCTCAGCT  | ACGGGGAGGA                             | 1800         |
|    | CCTGCAGATG  | GACTGGGATG   | GCCGCGGGAG  | GCTGCTGGTG  | AAGCTGTCCC  | CCGTCTACGC                             | 1860         |
|    | CGGGAAGACC  | TGCGGCCTGT   | GTGGGAATTA  | CAATGGCAAC  | CAGGGCGACG  | ACTTCCTTAC                             | 1920         |
|    | CCCCTCTGGG  | CTGGCAGAGC   | CCCGGGTGGA  | GGACTTCGGG  | AACGCCTGGA  | AGCTGCACGG                             | 1980         |
|    | GGACTGCCAG  | GACCTGCAGA   | AGCAGCACAG  | CGATCCCTGC  | GCCCTCAACC  | CGCGCATGAC                             | 2040         |
| 10 | CAGGTTCTCC  | GAGGAGGCGT   | GCGCGGTCCT  | GACGTCCCCC  | ACATTCGAGG  | CCTGCCATCG                             | 2100         |
|    | TGCCGTCAGC  | CCGCTGCCCT   | ACCTGCGGAA  | CTGCCGCTAC  | GACGTGTGCT  | CCTGCTCGGA                             | 2160         |
|    | CGGCCGCGAG  | TGCCTGTGCG   | GCGCCCTGGC  | CAGCTATGCC  | GCGGCCTGCG  | CGGGGAGAGG                             | 2220         |
|    | CGTGCGCGTC  | GCGTGGCGCG   | AGCCAGGCCG  | CTGTGAGCTG  | AACTGCCCGA  | AAGGCCAGGT                             | 2280         |
|    | GTACCTGCAG  | TGCGGGACCC   | CCTGCAACCT  | GACCTGCCGC  | TCTCTCTCTT  | ACCCGGATGA                             | 2340         |
| 15 | GGAATGCAAT  | GAGGCCTGCC   | TGGAGGGCTG  | CTTCTGCCCC  | CCAGGGCTCT  | ACATGGATGA                             | 2400         |
|    | GAGGGGGGAC  | TGCGTGCCCA   | AGGCCCAGTG  | CCCCTGTTAC  | TATGACGGTG  | AGATCTTCCA                             | 2460         |
|    | GCCAGAAGAC  | ATCTTCTCAG   | ACCATCACAC  | CATGIGCTAC  | TGTGAGGATG  | GCTTCATGCA                             | 2520         |
|    | CTGTACCATG  | AGTGGAGTCC   | CCGGAAGCTT  | GCTGCCTGAC  | GCTGTCCTCA  | GCAGTCCCCT                             | 2580         |
|    | GTCTCATCGC  | AGCAAAAGGA   | GCCTATCCTG  | TCGGCCCCCC  | ATGGTCAAGC  | TGGTGTGTCC                             | 2640         |
| 20 | CGCTGACAAC  | CTGCGGGCTG   | AAGGGCTCGA  | GTGTACCAAA  | ACGTGCCAGA  | ACTATGACCT                             | 2700         |
|    | GGAGTGCATG  | AGCATGGGCT   | GTGTCTCTGG  | CTGCCTCTGC  | CCCCCGGGCA  | TGGTCCGGCA                             | 2760         |
|    | agrangerma  | NACTORGOOM   | GROTOTOTO   | CTGCCTCTGC  | CCCCCCCCCC  | TOGTOGGGG                              | 2760         |
|    | TGAGAACAGA  | TGTGTGGCCC   | TGGAAAGGTG  | TCCCTGCTTC  | CATCAGGGCA  | AGGAGTATGC                             | 2820         |
|    | CCCTGGAGAA  | ACAGTGAAGA   | TTGGCTGCAA  | CACTIGIGIC  | TGTCGGGACC  | GGAAGTGGAA                             | 2880         |
| 25 | CTGCACAGAC  | CATGTGTGTG   | ATGCCACGTG  | CTCCACGATC  | GGCATGGCCC  | AGGAGTATGC<br>GGAAGTGGAA<br>ACTACCTCAC | 2940         |
|    | CTTCGACGGG  | CTCAAATACC   | TGTTCCCCGG  | GGAGTGCCAG  | TACGTTCTGG  | TGCAGGATTA                             | 3000         |
|    | CTGCGGCAGT  | AACCCTGGGA   | CCTTTCGGAT  | CCTAGTGGGG  | AATAAGGGAT  | GCAGCCACCC                             | 3060         |
|    |             |              |             |             |             | TIGAGCIGIT                             | 3120         |
|    | TGACGGGGAG  | GTGAATGTGA   | AGAGGCCCAT  | GAAGGATGAG  | ACTCACTITG  |                                        | 3180         |
| 30 | GTCTGGCCGG  | TACATCATTC   | TGCTGCTGGG  | CAAAGCCCTC  | TCCGTGGTCT  | GGGACCGCCA                             | 3240         |
|    | CCTGAGCATC  | TCCGTGGTCC   | TGAAGCAGAC  | ATACCAGGAG  | AAAGTGTGTG  | GCCTGTGTGG                             | 3300         |
|    | GAATTTTGAT  | GGCATCCAGA   | ACAATGACCT  | CACCAGCAGC  | AACCTCCAAG  | TGGAGGAAGA                             | 3360         |
|    | CCCTGTGGAC  | TTTGGGAACT   | CCTGGAAAGT  | GAGCTCGCAG  | TGTGCTGACA  | CCAGAAAAGT<br>CGATGGTGGA               | 3420         |
| 25 | GCCTCTGGAC  | TCATCCCCTG   | CCACCTGCCA  | TAACAACATC  | ATGAAGCAGA  | CGATGGTGGA                             | 3480<br>3540 |
| 35 | TTCCTCCTGT  | AGAATCCTTA   | CCAGTGACGT  | CTTCCAGGAC  | TGCAACAAGC  |                                        | 3600         |
|    | CGAGCCATAT  | CTGGATGTCT   | GCATITACGA  | CACCIGCTCC  | TGTGAGTCCA  |                                        |              |
|    |             |              |             |             |             | ATGGCAAGGT<br>ATCTCCGGGA               | 3660<br>3720 |
|    | GGTGACCTGG  | AGGACGGCCA   | CATTGTGCCC  | CCAGAGCTGC  | GAGGAGAGGA  | AAGTCACGTG                             | 3780         |
| 40 | GAACGGGTAT  | GAGTGTGAGT   | GGCGCTATAA  | CAGCIGIGUA  | CACCCCTGTC  | ATGCCCACTG                             | 3840         |
| 40 | COCOCCCC    | AAAATCCTCC   | AUCACCULTA  | CAGIGIGIG   | GTTGACCCTG  | AAGACTGTCC                             | 3900         |
|    | CCCICCAGGG  | AMMITCCIGG   | VIGWOCILLI  | CTCACCAAAC  | AAACTCACCT  | TONDACTORCO                            |              |
|    | mcaccccroac | CACTGCCAGA   | TTTCCCACTC  | TGATGTTGTC  | AACCTCACCT  | TGAATCCCAG<br>GTGAAGCCTG               | 4020         |
|    | CCAGGAGCCG  | agnagacanga  | TOGTGCCTCC  | CACAGATGCC  | CCGGTGAGCC  | CCACCACTCT                             | 4080         |
| 45 | GTATGTGGAG  | GACATCTCGG   | AACCGCCGTT  | GCACGATTTC  | TACTGCAGCA  | GGCTACTGGA                             | 4140         |
|    | CCTGGTCTTC  | CTGCTGGATG   | GCTCCTCCAG  | GCTGTCCGAG  | GCTGAGTTTG  | AAGTGCTGAA                             | 4200         |
|    | GGCCTTTGTG  | GTGGACATGA   | TGGAGCGGCT  | GCGCATCTCC  | CAGAAGTGGG  | TCCGCGTGGC                             | 4260         |
|    | CGTGGTGGAG  | TACCACGACG   | GCTCCCACGC  | CTACATCGGG  | CTCAAGGACC  | GGAAGCGACC                             | 4320         |
|    | GTCAGAGCTG  | CGGCGCATTG   | CCAGCCAGGT  | GAAGTATGCG  | GGCAGCCAGG  | TGGCCTCCAC                             | 4380         |
| 50 | CAGCGAGGTC  | TTGAAATACA   | CACTGTTCCA  | AATCTTCAGC  | AAGATCGACC  | GCCCTGAAGC                             | 4440         |
|    | CTCCCGCATC  | GCCCTGCTCC   | TGATGGCCAG  | CCAGGAGCCC  | CAACGGATGT  | CCCGGAACTT                             | 4500         |
|    | TGTCCGCTAC  | GTCCAGGGCC   | TGAAGAAGAA  | GAAGGTCATT  | GTGATCCCGG  |                                        | 4560         |
|    | GCCCCATGCC  | AACCTCAAGC   | AGATCCGCCT  | CATCGAGAAG  | CAGGCCCCTG  | AGAACAAGGC                             | 4620         |
|    | CTTCGTGCTG  | AGCAGTGTGG   | ATGAGCTGGA  | GCAGCAAAGG  | GACGAGATCG  | TTAGCTACCT                             | 4680         |
| 55 | CTGTGACCTT  | GCCCCTGAAG   | CCCCTCCTCC  | TACTCTGCCC  | CCCCACATGG  | CACAAGTCAC                             | 4740         |
|    | TGTGGGCCCG  | GGGCTCTTGG   | GGGTTTCGAC  | CCTGGGGCCC  | AAGAGGAACT  | CCATGGTTCT                             | 4800         |
|    |             |              |             |             |             | TCAACAGGAG                             | 4860         |
|    |             | ATGGAGGAGG   |             |             |             |                                        | 4920<br>4980 |
| 60 | CACGGTGCTG  | CAGTACTCCT   | ACATGGTGAC  | CGTGGAGTAC  | CCCTTCAGCG  | AGGCACAGTC                             | 5040         |
| 00 | CAAAGGGGAC  | ATCCTGCAGC   | GGGTGCGAGA  | GATCUGCTAC  | CAGGGGGGCA  | ACAGGACCAA                             | 5100         |
|    | CACTGGGCTG  | GCCCTGCGGT   | ACCTCTCTGA  | CCACAGCTTC  | TIGGTCAGCC  | AGGGTGACCG<br>ATGAGATCAA               | 5160         |
|    | GGAGCAGGCG  | CCCAACCTGG   | TCTACATGGT  | CACCGGAAAT  | CCIGCUICIG  | CCAACGTGCA                             | 5220         |
|    | GAGGCTGCCT  | ACCAMMOCATCO | CCCCCCAATCC | CCCTATCCTC  | ATCCACCACT  | TTGAGACGCT                             | 5280         |
| 65 | GGAGCIGGAG  | AGGMIIGGCI   | TOCTOCTOCA  | CACCTATCCTC | TOOGGAGAGG  | GGCTGCAGAT                             | 5340         |
| 05 | CCCCCGAGAG  | MODERATE     | CTCACTCCAC  | CCACCCCCTC  | CACCITGATCC | TTCTCCTGGA                             | 5400         |
|    | maccrecre   | ACTUTUCCOAG  | CTONCIONIO  | TOTATION    | ANGAGTTTCG  | CCAAGGCTTT                             | 5460         |
|    | CATTTCAAAA  | GCCAATATAG   | GGCCTCGTCT  | CACTCAGGTG  | TCAGTGCTGC  | AGTATGGAAG                             | 5520         |
|    | CATCACCACC  | ATTGACGTGC   | CATGGAACGT  | GGTCCCGGAG  | AAAGCCCATT  | TGCTGAGCCT                             | 5580         |
| 70 | TGTGGACGTC  | ATGCAGCGGG   | AGGGAGGCCC  | CAGCCAAATC  | GGGGATGCCT  | TGGGCTTTGC                             | 5640         |
|    | TGTGCGATAC  | TTGACTTCAG   | AAATGCATGG  | TGCCAGGCCG  | GGAGCCTCAA  | AGGCGGTGGT                             | 5700         |
|    | CATCCTGGTC  | ACGGACGTCT   | CTGTGGATTC  | AGTGGATGCA  | GCAGCTGATG  | CCGCCAGGTC                             | 5760         |
|    | CAACAGAGTG  | ACAGTGTTCC   | CTATTGGAAT  | TGGAGATCGC  | TACGATGCAG  | CCGCCAGGTC<br>CCCAGCTACG               | 5820         |
|    | GATCTTGGCA  | GGCCCAGCAG   | GCGACTCCAA  | CGTGGTGAAG  | CTCCAGCGAA  | TCGAAGACCT                             | 5880         |
| 75 | CCCTACCATG  | GTCACCTTGG   | GCAATTCCTT  | CCTCCACAAA  | CTGTGCTCTG  | GATTTGTTAG                             | 5940         |
|    | GATTTGCATG  | GATGAGGATG   | GGAATGAGAA  | GAGGCCCGGG  | GACGTCTGGA  | CCTTGCCAGA                             | 6000         |
|    |             |              |             |             |             |                                        |              |
|    |             |              |             |             |             |                                        |              |

|    | CCAGTGCCAC | ACCGTGACTT | GCCAGCCAGA | TGGCCAGACC | TIGCTGAAGA | GTCATCGGGT | 6060  |
|----|------------|------------|------------|------------|------------|------------|-------|
|    | CAACTGTGAC | CGGGGGCTGA | GGCCTTCGTG | CCCTAACAGC | CAGTCCCCTG | TTAAAGTGGA | 6120  |
|    | AGAGACCTGT | GGCTGCCGCT | GGACCTGCCC | CTGCGTGTGC | ACAGGCAGCT | CCACTCGGCA | 6180  |
|    | CATCGTGACC | TTTGATGGGC | AGAATTTCAA | GCTGACTGGC | AGCTGTTCTT | ATGTCCTATT | 6240  |
| 5  | TCAAAACAAG | GAGCAGGACC | TGGAGGTGAT | TCTCCATAAT | GGTGCCTGCA | GCCCTGGAGC | 6300  |
|    | AAGGCAGGGC | TGCATGAAAT | CCATCGAGGT | GAAGCACAGT | GCCCTCTCCG | TCGAGCTGCA | 6360  |
|    | CAGTGACATG | GAGGTGACGG | TGAATGGGAG | ACTGGTCTCT | GTTCCTTACG | TGGGTGGGAA | 6420  |
|    |            |            | GTGCCATCAT |            |            |            | 6480  |
|    | CATCTTCACA | TTCACTCCAC | AAAACAATGA | GTTCCAACTG | CAGCTCAGCC | CCAAGACTTT | 6540  |
| 10 | TGCTTCAAAG | ACGTATGGTC | TGTGTGGGAT | CTGTGATGAG | AACGGAGCCA | ATGACTTCAT | 6600  |
|    | GCTGAGGGAT | GGCACAGTCA | CCACAGACTG | GAAAACACTT | GTTCAGGAAT | GGACTGTGCA | 6660  |
|    | GCGGCCAGGG | CAGACGTGCC | AGCCCATCCT | GGAGGAGCAG | TGTCTTGTCC | CCGACAGCTC | 6720  |
|    |            |            | TACCACTGTT |            |            |            | 6780  |
|    |            |            | AGCAGGACAG |            |            |            | 6840  |
| 15 | CCCCTCTTAT | SCCCACCTCT | GTCGGACCAA | CGGGGTCTGC | GTTGACTGGA | GGACACCTGA | 6900  |
|    | TTTCTGTGCT | ATGTCATGCC | CACCATCTCT | GGTCTACAAC | CACTGTGAGC | ATGGCTGTCC | 6960  |
|    |            |            | TGAGCTCCTG |            |            |            | 7020  |
|    |            |            | TGGAAGGCAG |            |            |            | 7080  |
|    |            |            | AGCACCAGTT |            |            |            | 7140  |
| 20 | CTGTCAGATC | TGCACATGCC | TCAGCGGGCG | GAAGGTCAAC | TGCACAACGC | AGCCCTGCCC | 7200  |
|    | CACGCCCAAA | GCTCCCACGT | GTGGCCTGTG | TGAAGTAGCC | CGCCTCCGCC | AGAATGCAGA | 7260  |
|    | CCACTGCTGC | CCCGAGTATG | AGTGTGTGTG | TGACCCAGTG | AGCTGTGACC | TGCCCCCAGT | 7320  |
|    |            |            | TCCAGCCCAC |            |            |            | 7380  |
|    |            |            | AGGAGGAGTG |            |            |            | 7440  |
| 25 |            |            | GGAAGACCCA |            |            |            | 7500  |
|    |            |            | GCTGTCCCCT |            |            |            | 7560  |
|    |            |            | CCTGCCTTCC |            |            |            | 7620  |
|    |            |            | GGGAGGAGGG |            |            |            | 7680  |
|    |            |            | GCGTGGCCCA |            |            |            | 7740  |
| 30 |            |            | TTCTGCATGA |            |            |            | 7800  |
|    | TGCCTGTGAG | GTGGTGACTG | GCTCACCGCG | GGGGGACTCC | CAGTCTTCCT | GGAAGAGTGT | 7860  |
|    |            |            | CGGAGAACCC |            |            |            | 7920  |
|    |            |            | AAAGGAACGT |            |            |            | 7980  |
|    |            |            | GCTGTAAGAC |            |            |            | 8040  |
| 35 |            |            | TCAATGGCAC |            |            |            | 8100  |
|    |            |            | GCTGCATGGT |            |            |            | 8160  |
|    |            |            | GCAACCCCTG |            |            |            | 8220  |
|    |            |            | GTTTGCCTAC |            |            |            | 8280  |
|    |            |            | ATGAGACGCT |            |            |            | 8340  |
| 40 |            |            | ACTTCTGGGA |            |            |            | 8400  |
|    |            |            | AGGGAGGTAA |            |            |            | 8460  |
|    |            |            | GCAACGACAT |            |            |            | 8520  |
|    | ANGCTGTANG | TCTGAAGTAG | AGGTGGATAT | CCACTACTGC | CAGGGCAAAT | GTGCCAGCAA | 8580  |
|    |            |            | TCAACGATGT |            |            |            | 8640  |
| 45 | ACGGACGGAG | CCCATGCAGG | TGGCCCTGCA | CTGCACCAAT | GGCTCTGTTG | TGTACCATGA | 8700  |
|    |            |            | GCAAATGCTC |            |            |            | 8760  |
|    |            |            | GCTGCCTGCC |            |            |            | 8820  |
|    |            |            | CTTGTGCCCT |            |            |            | 8880  |
|    |            |            | TTGTGCCCTT |            |            |            | - 300 |
| 50 |            |            |            |            |            |            |       |
|    |            |            |            |            |            |            |       |

## Seq ID No: 149 Protein sequence: Protein Accession #: NP\_000543.1

| 55 | 1          | 11         | 21         | 31         | 41         | 51         |      |
|----|------------|------------|------------|------------|------------|------------|------|
|    | Ī          | 1          | 1          | I          | 1          | 1          |      |
|    | MIPARFAGVL | LALALILPGT | LCAEGTRGRS | STARCSLEGS | DEVNTFDGSM | YSFAGYCSYL | 60   |
|    | LAGGCOKRSF | SIIGDFONGK | RVSLSVYLGE | FFDIHLFVNG | TVTQGDQRVS | MPYASKGLYL | 120  |
|    | ETEAGYYKLS | GEAYGFVARI | DGSGNFQVLL | SDRYFNKTCG | LCGNFNIFAE | DDFMTQEGTL | 180  |
| 60 | TSDPYDFANS | WALSSGEOWC | ERASPPSSSC | NISSGEMOKG | LWEQCQLLKS | TSVFARCHPL | 240  |
|    | VDPEPFVALC | EKTLCECAGG | LECACPALLE | YARTCAQEGM | VLYGWTDHSA | CSPVCPAGME | 300  |
|    | YRQCVSPCAR | TCQSLHINEM | CQERCVDGCS | CPECQLLDEG | LCVESTECPC | VHSGKRYPPG | 360  |
|    |            |            | NEECPGECLV |            |            |            | 420  |
|    |            |            | TRSVTVRLPG |            |            |            | 480  |
| 65 |            |            | DWDGRGRLLV |            |            |            | 540  |
|    |            |            | DLQKQHSDPC |            |            |            | 600  |
|    |            |            | CLCGALASYA |            |            |            | 660  |
|    |            |            | RACLEGGFCP |            |            |            | 720  |
|    |            |            | SGVPGSLLPD |            |            |            | 780  |
| 70 |            |            | SMGCVSGCLC |            |            |            | 840  |
|    |            |            | HVCDATCSTI |            |            |            | 900  |
|    |            |            | CKKRVTILVE |            |            |            | 960  |
|    |            |            | SVVLKQTYQE |            |            |            | 1020 |
|    |            |            | SSPATCHNNI |            |            |            | 1080 |
| 75 |            |            | CDTIAAYAHV |            |            |            | 1140 |
|    | RCENRYNSCA | PACOVTCOHP | EPLACPVOCV | EGCHAHCPPG | KILDELLQTC | VDPEDCPVCE | 1200 |

```
VAGRRPASCK KVTLNPSDPE HCOICHCDVV NLTCEACOEP GGLVVPPTDA PVSPTTLYVE 1260
 DISEPPLHDF YCSRLLDLVF LLDGSSRLSE AEFEVLKAFV VDMMERLRIS QKWVRVAVVE 1320
 YHDGSHAYIG LKDRKRPSEL RRIASOVKYA GSOVASTSEV LKYTLFOIFS KIDRPEASRI
 ALLIMASQEP QRMSRNFVRY VQGLKKKKVI VIPVGIGPHA NLKQIRLIEK QAPENKAFVL
 1440
 SSVDELEGOR DEIVSYLCDL APEAPPPTLP PHMAGVTVGP GLLGVSTLGP KRNSMVLDVA
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 FVLEGSDKIG EADFNRSKEF MEEVIQRMDV GQDSIHVTVL QYSYMVTVEY PFSEAQSKGD
 1560
 ILORVREIRY OGGNRTNIGL ALRYLSDHSF LVSOGDREGA PNLVYMVIGN PASDEIKRLP
 1620
 1680
 GDIQUUPIGU GPNANUQELE RIGWPNAPIL IQDFETLPRE APPLUIQRCC SGEGLQIPTL
 SPAPDCSQPL DVILLIDGSS SPPASYFDEM KSFAKAFISK ANIGPRLTQV SVLQYGSITT
 1740
10
 IDVPWNVVPE KAHLLSLVDV MOREGGPSOI GDALGFAVRY LTSEMHGARP GASKAVVILV
 1800
 TDVSVDSVDA AADAARSNRV TVFPIGIGDR YDAAQLRILA GPAGDSNVVK LQRIEDLPTM
 1860
 VILGNSFLHK LCSGEVRICM DEDGNEKRPG DVWILPDOCH TVICOPDGOT LLKSHRVNCD
 1920
 RGLRPSCPNS QSPVKVBETC GCRWTCPCVC TGSSTRHIVT FDGQNFKLTG SCSYVLFQNK 1980
 EQDLEVILHN GACSFGAROG CMKSIEVKHS ALSVELHSDM EVTVNGRLVS VPYVGGNMEV
 2040
15
 NVYGAIMHEV RFNHLGHIFT PTPQNNEPQL QLSPKTFASK TYGLCGICDE NGANDFMLRD 2100
 GTVTTDWKTL VOEWTVORPG OTCOPILEEO CLVPDSSHCO VLLLPLFARC HKVLAPATFY
 2160
 ALCOCOSCHO BOVCEVIASY AHLCRINGVC VDWRIPDFCA MSCPPSLVYN HCEHGCPRHC
 2220
 DGNVSSCGDH PSEGCFCPPD KVMLEGSCVP EEACTQCIGE DGVQHQFLEA WVPDHQPCQI
 2280
 CTCLSGRKVN CTTQPCPTAK APTCGLCEVA RLRQNADQCC PEYECVCDPV SCDLPPVPHC
 2340
20
 ERGLOPTLYN PGECRPNFTC ACRKEECKRV SPPSCPPHRL PTLRKTQCCD EYECACNCVN 2400
 STYSCPLGYL ASTATNDCGC TTTTCLPDKV CVHRSTIYPV GQFWEBGCDV CTCTDMEDAV
 2460
 MGLRVAQCSQ KPCEDSCRSG FTYVLHEGEC CGRCLPSACE VVTGSPRGDS QSSWKSVGSQ
 2520
 WASPENPOLI NECVRYKEEV FIGORNVSCP OLEVPYCPSG FOLSCKTSAC CPSCRCERME 2580
 ACMINGTVIG PGKTVMIDVC TTCRCMVQVG VISGFKLECR RTTCNPCPLG YKEENNTGEC
CGRCLPTACT IQLRGGQIMT LKRDETLQDG CDTHFCKVNE RGBYFWEKRV TGCPPFDEHK
 2640
25
 2700
 CLAEGGKIMK IPGTCCDTCE EPECNDITAR LQYVKVGSCK SEVEVDIHYC QGKCASKAMY 2760
 SIDINDVODO CSCCSPTRTE PMOVALHCTN GSVVYHEVLN AMECKCSPRK CSK
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30 seq ID NO: 150 <u>DNA sequence</u> Nucleic Acid Accession #: NM\_001508.1

Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

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35
 11
 21
 31
 41
 51
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAAA TCATTGATCA CAGTCATGTC
 60
 CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTGTA CCTGATCATC
 120
 TTCGTGATGG GCCTTCTGGG GAACAGCGTC ACCATTCGGG TCACCCAGGT GCTGCAGAAG
 180
40
 AAAGGATACT TGCAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTCGGACATC
 240
 TIGGTGTTCC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCCTGACC
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 GCTACGCTGC TGCACGTGCT GACGCTCAGC TTTGAGCGCT ACATCGCCAT CTGTCACCCC
 TTCAGGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG
 480
45
 GTCACCTCCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCCTG
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 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCGCT CCAGCACCCG CCACCACGAG
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 720
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 780
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 ACGCGGCCTC CGCAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG
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 CCGCTCCTGT ACACGGTGTC CTCGCAGCAG TTTCGGCGGG TGTTCGTGCA GGTGCTGTGC 1080
55
 TGCCGCCTGT CGCTGCAGCA CGCCAACCAC GAGAAGCGCC TGCGCGTACA TGCGCACTCC
 1140
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 AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA
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60

Seq ID No: 151 Protein sequence: Protein Accession #: NP\_001499.1

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65
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 21
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 41
 51
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 KGYLOKEVTD HMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY
 120
 ATLLHVLTLS FERYLAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMSTEYPL
 180
70
 VNVPSHRGLT CNRSSTRHHE QPETSNMSIC THLSSRWIVF QSSIFGAFVV YLVVLLSVAF
 240
 MCWNMMOVLM KSOKGSLAGG TRPPOLRKSE SEESRTARRO TIIFLRLIVV TLAVCWMPNO
 300
 TERTMANARY KHOWTESYER AYMILLPESE TERVISSYIN PLLYTYSSOC FRRVEVOVIC
 360
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEPO
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 SKSOSLSLES LEPNSGAKPA NSAAENGFOE HEV
75
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Seq ID NO: 152 DNA sequence

Nucleic Acid Accession #: none found

Coding sequence: 3-65 (underlined sequences correspond to start and stop codons)

5 31 41 51 TTATTATTTT GTGTAAACTA TATTCTGCTT ATAGAGAGTC TCTGAGACTA AAATTGACAA 60 CTTGAAAAGT ATTCCAAGGA ATATTATGAA AATAGGGCAA CATGGACTGT TTAAGATCTC 120 CATGUARTE ARATTCATGC ARGGRARCAR CTCATAGARA AGRIRARTAT GGATGCCCTT 180 10 CACATGTTAT CAACCTCGTA ACTTTTGGTG CTTGCTGAAT CAGTCCATGA AAAGCTACAG 240 CCCGCTCTTT GGGAATGCTA CATACCCATT TCTGGTATTT AAAAAATATC TAGGAGGAGC 300 TALATGACAA AACACAGCAG TGTTTTGAGG GAGAAAGGAC CATCATTTAT AATGCTCTGT 360 ACATACTACC AGAGCTGCTT GGAAAATTAA AGGCCACTTG TGGCTTTTTC CTACCAACTG 420 ATACGTTTAA ATTTGCCCTA GGATTSAGCT AACAGCAAAA AAAAAAAAA AAAAAAAARA 480 GAGAGAAAGA AAGGAGKAAA CAGTGGTAAT AAAAAAATCC ATCTGTCTTC TTGCTATGTT 540 AATATTAATA AATCATAATA TGACAAGACC CTCACTGAAT AAGAGTATIT TCAGTCATCA 600 GAAGCCAGCT GTTGGTAGGC ATTAATGAGT TTAAAATTGT TCTCAATTGA AAAAACATCA 660 CACTATTTTG CCAAAACCAA AGTAATTATA ATACTGTGTC CTCCTGTAAT TTTTTGAGAA 720 GTGGTTATAA AGGGCATATT TACATAAATT CTACTTTATT CCTCAACTTC TTTGATGAAT 780 GTAACCCAAT TTTACTTCTT TAAAAAGTCT CAATTCAAGC TGGATTAGCC AGCTCAGCAT 20 840 AATCAACTAG ACAGTGGTTT GTTAAATTTA GCAGCATACT TCGTTCCCAT TCTAATTAAA 900 GTCATGAGTT CTTGAATCCC AGAGAAATAA TGCTTAGGAA CTTCTCTCAA TCTGCTTGGC 960 TTGGCCTAGA GAAGTGGCCA TTTTATCAAC AGGRAAAAAA AAAATTTTCT CTACTACAAC 1020 CCCGTTGCCT TCTGAAAAAC AGCAAGTTAT TTCTTTATAT AATTATCATT TTATTATTTT 1080 25 ATGGAAAATT AATTTATTAA TTAATAGCCT ATTATGTGTT CTCACTTGCT TCTCTAAGTA 1140 ATATTTTGAG ATAAAATGTT GAATAAAACC ATGGATTATA GAGAAAAGTC AAAATATATG 1200 TGTAATATT AATTATTTA TAAGTTTTAT AATAAAGTAT TCCATTTCTT TATCTT

30 Seq ID No: 153 Protein sequence: Protein Accession #: none found

Seq ID NO: 154 DNA sequence

Nucleic Acid Accession #: none found

40 Coding sequence: 1-36 (underlined sequences correspond to start and stop codons)

21 41 CTGGATGATA TGGAAGAAAT GGATGGGTTA AGG<u>TAA</u>AAGG CTGATCACAG ATGGGTTCCT 60 CTCAAGGTTA AAATAGTTTA AGTGCCAGAA GAAAAGGTGG GCACCAGCGA ATTAAGAACC 120 ATCTTTGAAT GGTCCCCTTG GTTAAATACT TAACTTTTGT CATCAGTGTC TGCATTTATG 100 AAATGAAGAG GAATTCACTA ATATGCTACG TGATCTTTTG TTTGTCATGA AAAGAGTTAC 240 TOTTGTGTAG TTCTCTGTTC CAGGGCTGCC TTTGCTCCAC AAAGCACTGA GAAGCAGTGG 300 CCCTGTACAA CCATACTGCC TCTCAACACT GTGTAATAGG CTAACACCGC CCAGCGAACC 50 360 

Seq ID No: 155 Protein sequence:

Protein Accession #: none found

1 11 21 31 41 5

Seq ID NO: 156 DNA sequence

11

60

Nucleic Acid Accession #: NM 032961.1

21

65 Coding sequence: 827-3949 (underlined sequences correspond to start and stop codons)

31

41

51

|    | concome                                 | ammamaamaa     | CATICACCAAC                             | ANDADADACC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GAGGACAGTC      | mmea a amame                           | 480  |
|----|-----------------------------------------|----------------|-----------------------------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------|----------------------------------------|------|
|    |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 |                                        |      |
|    |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 | CGCTGACTAT                             | 540  |
|    | TGTATTATTG                              | TTATTTTATT     | AATTAGTCAG                              | TGGAAAGATT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ACAGATGAGG      | AAAGGGGACG                             | 600  |
|    | CCTGTCACCC                              | TTCCTGTGCT     | AAGATTTAAA                              | AAAAAATGAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GCTGGATTGC      | GGGAAGCTCT                             | 660  |
| 5  | AAAATGAAGC                              | BARAGGAGTA     | AGATTTTTAA                              | AGACAGAAAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCACAGGAGC      | CCCCACGTAG                             | 720  |
| -  | OCICA OTHERDINA                         | mmmama mmmm    | TOTAL CASTITUTE                         | THE PROPERTY OF THE PROPERTY O | GTGGTGGTCC      | GGGAGGTGAT                             | 780  |
|    | -CCGMCIIIIM                             | 1110101111     | 22222222                                | maammaaamm                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | mmoar armar     | TTGTGCTATT                             | 840  |
|    | TGGGTGGCTG                              | ACTGGCTGCG     | GGAAGCTACT                              | TCCTTTCCTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TTOGMGMTGA      | TIGIGCIATI                             |      |
|    | ATTGTTTGCC                              | TTGCTCTGGA     | TGGTGGAAGG                              | AGTCTTTTCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CAGCTTCACT      | ACACGGTACA                             | 900  |
|    | GGAGGAGCAG                              | GAACATGGCA     | CTTTCGTGGG                              | GAATATCGCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GAAGATCTGG      | GTCTGGACAT                             | 960  |
| 10 | TACAAAACTT                              | TCGGCTCGCG     | GGTTTCAGAC                              | GGTGCCCAAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TCAAGGACCC      | CTTACTTAGA                             | 1020 |
|    | CCACA ACCAN                             | GAGACAGGGG     | TOCTOTACOT                              | CARCCACARA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATAGACCCCC      | AACAAATCTG                             | 1080 |
|    | CCICAACCIG                              | GAGACAGGGG     | TOCTOTACOI                              | ganconorma.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | OTTO COCCO      | GGGWGGA GGW                            | 1140 |
|    | CAAACAGAGC                              | CCCTCCTGTG     | TCCTGCACCT                              | GGAGGTCTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CIGGAGAACC      | CCCTGGAGCT<br>TCCCGGAGCC               |      |
|    | GTTCCAGGTG                              | GAGATCGAGG     | TGCTGGACAT                              | TAATGACAAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCCCCCTCTT      | TCCCGGAGCC                             | 1200 |
|    | AGACCTGACG                              | GTGGAAATCT     | CTGAGAGCGC                              | CACGCCAGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ACTCGCTTCC      | CCTTGGAGAG                             | 1260 |
| 15 | CGCATTCGAC                              | CCAGACGTGG     | GCACCAACTC                              | CTTGCGCGAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TACGAGATCA      | CCCCCAACAG                             | 1320 |
|    | CTACTTCTCC                              | CTGGACGTGC     | aGACCCAGGG                              | GGATGGCAAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CGATTCGCTG      | AGCTGGTGCT                             | 1380 |
|    |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 | CCGCGGTGGA                             | 1440 |
|    |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 | CAGGCCTGCC                             | 1500 |
|    |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 |                                        |      |
|    |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 | ACTCCAATGA                             | 1560 |
| 20 | CAATGTGCCC                              | GCTTTCGACC     | AACCCGTCTA                              | CACTGTGTCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CTACCAGAGA      | ACTCTCCCCC                             | 1620 |
|    | AGGCACTCTC                              | GTGATCCAGC     | TCAACGCCAC                              | CGACCCGGAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GAGGGCCAGA      | ACCCTGACCT                             | 1680 |
|    | AGGCACTOTC                              | mmanacanaca    | * C************                         | concededate                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | GAGCTTTTCG      | Carmencec                              | 1740 |
|    | CGIGIACICC                              | TICAGCAGCC     | ACMITICUCC                              | ccooococoo                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GMGCITITCG      | GACICICOCC                             |      |
|    | GCGCACTGGC                              | AGACTGGAGG     | TAAGCGGCGA                              | GTTGGACTAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GAAGAGAGCC      | CAGTGTACCA                             | 1800 |
|    | AGTGTACGTG                              | CAAGCCAAGG     | ACCTGGGCCC                              | CAACGCCGTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCTGCGCACT      | GCAAGGTGCT                             | 1860 |
| 25 | AGTGCGAGTA                              | CTGGATGCTA     | ATGACAACGC                              | GCCAGAGATC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AGCTTCAGCA      | CCGTGAAGGA                             | 1920 |
|    | AGCGGTGAGT                              | gaggggggg      | CGCCCCGGCAC                             | TOTOGOTOGOC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | CTTTTCAGCG      | TGACTGACCG                             | 1980 |
|    | CCA CECCACACAC                          | Cacaaacacac    | POCCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO | Caractrocc                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GGAGACGTGC      | Chinacoccou                            | 2040 |
|    | CGACTCAGAG                              | GAGAATGGGC     | MOGIGCHOIG                              | CGMGCTACTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GGMGMCGTGC      | CITICOGCCI                             |      |
|    | CAAGTCTTCC                              | TTTAAGAATT     | ACTACACCAT                              | CGTTACCGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GCCCCCTGG       | ACCGAGAGGC                             | 2100 |
|    | GGGGGACTCC                              | TACACCCTGA     | CTGTAGTGGC                              | TCGGGACCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GGCGAGCCTG      | CGCTCTCCAC                             | 2160 |
| 30 | CAGTAAGTCG                              | ATCCAGGTAC     | AAGTGTCGGA                              | TGTGAACGAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AACGCGCCGC      | GTTTCAGCCA                             | 2220 |
|    | GCCGGTCTAC                              | CACCTCTATC     | TOROTORARA                              | CARCOTOCCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GGCGCCTACA      | TCTACGCGGT                             | 2280 |
|    | arcadacaraa                             | CACCOCCATC     | 1000000000                              | OCCOCCA COMM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | CCCCC CTTCT     | TCCTCGAGTG                             | 2340 |
|    | GAGCGCCACC                              | GACCGGGAIG     | AGGGCGCCAA                              | COCCCAGCII                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GCCIACICIA      | ICCICGMGIG                             | 2400 |
|    |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 | ACGGCTACTT                             |      |
|    |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 | AGGTGGAAGC                             | 2460 |
| 35 | CCGGGACGCT                              | GGCAGCCCCC     | AGGCGCTGGC                              | TGGTAACGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ACTGTCAACA      | TCCTCATAGT                             | 2520 |
|    | GGATCAAAAT                              | GACAACGCCC     | CTGCCATCGT                              | GGCGCCTCTA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCAGGGCGCA      | ACGGGACTCC                             | 2580 |
|    | 200000000000000000000000000000000000000 | anconacca      | CIGCCIIICGI                             | COCCCCTTAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CTGCTCACCC      | accaraccac                             | 2640 |
|    | MGCGCGIGMG                              | GIGCIGCCCC     | GCICGGCGGA                              | GCCGGGTTAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CIGCICACCC      | 0001000000                             | 2700 |
|    | CGTGGACGCG                              | GACGACGGCG     | AGAACGCCCG                              | GCTCACTTAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AGCATCGTGC      | GTGGCAACGA                             | 2700 |
| 40 | AATGAACCTC                              | TTTCGCATGG     | ACTGGCGCAC                              | CGGGGAGCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CGCACAGCAC      | GCCGAGTCCC                             | 2760 |
| 40 | GGCCAAGCGC                              | GACCCCCAGC     | GGCCTTATGA                              | GCTGGTGATC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GAGGTGCGCG      | ACCATGGGCA                             | 2820 |
|    | GCCGCCCCTT                              | TCCTCCACCG     | CCACCCTGGT                              | GGTTCAGCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GTGGATGGCG      | CCGTGGAGCC                             | 2880 |
|    | CCAGGGGGGG                              | GGCGGGAGCG     | CAGGCGGAGG                              | GTCAGGAGAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CACCAGCGCC      | CCGTGGAGCC<br>CCAGTCGCTC               | 2940 |
|    | magagagaga                              | as a saconocca | magaggggag                              | CONCARCORC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | amon monocom    | TGGGCTCGGT                             | 2000 |
|    | 10000000                                | GRANCCICGC     | TAGACCICAC                              | CCICATCCIC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATCATCGCGT      | 10000010001                            | 3060 |
| 40 | GTCCTTCATC                              | Treergergg     | CCATGATCGT                              | GCIGGCCGIG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CGTTGCCAAA      | AAGAGAAGAA                             |      |
| 45 | GCTCAACATC                              | TATACTTGTC     | TGGCCAGCGA                              | TTGCTGCCTC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TGCTGCTGCT      | GCTGCGGTGG                             | 3120 |
|    | CGGAGGTTCG                              | ACCTGCTGTG     | GCCGCCAAGC                              | CCGGGCGCGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AAGAAGAAAC      | TCAGCAAGTC                             | 3180 |
|    | AGACATCATG                              | CTGGTGCAGA     | GCTCCAATGT                              | ACCCAGTAAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCGGCCCAGG      | TGCCGATAGA                             | 3240 |
|    | aga amagaga                             | coommocom      | CCC2 CC2 CC2                            | CARCCACAAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TACTOCTATO      | AGGTATGCCT                             | 3300 |
|    | GGAGICCGGG                              | 9901119901     | GCCACCACCA                              | CANCOMONAL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | COCCUCIO        | CTTCGCGGAG                             | 3360 |
| 50 | GACCCCTGAG                              | TCCGCCAAGA     | CCGACCIGAT                              | GITTCTTMAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCCIGCMGCC      | CTTCGCGGAG                             |      |
| 50 | TACGGACACT                              | GAGCACAACC     | CCTGCGGGGC                              | CATCGTCACC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GGTTACACCG      | ACCAGCAGCC                             | 3420 |
|    | TGATATCATC                              | TCCAACGGAA     | GCATTTTGTC                              | CAACGAGACT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AAACACCAGC      | GAGCAGAGCT                             | 3480 |
|    | CAGCTATCTA                              | GTTGACAGAC     | CTCGCCGAGT                              | TAACAGTTCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GCATTCCAGG      | AAGCCGACAT                             | 3540 |
|    | POST POST COL                           | AAGGACAGTG     | GTCATGGAGA                              | CACTICAACAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | GGAGATAGTG      | ATCATGATGC                             | 3600 |
|    | UP CCD P CCC                            | CCCCACTC       | CICUIGONGA                              | TOTOMORPO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | AATTCCACTC      | AGGAATGTAA                             | 3660 |
| 55 | CACCAMCCGT                              | GCCCM31CAG     | CAGGINIGGA                              | TOTOTTOTO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | CHICACHUTCH CTG | AMOUNT COCCO                           |      |
| JJ | AGCTCTGGGC                              | CACTUAGATO     | GGTGCTGGAT                              | GCCTTCTTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GICCUTTCTG      | MIGGACGCCA                             | 3720 |
|    | GGCTGCTGAT                              | TATCGCAGCA     | ATCTGCATGT                              | TCCTGGCATG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GACTCTGTTC      | CAGACACTGA                             | 3780 |
|    | GGTGTTTGAA                              | ACTCCAGAAG     | CCCAGCCTGG                              | GGCAGAGCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TCCTTTTCCA      | ATGGACGCCA<br>CAGACACTGA<br>CCTTTGGCAA | 3840 |
|    | 20202220000                             | CONCACACCA     | CTCTGGAGAG                              | CANCGAGCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GATGGACTGC      | TGACTAATAC                             | 3900 |
|    | CCC2 CCCCC                              | TACARACCAC     | CATATITICAC                             | ACCCA A A ACCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ATATICOTACE     | CAATTCTACA                             | 3960 |
| 60 | GCGMGCGCCI                              | TACAAACCAC     | CAIATTIGAC                              | ACCOMMUNICO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | AINIGCING!      | CAMITCIACA                             | 4020 |
| 00 |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 | CAACTTTTCA                             |      |
|    |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 | TTCGGATGGA                             | 4080 |
|    | GTCATCATGG                              | CCAATTATAG     | GACCTAATTG                              | CTCTCAGCAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GCCTGAGAAA      | TGAGTTGAAA                             | 4140 |
|    | TGTGCAGAAC                              | TGTAGAAACT     | TTAGAGGCAA                              | CAGATTTTGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CTCCCCGATC      | AGTGTGTGCC                             | 4200 |
|    | TOTTTACAGO                              | ACTATOTATO     | THEOLOGICAL                             | CARATGTCAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TGAGCCCTTT      | AGATGTTTAT                             | 4260 |
| 65 | I GTT I ACAGC                           | ACTATOTATO     | COMPARATOR                              | CHRIGICAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | COCCAMBLE       |                                        | 4320 |
| 00 | ATTCACCACG                              | AGAAGCCAGT     | CATAAAGATA                              | MADGAAATTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GIGCATTATA      | AATGCAATAT                             |      |
|    | CACTGTTTTA                              | AACTTGACTG     | TTTTATATTA                              | TTTTTGTGTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATCAAGTGTT      | CCGCAAGCTA                             | 4380 |
|    | TTCCAACTTT                              | ACAAGAGAAA     | TTGTGATTAT                              | GITCTTTTCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCTGTGGGTT      | ATAAAAAATG                             | 4440 |
|    | TTGTATTCTG                              | AAGACCCACA     | AAATATCAAA                              | GACATTCTGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AGTTTATACA      | CCGTGTTGCA<br>TATTATATTA<br>ATACAGTCCA | 4500 |
|    | A A CONCOUNTED A C                      | TOTALOTATION   | CARACCTTOT                              | ADDTADATAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | BARATATATA      | TATTATATA                              | 4560 |
| 70 | MAGIGITIAC                              | COLMCIAITT     | CHAMGETTET                              | COMPCOMMUNICAL PROPERTY.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ANAPORTOR       | PARCECACA IN                           | 4620 |
| /0 | TATAATTTTC                              | CIAMAATGTG     | GIACAACICA                              | GITGGTTTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | MALI GOMI GC    | ATHCHOTCCA                             |      |
|    | CATCATACAA                              | TAAAATAAAA     | GGTAATTCAG                              | GGTCCCAAAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ACAAACTTAC      | TAAGAAAAA                              | 4680 |
|    | TCATTAATAG                              | TTTTCTCCCA     | ATTTCCATAT                              | CTTACTCAAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CGTGTTTTTC      | CITCITTAAA                             | 4740 |
|    | ACAAAATGAT                              | GCTCTAAGCT     | ACAAAATTTT                              | GTCAAAAACT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CATATTGAAT      | TTTCAATGCC                             | 4800 |
|    | ANACATOTAC                              | CTATTOATOT     | TATCAGACAG                              | AGCACTGACT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATGTACTATC      | AAACTATCTA                             | 4860 |
| 75 |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 |                                        |      |
| 13 | ACAATCTGCA                              | TMMGTCTGAT     | TUTATTTUTA                              | TOMCTTTGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TTTAGAATCA      | CIIMMIGCIT                             | 4920 |
|    | TTATAAAGAA                              | TCGATAAATT     | CACCTGTATT                              | TGTTGTTAGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AAAAAACTGG      | GIGTCTGTAC                             | 4980 |
|    |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 |                                        |      |
|    |                                         |                |                                         |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                 |                                        |      |

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ATTITUTUS GRANATARS SAATIGAGG THACTASTIT AGGARGEAT CAGTCAIACE
ACCACACAG AATTITATET TACATAGTT SECRETARIA TACATAGTT AGGARGEAT CAGTCAIACE
TATATITUTA TATGGARATETA THACHGARTHA GRAACACTOT AACTGOTAAA GAATAACTAT 5140
AAAACTAGAA AGGICTAAAN THACAGATATA GAAGACACTOT AACTGOTAAA GAATAACTAT 5240
AAAACTAGAA AGGICTAAAN THACAGATATA GAAGACACTOT TACATTATAT GAAGAACATA 5340
TATTITUTA GATTCAGCT TACAAAANTA AGCTTGACTT THACTTTAT GTCAACAATA 5340
TATATITUTA AANTTAGTAG AGCCCATAAA AAAAAAAAA AAAA
```

Seq ID No: 157 Protein sequence:
10 Protein Accession #: NP\_116586.1

|    | 1          | 11         | 21         | 31         | 41         | 51         |      |
|----|------------|------------|------------|------------|------------|------------|------|
|    | 1          | 1          | 1          | 1          | 1          | 1          |      |
| 15 | MIVLLEPALL | WMVEGVFSOL | HYTVOEEOEH | GTFVGNIAED | LGLDITKLSA | RGFQTVPNSR | 60   |
|    | TPYLDLNLET | GAFAANEKID | REGICKOSPS | CATHTRALTE | NPLELFQVEI | EVLDINDNPP | 120  |
|    | SFPEPDLTVE | ISESATPGTR | FPLESAFDPD | VGTNSLRDYE | ITPNSYFSLD | VQTQGDGNRF | 180  |
|    | AELVLEKPLD | RECOAVHRYV | LTAVDGGGGG | GVGEGGGGG  | GAGLPPOQQR | TGTALLTIRV | 240  |
|    | LOSNONVPAF | DOPVYTVSLP | ENSPPGTLVI | QLNATDPDRG | QNGEVVYSFS | SHISPRAREL | 300  |
| 20 | FGLSPRTGRL | EVSGELDYEE | SPVYOVYVQA | KDLGPNAVPA | HCKVLVRVLD | ANDNAPEISF | 360  |
|    | STVKEAVSEG | AAPGTVVALF | SVTDRDSEEN | GQVQCELLGD | VPFRLKSSFK | NYYTIVTEAP | 420  |
|    |            |            |            |            |            | YVTENNVPGA | 480  |
|    |            |            |            |            |            | FDYRQLKDFS | 540  |
|    | FQVEARDAGS | POALAGNATV | NILIVDQNDN | APAIVAPLPG | RNGTPAREVL | PRSABPGYLL | 600  |
| 25 |            |            |            |            |            | QRPYBLVIEV | 660  |
|    |            |            |            |            |            | SLDLTLILII | 720  |
|    | ALGSVSFIFL | LAMIVLAVRC | QKEKKLNIYT | CLASDCCLCC | CCCGGGGSTC | CGRQARARKK | 780  |
|    |            |            |            |            |            | KTDLMFLKPC | 840  |
|    |            |            |            |            |            | RPRRVNSSAF | 900  |
| 30 |            |            | SDHDATNRAQ |            |            |            | 960  |
|    | SDGROAADYR | SNLHVPGMDS | VPDTEVFETP | EAQPGAERSF | STFGKEKALH | STLERKELDG | 1020 |
|    | LITHTRAPYK | PPYLTRKRIC |            |            |            |            |      |

Seq ID NO: 158 DNA sequence
35 Nucleic Acid Accession #: NM 022159.1

Coding sequence: 70-1890 (underlined sequences correspond to start and stop codons)

|    | 1          | 11         | 21                 | 31         | 41         | 51         |      |
|----|------------|------------|--------------------|------------|------------|------------|------|
| 40 | 1          | 1          | 1                  | 1          |            |            |      |
|    | GTGAAATTTA | AACTCCAGTC | CTGTGGCGAA         | AATGCTAATT | GCACTAACAC | AGAAGGAAGT | 60   |
|    |            |            |                    |            |            | GTTTATCACT | 120  |
|    |            |            | AGAAAATGTG         |            |            |            | 180  |
|    | ATAGCTGCAA | ATATTAATAA | AACTTTAACA         | AAAATCAGAT | CCATAAAAGA | ACCIGIGGCT | 240  |
| 45 |            |            | AAATTCTGTG         |            |            |            | 300  |
|    |            |            | ATCATCTTCA         |            |            |            | 360  |
|    |            |            | CTCAACTCTT         |            |            |            | 420  |
|    |            |            | AGTTTGGGAC         |            |            |            | 480  |
|    |            |            | TGTTGAACAA         |            |            |            | 540  |
| 50 |            |            | AAATTCAACG         |            |            |            | 600  |
|    |            |            | TCATCCTCAT         |            |            |            | 660  |
|    |            |            | ATATGATTCA         |            |            |            | 720  |
|    |            |            | GCTTTCATCA         |            |            |            | 780  |
|    |            |            | GGAAAGAGTC         |            |            |            | 840  |
| 55 |            |            | TGAACTTGAA         |            |            |            | 900  |
|    |            |            | TCTATGTGCA         |            |            |            | 960  |
|    |            |            | CTGTGAGCTG         |            |            |            | 1020 |
|    |            |            | TTTTGCAATT         |            |            |            | 1080 |
|    |            |            | AAGGATCACT         |            |            |            | 1140 |
| 60 |            |            | CTTCTGGTTC         |            |            |            | 1200 |
|    |            |            | TAGCCTATTT         |            |            |            | 1260 |
|    |            |            | CTTCTGTTCA         |            |            |            | 1320 |
|    |            |            | GTGCATTGAA         |            |            |            | 1380 |
|    |            |            | TTTGCACAAG         |            |            |            | 1440 |
| 65 |            |            | GGCAGCACTA         |            |            |            | 1500 |
|    |            |            | CAACTTTATT         |            |            |            | 1560 |
|    |            |            | TTTTGGAGTC         |            |            |            | 1620 |
|    |            |            | TTGCTTTGAG         |            |            |            | 1680 |
|    |            |            | CACCACCTGG         |            |            |            | 1740 |
| 70 |            |            | CTTCACAGTC         |            |            |            | 1800 |
|    |            |            | TAGAAAGATT         |            |            |            | 1860 |
|    |            |            | TTTAAGG <u>TAA</u> |            |            |            | 1920 |
|    |            |            | CTGTGGATGA         |            |            |            | 1980 |
|    |            |            | AAAAAGTATT         |            |            |            | 2040 |
| 75 |            |            | AATTATGTAT         |            |            |            | 2100 |
|    | AATAGTTCTG | TCAAAAATAG | TATTGCAGAT         | ATTTGGAAAG | TAATTGGTTT | CICAGGAGTG | 2160 |

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ATATCACTGC ACCCAAGGAA AGATTTTCTT TCTAACACGA GAAGTATATG AATGTCCTGA 2220
 AGGARACCAC TGGCTTGATA TTTCTGTGAC TCGTGTTGCC TTTGAAACTA GTCCCCTACC 2280
 ACCTOGGTAA TGAGCTCCAT TACAGAAAGT GGAACATAAG AGAATGAAGG GGCAGAATAT
 2340
 CAAACAGTGA AAAGGGAATG ATAAGATGTA TTTTGAATGA ACTGTTTTTT CTGTAGACTA
 2400
 5
 GCTGAGAAAT TGTTGACATA AAATAAAGAA TTGAAGAAAC ACATTTTACC ATTTTGTGAA
 2460
 TTGTTCTGNA CTTAANTGTC CACTAAAACA ACTTAGACTT CTGTTTGCTA AATCTGTTTC 2520
 TTTTTCTAAT ATTCTAAAA
 Seg ID No: 159 Protein seguence:
10
 Protein Accession #: NP 071442.1
 51
 11
 21
 21
 41
15
 MCVPGFRSSS NODRFITNDG TVCIENVNAN CHLDNVCIAA NINKTLTKIR SIKEPVALLQ
 EVYRNSVTDL SPTDIITYIE ILAESSSLLG YKNNTISAKD TLSNSTLTEF VKTVNNFVQR
 120
 DTFVVWDKLS VNHRRTHLTK LMHTVEQATL RISQSFQKTT EFDTNSTDIA LKVFFFDSYN
 180
 MKHIHPHMMM DGDYINIFPK RKAAYDSNGN VAVAFLYYKS IGPLLSSSDN FLLKPQNYDN
 240
 SEEEERVISS VISVSMSSNP PTLYELEKIT FTLSHRKVTD RYRSLCAFWN YSPDTMNGSW
 300
20
 SSEGCELTYS NETHTSCRCN HLTHFAILMS SGPSIGIKDY NILTRITOLG IIISLICLAI
 CIFTFWFFSE IQSTRTTIHK NLCCSLFLAE LVFLVGINTN TNKLFCSIIA GLLHYFFLAA
 420
 FAWMCIEGIH LYLIVYGVIY NKGFLHKNFY IFGYLSPAVV VGFSAALGYR YYGTTKVCWL
 480
 STENNFIWSF IGPACLIILV NLLAFGVIIY KVFRHTAGLK PEVSCFENIR SCARGALALL
 540
 FLLGTTWIFG VLHVVHASVV TAYLFTVSNA FOGMFIFLFL CVLSRKIQEE YYRLFKNVPC
 600
25
 CEGCLE
 Seq ID NO: 160 DNA sequence
 Nucleic Acid Accession #: none found
30
 Coding sequence: 1-216 (underlined sequences correspond to start and stop codons)
 11
 21
 31
 41
 51
35
 TGTCTGCTTA TGCGGTGGCT CGCTGCTCAG AACAGGATGG CAGAGATGAG CACCACCATC
 60
 AAAAACTCAA GGACCAGTGC TGTGGGTCCA GTCATCTGTT TCATGGAATT CACCAGTCTG
 120
 GTATCTTCAA AATCCAGAAG GATGATGGCA GATGGCAGGA AGGAGGAAGA GGGTAATCTG
GAAGAGTTTC CTGACCTACT CTGCTGCTGT GAT<u>TAA</u>ACAA CCACCAGGAA ATTTTGATGA
 180
 240
 CACTGTTCTC CTGAGCTCCT CCCTTTCCTC GGGGAAGAAA AGCATTGAAA CTACAAAAAT
 300
40
 AAAGTGTTAT TTGGCTGGAG TGAGGTCTCA TGTCTGCTTA TGCGGTGGCT CGCTGCTCAG
 360
 AACAGGGAAC CATTGGAGAT ACTCATTACT CTTTGAAGGC TTACAGTGGA ATGAATTCAA
 420
 ATACGACTTA TTTGAGGAAT TGAAGTTGAC TTTATGGAGC TGATAAGAAT CTTCTTGGAG
 480
 AAAAAAAGAC TGGTACTTCT GAATTAACCA AAATCACAGT ATTCTGAAGA TGATTCTACA
 540
 AAGCCTGCTG TTTCTACAAA GGCTGCTGAT GATTTCTACA AAGCCTGCTG TAGTGTTGCT
 600
45
 GTGGCCTCTG CTTAAAAAAG TAGAAAACAC ATTGATGCAG CATGTTCACC CCAACCTCCC
 660
 TGCCTARAGG CTCAGGGACC ATCTTGGAAG AGGAAGGCGG GTGAGATTGT AAGAGCCGAA
TTAGGGGGAT GGAGTGTGGA GAATAAGGAC ACTTCATCTT GGATGCTCAC CTGCCAAATT
 720
 780
 GACTTCTGAT GAAAGCCAGC TCCAGAAATG TGCCTACAGT TACTACTTTC ACCTAAACCC
 840
 TGCCCTTAGT CAAATCCTTC TCTTCTTCTA AGCAATCAAC TTCAATTCCT TGTATAACCC
 900
 ACAGTATARA AGGCTTTTA TACCATTCTA TCCTATTGCA TGTAAGCCTT GGGTCTGGGA GGTAACAGTG TGGGATTCCA CCATCTCATC TCCCTGCCAC CCAAACATGC CTGCTCTTCT 1020
 TTAAGCAATA TTAAATGTTT GTACTTCA
 Seq ID No: 161 Protein sequence:
55
 Protein Accession #: none found
 31
 41
 51
 11
 21
 CLLMRWLAAQ NRMAEMSTTI KNSRTSAVGP VICHMEFTSL VSSKSRRMMA DGRKEEBGNL
60
 60
 EEFPDLLCCC D
 Seq ID NO: 162 DNA sequence
 Nucleic Acid Accession #: none found
65
 Coding sequence: 1-159 (underlined sequences correspond to start and stop codons)
 37
 51
 11
 21
 41
70
 GAGACCCTCC AGAGGCAGGG CCCAGGATTG AAGAGGGAAG CCCTGCTCCA CACGTGTTCA
 60
 TCAGGAAGGA CCCACAGACT GCTGCTCCTG GAGGCCTCTC GGTTTATGGA TGTGTGTTTG
 120
 TTCCATAAAC CCTCAGAGGG TCACCTGGAG ACCCGCTAAA ATGCAGGTTC TTGGGCCACA
 180
 TCCTAGACCT TCTGACCGAC CCAGGGAGTG GGGCCCAGGA AGCTGCATTT GACAGATATC
 240
 CCCGTGTGAT CATCATGCAC ACAGGAGTGA GAGAACCAGT GTTCTCCCCG GGCAGAAGGG
 300
75
```

360

AAGCTCGTGT GCAGGACACC TCACACCTCC TTTCCCATTC CCCTGCCAGG CTCTCCCTGC

TGA CATTGTT TTTCCCGGGG AGCTGTGAAT TCTGAAGATT AGGTTGCTTC TCACCCCAAG

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CTCCAGAAGT CCAGGCTGAG CCAAACCAAG CTTCAAGTTG TGCCTGGACT TGGAGAACCA
 480
 GGAGGTGAGG GGACTGACTA CTTGAAGATC ACATGGAGGA GGAGTCTGAT CCAGGCCCAG
 540
 GCACCAAGGA AAGGCCATGC AAGGACACAG GGAGAAGGGC AGCTGTCTGT AAGCCAGAAA
 600
 GAGCCTICAC TAGAAACCAA ATCAGCCAGA ACCITCATCT TGGACTITCC AGCCTTCAGA
 660
 5
 GATGTGAAAA AATAAATTTC TGTTGATTAA CCTAAAAAA
 Seq ID No: 163 Protein sequence:
 Protein Accession #: none found
10
 31
 41
 51
 11
 21
 ETLOROGPGL KREALLHTCS SGRTHRLLLL EASRFMDVCL FHKPSEGHLE TR
15
 Sec ID NO: 164 DNA sequence
 Nucleic Acid Accession #: NM_020241.1
 Coding sequence: 4-1557 (underlined sequences correspond to start and stop codons)
20
 21
 31
 51
 11
 41
 GCCATGCAGA CCCCGCGAGC GTCCCCTCCC CGCCCGGCCC TCCTGCTTCT GCTGCTGCTA
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 CTGGGGGGGG CCCACGGCCT CTTTCCTGAG GAGCCGCCGC CGCTTAGCGT GGCCCCCAGG
 120
 GROTACCTGA ACCACTATCC CGTGTTTGTG GGCAGCGGGC CCGGACGCCT GACCCCCGCA
 180
 GAAGGTGCTG ACGACCTCAA CATCCAGCGA GTCCTGCGGG TCAACAGGAC GCTGTTCATT
 240
 GGGGACAGGG ACAACCTCTA CCGCGTAGAG TTGGAGCCCC CCACGTCCAC GGAGCTGCGG
 300
 TACCAGAGGA AGCTGACCTG GAGATCTAAC CCCAGCGACA TAAACGTGTG TCGGATGAAG
 360
 GGCAAACAGG AGGGCGAGTG TCGAAACTTC GTAAAGGTGC TGCTCCTTCG GGACGAGTCC
 ACGCTCTTG TGTGCGGTTC CAACGCCTTC AACCCGGTGT GCGCCAACTA CAGCATAGAC
 480
30
 ACCCTGCAGC CCGTCGGAGA CAACATCAGC GGTATGGCCC GCTGCCCGTA CGACCCCAAG
 540
 CACGCCAATG TTGCCCTCTT CTCTGACGGG ATGCTCTTCA CAGCTACTGT TACCGACTTC
 600
 CTAGCCATTG ATGCTGTCAT CTACCGCAGC CTCGGGGACA GGCCCACCCT GCGCACCGTG
 660
 AAACATGACT CCAAGTGGTT CAAAGAGCCT TACTTTGTCC ATGCGGTGGA GTGGGGCAGC
 720
 CATGTCTACT TCTTCTCCG GGAGATTGCG ATGGAGTTTA ACTACCTGGA GAAGGTGGTG
 780
35
 GTGTCCCGCG TGGCCCGAGT GTGCAAGAAC GACGTGGGAG GCTCCCCCCG CGTGCTGGAG
 840
 AAGCAGTGGA CGTCCTTCCT GAAGGCGCGG CTCAACTGCT CTGTACCCGG AGACTCCCAT
 900
 TICTACTICA ACGIGCIGCA GGCTGTCACG GGCGTGGTCA GCCTCGGGGG CCGGCCCGTG
 960
 GTCCTGGCCG TTTTTTCCAC GCCCAGCAAC AGCATCCCTG GCTCGGCTGT CTGCGCCTTT
 3020
 GACCTGACAC AGGTGGCAGC TGTGTTTGAA GGCCGCTTCC GAGAGCAGAA GTCCCCCGAG
 1080
40
 1140
 GCCCCCGGGA TGCAGTACAA TGCCTCCAGC GCCTTGCCGG ATGACATCCT CAACTTTGTC
 1200
 AAGACCCACC CTCTGATGGA CGAAGCGGTG CCCTCGCTGG GCCATGCGCC CTGGATCCTG
 1260
 CGGACCCTGA TGAGGCACCA GCTGACTCGA GTGGCTGTGG ACGTGGGAGC CGGCCCCTGG
 1320
 GGCAACCAGA COGTTGTCTT CCTGGGTTCT GAGGCGGGGA CGGTCCTCAA GTTCCTCGTC
 1380
45
 COGCCCAATG CCAGCACCTC AGGGACGTCT GGGCGTGTGT GTCAAGTGGG CCACGCGTGC
 1440
 AGGGTGTGTG TCCACGAGCG ACGATCGTGG TGGCCCCAGC GGCCTGGGCG TTGGCTGAGC
 1500
 CGACGCTGGG GCTTCCAGAA GGCCCGGGGG CCTCCGAGGT GCCGGTTAGG AGTTTGAACC
 1560
 CCCCCACTC TGCAGAGGGA AGCGGGGACA ATGCCGGGGT TTCAGGCAGG AGACACGAGG
 1620
 AGGGCCTGCC CGGAAGTCAC ATCGGCAGCA GCTGTCTAAA GGGCTTGGGG GCCTGGGGGG
 1680
50
 COGCGAAGGT GGGTGGGGCC CCTCTGTRAA TACGGCCCCA GGGTGGTGAG AGACTCCCAT 1740
GCCACCCGTC CCCTTGTGAC CTCCCCCCTC TWACCTCCAG CTGACCATGC ATGCCACGTG 1800
 Sec ID No: 165 Protein sequence:
55
 Protein Accession #: NP_064626.1
 31
 41
 51
 MOTPRASPPR PALLLLLLL GGAHGLFPEE PPPLSVAPRD YLNHYPVFVG SGPGRLTPAE
60
 GADDLNIQRV LRVNRTLFIG DRDNLYRVEL EPPTSTELRY QRKLTWRSNP SDINVCRMKG
 120
 KOEGECRNFV KVLLLRDEST LFVCGSNAFN PVCANYSIDT LOPVGDNISG MARCPYDPKH
 180
 ANVALFSDGM LFTATVTDFL AIDAVIYRSL GDRPTLRTVK HDSKWFKEPY FVHAVEWGSH
 240
 UVFFFRRIAM RENYLEKYUV SRVARUCKNI VGGSPRVIEK OWTSFLKARL NCSVPGDSHF
 300
 YFNVLQAVTG VVSLGGRPVV LAVFSTPSNS IPGSAVCAFD LYQVAAVFEG RFREQKSPES
 360
65
 IWTPVPEDQV PRPRPGCCAA PGMOYNASSA LPDDILNFVK THPLMDEAVP SLGHAPWILR
 420
 TLMRHQLTRV AVDVGAGPWG NQTVVFLGSE AGTVLKFLVR PNASTSGTSG RVCQVGHACR
 490
 VCVHERRSWW PORPGRWLSR RWGFOKARGP PRCRLGV
 Sec ID NO: 166 DNA sequence
70
 Nucleic Acid Accession #: NM_032108.1
 Coding sequence: 39-2705 (underlined sequences correspond to start and stop codons)
 31
 47
75
 TOCGAGGOST CACCTCCTCC TGTCGCCTGG CCCTCGCCAT GCAGACCCCG CGAGCGTCCC
 CTCCCCGCCC GGCCCTGCTG CTTCTGCTGC TGCTACTGGG GGGCGCCCAC GGCCTCTTTC
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|                      | CIGAGGACCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | GCCGCCGCTT                                                                                                                                                                                                                                                   | AGCGTGGCCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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                                                                                                                                               | TATCCCGTGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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|                      | TTGTGGGCAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | CGGGCCCGGA                                                                                                                                                                                                                                                   | CGCCTGACCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCGCAGAAGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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  | TTATGCGCGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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                                                                                                | TTTTTTTGCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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|                      | CTATGGATTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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  | ATTRCACAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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                                                                                                | TTTTTTTGCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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| 50                   | CTTTTGCGGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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  | ATTGCACAAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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                                                                                                | TTTTTTTGCA<br>GGGTGGCGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | AGGCAGGGGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 3060                                                                                                                      |
| 50                   | CTTTTGCGGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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  | ATTGCACAAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           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                                                                                                | TTTTTTTGCA<br>GGGTGGCGGC<br>ACCTAAGCCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | AGGCAGGGGA<br>TCCCCCACCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 3060<br>3120                                                                                                              |
| 50                   | GGCTTGGACG<br>CTGGAAAGGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        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  | ATTGCACAAC<br>ATGGGGGGCC<br>CCCAGGCCCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | TCCGTTCTCG<br>ACAGCTGCAG<br>TGGCGTGTGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | TTTTTTTGCA<br>GGGTGGCGGC<br>ACCTAAGCCC<br>GGGTGTGCGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | TCCCCCACCC<br>GCGTGTGCGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 3060<br>3120<br>3180                                                                                                      |
| 50                   | CTTTTGCGGT<br>GGCTTGGACG<br>CTGGAAAGGT<br>GCCGTGTTCG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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  | ATTGCACAAC<br>ATGGGGGGCC<br>CCCAGGCCCC<br>GCCGGGGAGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | TCCGTTCTCG<br>ACAGCTGCAG<br>TGGCGTGTGT<br>TGGGCGTGTGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | TTTTTTGCA<br>GGGTGGCGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | AGGCAGGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 3060<br>3120<br>3180<br>3240                                                                                              |
| 50                   | CTTTTGCGGT<br>GGCTTGGACG<br>CTGGAAAGGT<br>GCCGTGTTCG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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  | ATTGCACAAC<br>ATGGGGGGCC<br>CCCAGGCCCC<br>GCCGGGGAGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | TCCGTTCTCG<br>ACAGCTGCAG<br>TGGCGTGTGT<br>TGGGCGTGTGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | TTTTTTGCA<br>GGGTGGCGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | AGGCAGGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 3060<br>3120<br>3180<br>3240                                                                                              |
| 50                   | GCTTTTGGGGT<br>GGCTTGGACG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGTGGGCG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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  | ATTGCACAAC<br>ATGGGGGGCC<br>CCCAGGCCCC<br>GCCGGGGAGG<br>GTGGGCCACG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | TCCGTTCTCG<br>ACAGCTGCAG<br>TGGCGTGTGT<br>TGGGCGTGTG<br>CGTGCAGGGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | TTTTTTGCA<br>GGGTGGCGGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>GTGTGTCCAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | 3060<br>3120<br>3180<br>3240<br>3300                                                                                      |
|                      | CTTTTGCGGT<br>GGCTTGGACG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGTGGCC<br>CGTGGTGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  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  | ATTGCACAAC<br>ATGGGGGGCC<br>CCCAGGCCCC<br>GCCGGGGAGG<br>GTGGGCCACG<br>GGGCGTTGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | TCCGTTCTCG<br>ACAGCTGCAG<br>TGGCGTGTGT<br>TGGGCGTGTG<br>CGTGCAGGGT<br>TGAGCCGACG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | TTTTTTGCA<br>GGGTGGCGGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>GTGTGTCCAC<br>CTGGGGCCTTC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 3060<br>3120<br>3180<br>3240<br>3300<br>3360                                                                              |
|                      | CTTTTGCGGT<br>GGCTTGGACG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGTGGCC<br>CGTGGTGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  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  | ATTGCACAAC<br>ATGGGGGGCC<br>CCCAGGCCCC<br>GCCGGGGAGG<br>GTGGGCCACG<br>GGGCGTTGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | TCCGTTCTCG<br>ACAGCTGCAG<br>TGGCGTGTGT<br>TGGGCGTGTG<br>CGTGCAGGGT<br>TGAGCCGACG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | TTTTTTGCA<br>GGGTGGCGGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>GTGTGTCCAC<br>CTGGGGCCTTC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 3060<br>3120<br>3180<br>3240<br>3300<br>3360                                                                              |
| 50<br>55             | CTTTTGCGGT<br>GGCTTGGACG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGTGGCC<br>CGTGGTGGCC<br>GGGGGTCTCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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  | ATTGCACAAC<br>ATGGGGGGCC<br>CCCAGGCCCC<br>GCCGGGGAGG<br>GTGGGCCACG<br>GGGCGTTGGC<br>TTAGGAGTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | TCCGTTCTCG ACAGCTGCAG TGGCGTGTGT TGGGCGTGTG CGTGCAGGGT TGAGCCGACG GAACCCCCCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | TTTTTTGCA<br>GGGTGGCGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>GTGTGTCCAC<br>CTGGGGCTTC<br>CACTCTGCAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC<br>AGGGAAGCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420                                                                      |
|                      | CTTTTGCGGT<br>GGCTTGGACG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGTGGGCC<br>CGTGGTGGCC<br>GGGGGTCTCC<br>GGACAATGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | TTTCTAACCA<br>CCGGTGGGGA<br>CCCTCCCCAA<br>TGTGCAAGGG<br>TGTGTGTAA<br>CCAGCGGCCT<br>GAGGTGCCGG<br>GGGGTTTCAG                                                                                                                                                  | ATTGCACAAC ATGGGGGGCCCC CCCAGGCCCC GCCGGGAGG GTGGGCCACG GGGCGTTGGC TTAGGAGTTT GCAGGAGACA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TCCGTTCTCG ACAGCTGCAG TGGCGTGTGT TGGGCGTGTG CGTGCAGGGT TGAGCCGACG GAACCCCCCC CGAGGAGGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TTTTTTGCA<br>GGGTGGCGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>CTGTGCCCAC<br>CTGGGGCTTC<br>CACTCTGCAG<br>CTGCCCGGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC<br>AGGGAAGCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 3060<br>3120<br>3180<br>3240<br>3300<br>3360                                                                              |
|                      | CTTTTGCGGT<br>GGCTTGGACG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGTGGGCC<br>CGTGGTGGCC<br>GGGGGTCTCC<br>GGACAATGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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  | ATTGCACAAC ATGGGGGGCCCC CCCAGGCCCC GCCGGGAGG GTGGGCCACG GGGCGTTGGC TTAGGAGTTT GCAGGAGACA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TCCGTTCTCG ACAGCTGCAG TGGCGTGTGT TGGGCGTGTG CGTGCAGGGT TGAGCCGACG GAACCCCCCC CGAGGAGGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TTTTTTGCA<br>GGGTGGCGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>CTGTGCCCAC<br>CTGGGGCTTC<br>CACTCTGCAG<br>CTGCCCGGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC<br>AGGGAAGCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420                                                                      |
|                      | CTTTTGCGGT<br>GGCTTGGACG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGTGGGCC<br>CGTGGTGGCC<br>GGGGGTCTCC<br>GGACAATGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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  | ATTGCACAAC<br>ATGGGGGGCC<br>CCCAGGCCCC<br>GCCGGGGAGG<br>GTGGGCCACG<br>GGGCGTTGGC<br>TTAGGAGTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | TCCGTTCTCG ACAGCTGCAG TGGCGTGTGT TGGGCGTGTG CGTGCAGGGT TGAGCCGACG GAACCCCCCC CGAGGAGGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TTTTTTGCA<br>GGGTGGCGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>CTGTGCCCAC<br>CTGGGGCTTC<br>CACTCTGCAG<br>CTGCCCGGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC<br>AGGGAAGCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420                                                                      |
|                      | CTTTTGCGGT<br>GGCTTGGACG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGTGGGCC<br>CGTGGTGGCC<br>GGGGGTCTCC<br>GGACAATGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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  | ATTGCACAAC ATGGGGGGCCCC CCCAGGCCCC GCCGGGAGG GTGGGCCACG GGGCGTTGGC TTAGGAGTTT GCAGGAGACA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TCCGTTCTCG ACAGCTGCAG TGGCGTGTGT TGGGCGTGTG CGTGCAGGGT TGAGCCGACG GAACCCCCCC CGAGGAGGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TTTTTTGCA<br>GGGTGGCGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>CTGTGCCCAC<br>CTGGGGCTTC<br>CACTCTGCAG<br>CTGCCCGGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC<br>AGGGAAGCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420                                                                      |
| 55                   | CTTTTGGGT<br>GGCTTGGACG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGTGGGCC<br>GGGGGTCTCC<br>GGGGGTCTCC<br>GGACAATGCC<br>CAGCAGCTGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       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  | ATTIGACAAC ATGGGGGGCC CCCAGGGCCC GCCGGGAGG GTGGCCACG GGCGTTGGC TTAGGAGTTT GCAGGAGACA TGGGGGCCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | TCCGTTCTCG ACAGCTGCAG TGGCGTGTGT TGGGCGTGTG CGTGCAGGGT TGAGCCGACG GAACCCCCCC CGAGGAGGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TTTTTTGCA<br>GGGTGGCGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>CTGTGCCCAC<br>CTGGGGCTTC<br>CACTCTGCAG<br>CTGCCCGGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC<br>AGGGAAGCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420                                                                      |
|                      | CTTTTGGGT<br>GGCTTGGAG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGGTGGC<br>GGGGGTCTCC<br>GGACAATGCC<br>CAGCAGCTGT<br>Seq ID No:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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  | ATTGCACAC ATGGGGGGC CCCAGGGCCC CCCAGGGAGG GTGGGCCACG GGCCGTTGGC TTAGGAGATT GCAGGAGACA TGGGGCCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | TCCGTTCTCG ACAGCTGCAG TGGCGTGTGT TGGGCGTGTG CGTGCAGGGT TGAGCCGACG GAACCCCCCC CGAGGAGGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TTTTTTGCA<br>GGGTGGCGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>CTGTGCCCAC<br>CTGGGGCTTC<br>CACTCTGCAG<br>CTGCCCGGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC<br>AGGGAAGCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420                                                                      |
| 55                   | CTTTTGGGT<br>GGCTTGGAG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGGTGGC<br>GGGGGTCTCC<br>GGACAATGCC<br>CAGCAGCTGT<br>Seq ID No:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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  | ATTGCACAC ATGGGGGGC CCCAGGGCCC CCCAGGGAGG GTGGGCCACG GGCCGTTGGC TTAGGAGATT GCAGGAGACA TGGGGCCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | TCCGTTCTCG ACAGCTGCAG TGGCGTGTGT TGGGCGTGTG CGTGCAGGGT TGAGCCGACG GAACCCCCCC CGAGGAGGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TTTTTTGCA<br>GGGTGGCGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>CTGTGCCCAC<br>CTGGGGCTTC<br>CACTCTGCAG<br>CTGCCCGGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC<br>AGGGAAGCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420                                                                      |
| 55                   | CTTTTGGGT<br>GGCTTGGAG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGGTGGC<br>GGGGGTCTCC<br>GGACAATGCC<br>CAGCAGCTGT<br>Seq ID No:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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  | ATTGCACAC ATGGGGGGC CCCAGGGCCC CCCAGGGAGG GTGGGCCACG GGCCGTTGGC TTAGGAGATT GCAGGAGACA TGGGGCCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | TCCGTTCTCG ACAGCTGCAG TGGCGTGTGT TGGCCGTGTG CGTGCAGGGT TGAGCCGACG GAACCCCCCC CGAGGAGGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TTTTTTGCA<br>GGGTGGCGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>CTGTGCCCAC<br>CTGGGGCTTC<br>CACTCTGCAG<br>CTGCCCGGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC<br>AGGGAAGCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420                                                                      |
| 55                   | CTTTGCGGT GGCTTGGACG GCGTGTTCG GCTGTGGGCG GCGGGTCTCC GGACAATGCC CAGCAGCTGT Seq ID No: Protein Acc                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | TTTCTAACCA CCGGTGGGGA CCCTCCCCAA TGTGCAAGGG TGTGTGTCAA CCAAGGGCT GAGGTGCCGG GGGGTTTCAG CTAAAGGGCT  167 Protein cession #: 1                                                                                                                                  | ATTGCACAAC ATGGGGGCC CCCAGGCCCC GCCGGGGAGG GTGGGCCACG TTAGGAGTTTGC TTAGGAGTAT TGCAGGAGACA TGGGGGCCTG TGGGGGCCTG TGGCGTTAGCAGACA TGGGGGCCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TCCSTTTTCG ACAGCTGCAG TGGCGTGTGT TGGCCGTGTGT TGGCCGACG GAACCCCCC CCAGGAGGGC GGGCCGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | TTTTTTTGA<br>GGGTGGCGG<br>ACCTAAGCC<br>GGGTGTGGT<br>TGTGCGTGCC<br>CTGTGTCCAC<br>CTGGGGCTTC<br>CACTCTGCAG<br>CTGCCCGGAA<br>AAAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | AGGCAGGGGA<br>TCCCCCALCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC<br>AGGGAAGCGG<br>GTCACATOGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420                                                                      |
| 55                   | CTTTTGGGT<br>GGCTTGGAG<br>CTGGAAAGGT<br>GCCGTGTTCG<br>GCTGGTGGC<br>GGGGGTCTCC<br>GGACAATGCC<br>CAGCAGCTGT<br>Seq ID No:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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  | ATTGCACAC ATGGGGGGC CCCAGGGCCC CCCAGGGAGG GTGGGCCACG GGCCGTTGGC TTAGGAGATT GCAGGAGACA TGGGGCCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | TCCGTTCTCG ACAGCTGCAG TGGCGTGTGT TGGCCGTGTG CGTGCAGGGT TGAGCCGACG GAACCCCCCC CGAGGAGGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TTTTTTGCA<br>GGGTGGCGC<br>ACCTAAGCCC<br>GGGTGTGCGT<br>TGTGCGTGCC<br>CTGTGCCCAC<br>CTGGGGCTTC<br>CACTCTGCAG<br>CTGCCCGGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | AGGCAGGGA<br>TCCCCCACCC<br>GCGTGTGCGT<br>AGCGAAGGCT<br>GAGCGACGAT<br>CAGAAGGCCC<br>AGGGAAGCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420                                                                      |
| 55                   | CTTTGGGGT GGCTGGAAGGT GCGGTGTGG GCGGTGTGG GGGGGTGTCG GGGGGTCTCC CGACAATGCC CAGCAGCTGT Seq ID No: Protein Acc                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | TTTCTAACCA CCGGTGGGA CCCTCCCAA TGTGCAAGGG TGTGTGTCAA CCAGCGGCCT GAGGTGCCGG GGGGTTTCAG CTAAAGGGCT  167 Proteir cession #: 1 1 1                                                                                                                               | ATTGCACAC ATTGGGGGCC CCCAGGCCCC GCCAGGGCCC GCCAGGGCCAC GGCGTTGGC TTAGGAGTTT GCAGGAGACA TGCGGGCCTG  B SEQUENCE: NP_115484.1  21                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | TCCSTTCTCS TGGCGTGTGT TGGCCGTGTG TGGCCGTGTG GGTGCAGGGT TGAGCCCACG GAACCCCCCC CGAGGAGGGC GGGGCGCGCG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | TTTTTTTGA<br>GGGTGGCGC<br>ACCTAAGCC<br>GGGTGTGGT<br>TGTCGGTCC<br>CTGTGTCAC<br>CTGGGGCTTC<br>CACCTGCAC<br>CTGCCCGAA<br>AAAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AGGCAGGGGA<br>TCCCCCALCC<br>GCGTGTGCGT<br>AGGCAAGGCT<br>CAGGAAGGCA<br>CAGGAAGGCA<br>AGGGAAGCGG<br>GTCACATCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420<br>3480                                                              |
| 55                   | CTTTGGGGT GGCTGGAAGGT GCGGTGTGG GCGGTGTGG GGGGGTGTCG GGGGGTCTCC CGACAATGCC CAGCAGCTGT Seq ID No: Protein Acc                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    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  | ATTGCACAC ATTGGGGGCC CCCAGGCCCC GCCAGGGCCC GCCAGGGCCAC GGCGTTGGC TTAGGAGTTT GCAGGAGACA TGCGGGCCTG  B SEQUENCE: NP_115484.1  21                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | TCCSTTCTCS TGGCGTGTGT TGGCGTGTGT TGGCCGTGTG GGTGCAGGGT TGAGCCCACG GAACCCCCCC CGAGGAGGGC GGGGCGCGCG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | TTTTTTTGA<br>GGGTGGCGC<br>ACCTAAGCC<br>GGGTGTGGT<br>TGTCGGTCC<br>CTGTGTCAC<br>CTGGGGCTTC<br>CACCTGCAC<br>CTGCCCGAA<br>AAAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AGGCAGGGGA<br>TCCCCCALCC<br>GCGTGTGCGT<br>AGGCAAGGCT<br>CAGGAAGGCA<br>CAGGAAGGCA<br>AGGGAAGCGG<br>GTCACATCGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420<br>3480                                                              |
| 55                   | CTTTTGGGGT GGCTTGAAAGGT GCCGTGTTGG GCTGTGGGGG CGTGGTGGCG CGGGGTCTCC GGGCAATGCC CAGCAGTGTC Seq ID No: Protein Acc                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TTTCTRACCA CCGGTGGGA CCCTCCCAA TGTGCAGGGC TGTGTGTCAA CCAGCGGCCT GAGGTGCCGG GGGGTTTCAG CTAAAGGGCT 167 Proteir cession #: 1 1   PALLLLLLLL                                                                                                                     | ATTGCACAC ATTGGGGGCC CCCAGGCCCC GCCGGGAGG GTCGGCCAC GGCGTTGGC TTAGGAGTTT GCAGGAGACA TGGGGGCCTG  Sequence: NP_115484.1  21  GGAHGLPFED                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | TCCSTTTTCG ACAGCTGTGT TGGCGTGTT TGGCGTGTGT TGGCCGACG GAACCCCCCC CGAGGAGGGC GGGGCCGCG  31   PPPLSVAFRD                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | TTTTTTTGGG GGGTGGGGG ACCTAAGCCC GGGTGTGGGT TGTGGGTGCC CTGGGGCTTC CACCCTGCAC CTGCCCGGAA AAAG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ASGCAGGGGA TCCCCCACC GCGTGTGCGT TCCCCCACC GCGTGTGCGT GAGCGACGAT CAGAAGGCCC GTCACATCGG  51   SGGGRGTTPAE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420<br>3480                                                              |
| 55                   | CTTTGGGGT GGCTGGAAAGGT GCGGTGTTGG GCTGTGGGG GGGGGTCTC GGACAATGCC CAGCAGCTGT Seq ID No: Protein Acc                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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  | ATTGCACAC ATTGGGGGCC CCCAGGGCCC GCCAGGGCCC GCCAGGGAGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | TCCSTTCTCS TGGCGTGTGT TGGCGTGTGT TGGCGGTGTGT TGGCCGAGGGT TGAGCCGAC CGAGGAGGGC CGAGGAGGGC GGGCCGCG  31   PPPLSVAPRD PPPLSVAPRD PPPTSTELRY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TITITITISCA GGGTGGCSGC ACCTAAGCCC GGGTGTGCGT TGTGCGTGCCC CTGGGGCTTC CACTCTGCAG CTGCCCGGAA ARAG  41   YLMHYPVFVG QRKLIWKSNP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AGGCAGGGG<br>TCCCCCACC<br>GCGTGTGCGT<br>AGGGAAGGCT<br>CAGAAGGCA<br>AGGGAAGGC<br>GTCACATCGG<br>51<br> <br> <br> <br> <br>  SGPGRILTPAE<br>SDINVCRMKG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420<br>3480                                                              |
| 55                   | CTTTGGGGT GGCTGGAAAGGT GCGGTGTTGG GCTGTGGGG GGGGGTCTC GGACAATGCC CAGCAGCTGT Seq ID No: Protein Acc                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              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  | ATTGCACAC ATTGGGGGCC CCCAGGGCCC GCCAGGGCCC GCCAGGGAGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | TCCSTTCTCS TGGCGTGTGT TGGCGTGTGT TGGCGGTGTGT TGGCCGAGGGT TGAGCCGAC CGAGGAGGGC CGAGGAGGGC GGGCCGCG  31   PPPLSVAPRD PPPLSVAPRD PPPTSTELRY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TITITITISCA GGGTGGCSGC ACCTAAGCCC GGGTGTGCGT TGTGCGTGCCC CTGGGGCTTC CACTCTGCAG CTGCCCGGAA ARAG  41   YLMHYPVFVG QRKLIWKSNP                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AGGCAGGGG<br>TCCCCCACC<br>GCGTGTGCGT<br>AGGGAAGGCT<br>CAGAAGGCA<br>AGGGAAGGC<br>GTCACATCGG<br>51<br> <br> <br> <br> <br>  SGPGRILTPAE<br>SDINVCRMKG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420<br>3480                                                              |
| 55                   | CTTTGGGGT GGCTTGGAGG CTGGAAAGGT GCCGTGTTGC GGGGGTCTCC GGACAATGCC CAGCAGCTGT  Seq ID No: Protein Acc  1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          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  | ATTGCACAC ATTGGGGGCC CCCAGGCCCC GCCGGGAGG GCCGGGAGGCCAC GGCGTTGGC GGAGGTTGGC TAGGAGACA TGCGGGCCTG  SEQUENCE: NP_115484.1  21    GGAHGLFPED DRDNLYRVEL LFVCGSNAFN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | TCCSTTCTCS ACAGCTGCAS TGGCGTGTGT TGGGCGTGTGT TGGGCCGCG GAACCCCCC CGAGGAGGGC GGGGCGCGC  31   PPPLSVAPRD EPPTSTELRY FVCANYSIDT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | TTTTTTTGGA GGGTGGGGG ACCTAAGCCC GGGTGTGGGC TGTGGGGCTC CACCTGGGCTC CACCCGGAA AAAG  41   YLNHYPVFVG QRKLTWESNP LQPYGDNISG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | ASGCAGGGGA TCCCCCACC GCGTGTGCGT TCCCCCACC GCGTGTGCGT GAGCGACGAT CAGAAGGCCT GAGCGAGGAT CAGAAGGCGG GTCACATCGG  51   SGPGRLTPAE SDINVCRMKG MARCPYDPKH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3420<br>3480                                                              |
| 55                   | CTTTGGGGT GGCTGGAAGGT GCGTGTGGG GCTGTGGGG GCTGTGGGG GGGGTCTCC GGACAATGCC CAGCAGCTGT Seq ID No: Protein Acc  1   MQTPRASPPR MQTPRASPPR KGGGGCTHC KGGGGCTHC KGGGGCTHC KGGGGCTHC KGGGGCTHC KGGGGCTHC KGGGGCTHC KGGGGCTHC ANYALFSDGM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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  | ATTGCACAAC ATTGGGGGCC CCAGGCCCC CCAGGCCCC CCAGGCCCAC GGCGTTGGC GGCGTTGGC TTAGGAGTTT GCAGGAGACA TGGGGGCCAC  1 SCTUENCE: NP_115484.1  21    GGAHGLFPED DRDNLYRVEL LFVCGSNAFN AIDAVIYNSL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | TCCSTTCTCS TGGCGTGTGT TGGCGGTGTG TGGCGGTGTG TGAGCCGACG GAACCCCCC CGAGGAGGGC GGGGCGCGC  31   PPPLSVAPRD EPPTSTELKY FVCANYSIDT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | TITITITIGA<br>GGGTGGCSGC<br>ACCTAAGCCC<br>GGGTGTGCCT<br>TIGTGCGTGCC<br>CTGGGGCTTC<br>CACTCTGCAG<br>CTGCCCGGAA<br>AAAG<br>41<br> <br>YLNHYPVFVG<br>GRKLTWKSNP<br>LQPVGDMISG<br>HDSKNFKEPY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | ASGCAGGGGA TCCCCCACC GCTGTGCGT GAGCGAGGAT CAGAAGGCCC AGGAAGCCC AGGAAGCCG GTCACATCGG  51   SGPGRITPAE SDINVCRMKC MARCPUPPKH FVHAVENGSH                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3480<br>60<br>120<br>180<br>240                                           |
| 55<br>60<br>65       | CTTTTGGGT GGCTTGGASG TGGAAGGT GCGGTGTGGC GGGGTCTCC GGACATGCC CAGCAGCTCT  Seq ID No: Protein Act                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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  | ATTGCACAAC ATTGGGGGCC CCCAGGCCCC GCCGGGAGG GTGGGCCACG GGGCGTTGGC TTAGGAGTTT GCAGGAGACA TGCGGGCCTG  SEQUENCE: NP_115484.1  21  GGAHGLFPED DRDNLYRVEL LFVCGSNAFN AIDAVIYKSL SEVARVCKNL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | TCCSTTCTCS TGGCGTGTGT TGGCCTGTGT TGGCCGTGTG GGTCCAGGGT TGAGCCCCC CGAGGAGGGC GGGGCGCG  31   PPPPLSVAPRD EPPTSTELEY FVCANYSLT GDRPTLETY WGGSPRULEK                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | TITITITIGGA GGGTGGCGGC ACCTAAGCCC GGGTGTGCGC TTGTGCGTGC CTGGGGCTTC CACTCTGCAG CTGCCCGGAA AAAG  41   YLMHYPVFVG QRKLIWKSNP LOPVGDNISG HDSKNFKEPL GWTSPLKNFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ASGCAGGGGA TCCCCCACC GCTGTGCGT GAGCGAGGAT GAGGAGAGCC AGGGAAGCC AGGGAAGCCG TCACATCGG  51   SGPGRI/TPAE SDINVCRMC FVIENVBRGSH FV | 3060<br>3120<br>3180<br>3240<br>3360<br>3420<br>3480<br>60<br>120<br>180<br>240<br>340                                    |
| 55                   | CTTTTGGGT GGCTTGGASG TGGAAGGT GCGGTGTGGC GGGGTCTCC GGACATGCC CAGCAGCTCT  Seq ID No: Protein Act                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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  | ATTGCACAAC ATTGGGGGCC CCCAGGCCCC GCCGGGAGG GTGGGCCACG GGGCGTTGGC TTAGGAGTTT GCAGGAGACA TGCGGGCCTG  SEQUENCE: NP_115484.1  21  GGAHGLFPED DRDNLYRVEL LFVCGSNAFN AIDAVIYKSL SEVARVCKNL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | TCCSTTCTCS TGGCGTGTGT TGGCCTGTGT TGGCCGTGTG GGTCCAGGGT TGAGCCCCC CGAGGAGGGC GGGGCGCG  31   PPPPLSVAPRD EPPTSTELEY FVCANYSLT GDRPTLETY WGGSPRULEK                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | TITITITIGGA GGGTGGCGGC ACCTAAGCCC GGGTGTGCGC TTGTGCGTGC CTGGGGCTTC CACTCTGCAG CTGCCCGGAA AAAG  41   YLMHYPVFVG QRKLIWKSNP LOPVGDNISG HDSKNFKEPL GWTSPLKNFL                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ASGCAGGGGA TCCCCCACC GCTGTGCGT GAGCGAGGAT GAGGAGAGCC AGGGAAGCC AGGGAAGCCG TCACATCGG  51   SGPGRI/TPAE SDINVCRMC FVIENVBRGSH FV | 3060<br>3120<br>3180<br>3240<br>3300<br>3360<br>3480<br>60<br>120<br>180<br>240                                           |
| 55<br>60<br>65       | CTTTGGGGT GGCTTGGANGGT GCGTGTGGGG GCGTGTGGGG GGGGTCTCC GGACATICC CAGCAGCTGT Seq ID No: Protein Acc  1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | TTTCTAACCA CCGGTGGGGA CCTCCCCAA TGTCCAAGGG TGTGTGTCAA CCACGGCCT 167 Proteir CCACAGGGCT 11 1 1 1 PALLLLLLL IL INVARTIFIG KVLLINEST EFNYLEKVW VSLGGRPV VSLGGRPV                                                                                                | ATTGCACAAC ATTGGGGGCC CCAGGGCCCC CCAGGCCCC GGCGCACG GGCGTTGGC GGCGTTGGC TGCGGGCACA TGCGGGCACA  A SECTUENCE: NP_115484.1  21    GGAHGLPPED DRDNLYRVEL LFVCGSNAFN AIDAVIYKSL SRVARVCKND LAVFSTPSNS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | TCCSTTCTCS TGGCGTGTGT TGGCGGTGTG TGGCGGTGTG TGAGCCCCC CGAGGAGGG GGGCGGCG  31   PPPLSVAPRD PPPLSVAPRD PVCANYSIDT GORPTLETVE VGGSPRVLEF TGGSPRVLEF TPGSSPCAF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TTTTTTTGCA GGGTGTGGGT GGGTGTGGT TGTGGGTGTG GTGTGTGCA CTGGGGGTT CACCTGGAGA AAAG  41   YUMHYPUFVG QRELTWRSNP LOPVGUNIG HUSKWFKEFF QKTESKEABL LUQVAAVES                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | AGGCAGGGGA TCCCCCACC GCTGTGCGT TCCCCCACC GCTGTGCGT GAGCGAGGAT CAGAAGGCT CAGAAGGCT AGGGAAGCG GTCACATCGG  51   SGPGRLTPAE SDINVCRMKC MARCPYDPKH FVIENVEWGSH NCSVPGDSHH FFYERVERSHS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 3060<br>3120<br>3180<br>3240<br>3306<br>3420<br>3480<br>60<br>120<br>180<br>240<br>300<br>360                             |
| 55<br>60<br>65       | CTTTTGGGGT GGCTTGGAGG CTGGAAGGT GCGTGTTGG GCTGTGGGC GGGGTCTCC CGGCAATGC CAGCAGCTGT  Seq ID No: Protein Act                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      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  | ATTGCACAAC ATGGGGGGC CCCAGGGCCCC GCCGGGAGG GGCGTTGGC TTAGGAGTTT GCAGGAACA TGGGGGCCTG  BCLGCAGAACA TGGGGGCCTG  GGAGGACA TGGGGGCTG LFVCGSNAFN AIDAVIYKSL LFVCGSNAFN AIDAVIYKSL STWARVCKND LAVESTPSNS ENWARVCKND LAVESTPSNS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TCCSTTCTCS TGGCGTGTG TGGCGTGTG TGGCGGTGTG TGAGCCGACG GAACCCCCC CCAGGAGGG GGGCGCG  31                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | TTTTTTGCA GGGTGGGGG ACCTAAGCC GGGTGTGCGT TGTGCGTGCC GTGTGTCCAC CTGCGGGCTTC CACCTGGAGA AAAG  41   I YINHYPVEVG QRKLYMESHP LDQVANTES HISKNEKEPY QRTSEKARL LTQVAAVEGG TERLINGEND                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | AGGCAGGGGA TCCCCCACC GCTGTGCGT GAGCGAGGACGAT GAGGAGGCC AGGGAAGCGG GTCACATCGG  51   SgpGRLTPAE SDLNVCRMCC FVHAVENGSH FVHAVENGSH FFFERQKSPES SLGHAPWILE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 3060<br>3120<br>3180<br>3240<br>3300<br>3420<br>3480<br>60<br>120<br>180<br>240<br>300<br>360<br>420                      |
| 55<br>60<br>65       | CTTTTGGGT GGCTTGGANGGT GCGGTGTTGG GCGGTTTGG GCGGGTGGCC GGGGGTCTCC CGACANGCCT  Seq ID No: Protein Act                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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  | ATTGCACAAC ATGGGGGGC CCCAGGGCCCC GCCGGGAGG GGGGGTGGCCACG GGGGGTTGGC TTAGGGGTCTG GCAGGAGACA TGGGGGCCTG GCAGGAGACA TGGGGGCCTG BCCCAGGAGCA TGGGGGCCTG AGGGGCCTG AGGGGCCCTG AGGGGCCCTG AGGGGCCCTG AGGGGCCCTG AGGGGCCCTG AGGGGCCCTG AGGGCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCTG AGGGCCCCCTG AGGGCCCCTG AGGGCCCCCTG AGGGCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCC | TCCGTTCTCG ACAGCTCGT TGGCGTGTGT TGGCGTGTGT CTGCGAGGT CTGCGAGGT CTGCGAGGT CTGCGAGGT CGGGGCGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | TTTTTTGCA GGGTGGGGG GGGTGGGGG GGTGTGGCG TGTGCGTGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | AGGCAGGGGA TCCCCCACC GCTGTGCCT AGCGAAGGCT GAGCGACGAT CAGAAGGCC AGGGAAGCCG AGCGAAGCCG SDINVCRMC MACPYDPKH FYUNAVERGS NCSVFGDSHF SLGHAPHILE LSVFLEEFFT LSVFLEEFFT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 3060<br>3120<br>3180<br>3240<br>3306<br>3420<br>3480<br>60<br>120<br>180<br>240<br>300<br>360<br>420                      |
| 55<br>60<br>65       | CTTTTGGGT GGCTTGGANGGT GCGGTGTTGG GCGGTTTGG GCGGGTGGCC GGGGGTCTCC CGACANGCCT  Seq ID No: Protein Act                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            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  | ATTGCACAAC ATGGGGGGC CCCAGGGCCCC GCCGGGAGG GGGGGTGGCCACG GGGGGTTGGC TTAGGGGTCTG GCAGGAGACA TGGGGGCCTG GCAGGAGACA TGGGGGCCTG BCCCAGGAGCA TGGGGGCCTG AGGGGCCTG AGGGGCCCTG AGGGGCCCTG AGGGGCCCTG AGGGGCCCTG AGGGGCCCTG AGGGGCCCTG AGGGCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCTG AGGGCCCCCTG AGGGCCCCTG AGGGCCCCCTG AGGGCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCCTG AGGGCCCCC | TCCGTTCTCG ACAGCTCGT TGGCGTGTGT TGGCGTGTGT CTGCGAGGT CTGCGAGGT CTGCGAGGT CTGCGAGGT CGGGGCGGGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | TTTTTTGCA GGGTGGGGG GGGTGGGGG GGTGTGGCG TGTGCGTGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | AGGCAGGGGA TCCCCCACC GCTGTGCCT AGCGAAGGCT GAGCGACGAT CAGAAGGCC AGGGAAGCCG AGCGAAGCCG SDINVCRMC MACPYDPKH FYUNAVERGS NCSVFGDSHF SLGHAPHILE LSVFLEEFFT LSVFLEEFFT                                                                                                                                                                                                                                                                                              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| 55<br>60<br>65       | CTTTTGGGT GGGTGGGGG GGGGGTGTGGGG GGGGGTTGTGGGG GGGGGTTCTC GGGACAGTGC CAGCAGTGC  Seq ID No- Protein Ac  1   MQTFRASPPR GADDATIGN NPWIGHTGBGA NPWIGHTGBGA NPWIGHTGBGA NPWIGHTGBGA NPWIGHTGGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | TTTCTAACCA CCCTCCCCAA TCTGCGAAGG TCTGTGTCAA CCCTCCCCAA TGTGTCAAG GGGTTTCAG GGGGTTCCAG GGGTTCCAG GCGTTCCAG LAAGGGCT  11    PALLLLLLL LAVNRTLFIG KVLLERDES LFTAYVDFL ENTALEVVDFL ENTALEVVDFL ENTLEKVVD VSLIGSEPVV VSLIGSEPVV VSLIGSEPVA AVDVJACPMG GGGTGGRLIAG | ATTGCACACA ATTGGACCC CCCAGGCCC CCCAGGCCC CCCAGGCCC CCCAGGCCC CCCAGGCCCC CTAGGACTT CGCACGCACCA TGGGGCCTC  1 SECUENCE: CTAGGACTT CCAGGCCCTC  1 SECUENCE: CTAGGACTT CAGGGCCTC  1 SECUENCE: CTAGGACTT CAGGGCCTC  1 SECUENCE: CTAGGACTT CAGGGCCTC  1 SECUENCE: CTAGGACTT CAGGGCCTC  1 SECUENCE: CTAGGACT CTAGGCCTC  CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCTC CTAGGCCCTC CTAGGCCTC CTAGGCCCTC CTAGGCCTC CTAGGCCCTC CTAGCCCTC CTAGGCCCTC CTAGGCC | TCOSTTCTOS ACAGCICAS TGGCOTTOT TGGCCOTOT COTGCAGGOT TGGCCOCC CCAGGAGGG CGGCCGCC  31   PPPLSVAPRD EPPTSTELKY FCANSISION GREPLETUK GREPLETUK GREPLETUK TGGREPLETUK T | TTTTTTGCA GGGTGGGGG ACCTAAGCC GGGTGTGGCT TGTGCGTGCC GTGGTGCC CTGGGGCTTC CACCTCTGCAG CTGCCCGGAA AAAG  41   LINHYPUFVG QRKLTMESHP LDQVAMTIS HDSKMFKEPY QRMSTLELLCQVAAVFBG THELMDESAP PRASTSGTSG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | AGGCAGGGGA TCCCCCACC GCGTGTGCGT TCCCCCACC GCGTGTGCGT AGCGAAGGCC AGGGAGCCC AGGGACCC AGGGACCC AGGGACCC AGGGACCC AGGGACCC AGGCACCC AGGGACCC AGGGACCC AGGGACCC AGGGACCC AGGCACCC AGCCACCC AGGCACCC AGCCACCC AGGCACCC AGGCACCC AGGCACCC AGGCACCC AGGCACCC AGGCACCC AGGC | 3060<br>3120<br>3180<br>3240<br>3360<br>3420<br>3480<br>60<br>120<br>180<br>240<br>306<br>420<br>480<br>540               |
| 55<br>60<br>65<br>70 | CTTTTGGGT<br>GGGTTGGAG<br>GGGTTGGAG<br>CCGGTGTTGG<br>CCGTGGTTGG<br>GGGGTTGGG<br>GGGGTTCC<br>CAGCAGCTGT<br>Seq ID No:<br>Protein Ac:<br>I<br>MOTFRASPER<br>GADDENTGR<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>VYFFRIAM<br>V | TTTCTAACCA CCTCCCCAA TGTGCAAGG CCTCCCCAA TGTGCAAGG TGTGTGCAAG GGGGTTCCAA GGGGTGCCAG GGGGTTCCAG CTAAAGGGCT  167 Proteir LEVNETLEFATVDEL ENTLELLLLLL ENTLELLENTERVW VYSLIGGEPV PRERGCCAA ANDVAGAPGA GGETGGELLS SCIPLEFORT                                      | ATTGCACACA ATTGGACACA ATTGGACCC CCCAGGCCC CCCAGGCCC CCCAGGCCC CCCAGGCACCA TGGGGCCTATAGGAGTT GCAGGACACT TGGGGCCTG BEGUAGGACAC TGGGGGCCTG CAGGACACA TGGGGGCCTG BEGUAGGACAC TGGGGCCTG BEGUAGGACAC TGGGGCCCTG BEGUAGGACAC TGGGGCCCTG BEGUAGGACAC TGGGGCCCTG BEGUAGGACAC TGGGGCCCTG BEGUAGGACAC TGGGGCCCTG BEGUAGGACC TGGGGCCCTG BEGUAGCAC TGGGGCCCTG BEGUAGGACC TGGGGCCCTG BEGUAGGACC TGGGGCCCTG BEGUAGGACC TGGGGCCCTG BEGUAGGACC TGGGCCCTG BEGUAGGACC TGGGCCCTG BEGUAGGACC TGGGCCCTG BEGUAGGACC TGGGCCCTG BEGUAGGACC TGGGCCCTG BEGUAGCAC TGGGCCCTG BEGUAGGACC TGGGCCCTG BEGUAGGACC BEGUAGCAC BEGU | TCGSTTTIGG ACAGGTCAGGT TGGCGTGTGT TGGGCGTGTGT TGGGCGTGTGT TGGGCGTGTGT TGGGCGTGGG GAGCCCCCC CGAGGAGGGC GGGGCGGGG GGGCGGGG GGGCGGGG GGGCGGGCGGG GGGCGGGCGGGCGGGGCGGGGGG  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LOPVOLTIS HINSHPKERF QWTSFLKARL LUQVAAVFBA THELMDEAUF PRASTSCTSC VPVARCQUS LURGAGCOUS LURGA | AGGCAGGGGA TCCCCCACCC GCGTGTGCGT AGCGACGTA GAGCGACGTA GAGCGACGTA GAGCGACGTA GAGCGACGTA  51                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 3060<br>3120<br>3180<br>3240<br>3300<br>3420<br>3480<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600 |
| 55<br>60<br>65       | CTTTTGGGT GGGTTGGAG GGGTTGGAG GCTGGGAAGGT GCGGGTTGGGG GCGGTGTGGGG GGGGTTCTC GGGGACATGC CAGCAGCTT  Seq ID No: Protein Ac:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        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  | ATTOGACACA A ATTOGACACA ATTOGACACACA ATTOGACACACA ATTOGACACACA ATTOGACACACACACA ATTOGACACACACACACACACACACACACACACACACACACAC                                                                                                                                              | ACAGTICIOS ACAGCICACIÓN TO CONTROL TO CONTROL  | TTTTTTGCA GGGTGGGGG GGGTGGGGG GGGTGTGGCT TGTGCGTGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | AGGCAGGGA TCCCCCACCC GCTGTTTCCT AGCCAACCC AGCGAGCCC AGCGAGCCC AGCGAGCCC AGGGAGCCC AGGCGACC AGGCACC AGCACC AGGCACC AGGC | 3060<br>3120<br>3180<br>3340<br>3360<br>3420<br>3480<br>60<br>120<br>240<br>300<br>420<br>420<br>420<br>460<br>660        |
| 55<br>60<br>65<br>70 | CTTTTGGGT GGGTTGGAG GGGTTGGAG GCTGGGAAGGT GCGGGTTGGGG GCGGTGTGGGG GGGGTTCTC GGGGACATGC CAGCAGCTT  Seq ID No: Protein Ac:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        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  | ATTGCACACA ATTGGACACA ATTGGACCC CCCAGGCCC CCCAGGCCC CCCAGGCCC CCCAGGCACCA TGGGGCCTATAGGAGTT GCAGGACACT TGGGGCCTG BEGUAGGACAC TGGGGGCCTG CAGGACACA TGGGGGCCTG BEGUAGGACAC TGGGGCCTG BEGUAGGACAC TGGGGCCCTG BEGUAGGACAC TGGGGCCCTG BEGUAGGACAC TGGGGCCCTG BEGUAGGACAC TGGGGCCCTG BEGUAGGACAC TGGGGCCCTG BEGUAGGACC TGGGGCCCTG BEGUAGCAC TGGGGCCCTG BEGUAGGACC TGGGGCCCTG BEGUAGGACC TGGGGCCCTG BEGUAGGACC TGGGGCCCTG BEGUAGGACC TGGGCCCTG BEGUAGGACC TGGGCCCTG BEGUAGGACC TGGGCCCTG BEGUAGGACC TGGGCCCTG BEGUAGGACC TGGGCCCTG BEGUAGCAC TGGGCCCTG BEGUAGGACC TGGGCCCTG BEGUAGGACC BEGUAGCAC BEGU | ACAGTICIOS ACAGCICACIÓN TO CONTROL TO CONTROL  | TTTTTTGCA GGGTGGGGG GGGTGGGGG GGGTGTGGCT TGTGCGTGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | AGGCAGGGA TCCCCCACCC GCTGTTTCCT AGCCAACCC AGCGAGCCC AGCGAGCCC AGCGAGCCC AGGGAGCCC AGGCGACC AGGCACC AGCACC AGGCACC AGGC | 3060<br>3120<br>3180<br>3240<br>3300<br>3420<br>3480<br>60<br>120<br>180<br>240<br>300<br>360<br>420<br>480<br>540<br>600 |

PTPHEHPHAL GPRAWDHGHP LLPASASSSL LLLAPARAPE QPPARGEPTP DGRLYAARPG
RASHGOFFLT PHASPORREV VASTGELDP ASSADGLERP WSPPPTGSLR RPLGHHAPPA
840
ATLARTHITTH SGRARPGORE RGCHARPGTD LAHLLPYGGA DRTAPPY

5 Seq ID NO: 168 DNA sequence

Nucleic Acid Accession #: AW205664 Coding sequence: 1-135 (underlined sequences correspond to start and stop codons)

- 10 11 21 31 41 51 CGGCACGAGG AGAACAGGGG CCTCTGCCTC AGTTTGCCCG GGAGCCAGGC AGGGCCCATC 60 CTAATTTGGA GCACAGTCTT CCCGGTGCCT AGACATGCCA AGGCCCCTCC CACGTGGTAC 120 15 ACCUTCTCCG TITAGTACCT GACCACCTGT TICAAAACGC AGGTGITTCT GGTTTAGAAA 180 CTTGGAAGGC GGAATGTGTT TTCGTGTCTT CTAGGAAGGG TCTGCTGAGG ACCAGACCAC 240 GTAAGCCTGA GTGGATCCTG ACTCAGCTGC AGCCCTTACC TGCCTCGTGC TGATGATCTA 300 TGCATGGCGT TATGTAGATC ACGTGCGGCA GAGACAGCCA CTGTCCTGTG TGCGGGTTTT 360 20
- Seq ID No: 169 Protein sequence: Protein Accession #: AW205664
- 25 1 11 · 21 31 41 51 | RHEENRGLCL SLPGSQPGPI LIWSTVFPVP RHAKAPPTWY TLSV
- 30 Seq ID NO: 170 DNA sequence Nucleic Acid Accession #: AB033100 Coding sequence: 32-2623 (underlined sequences correspond to start and stop codons)

| 35 | 1          | 11         | 21         | 31         | 41         | 51         |      |
|----|------------|------------|------------|------------|------------|------------|------|
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|    | AGGTCTGGGG | TCCTGAGGCT | GCTGGCAGAC | TATGGGTACA | ACGGCCAGCA | CAGCCCAGCA | 60   |
|    | GACGGTCTCG | GCAGGCACCC | CATTTGAGGG | CCTACAGGGC | AGTGGCACGA | TGGACAGTCG | 120  |
|    |            |            |            | CACTAGCTTG |            |            | 180  |
| 40 | CATCATCCCC | AACAAGGTGG | CCCCTGTTGT | GATCACGTAC | AACTGCAAGG | AGGAGTTCCA | 240  |
|    | GATCCATGAT | GAGCTGCTCA | AGGCTCATTA | CACGTTGGGC | CGGCTCTCGG | ACAACACCCC | 300  |
|    |            |            |            | CTTACCCCAG |            |            | 360  |
|    | GGATGTCACT | GAGAAGATGG | ATGTGCTGGG | CACCGTGGGA | AGCTGTGGGG | CCCCCAACTT | 420  |
|    |            |            |            | CGGCATGGGA |            |            | 480  |
| 45 |            |            |            | CGGACATAGG |            |            | 540  |
|    |            |            |            | AGATGAGGAC |            |            | 600  |
|    |            |            |            | GGGCCTTGGA |            |            | 660  |
|    |            |            |            | CGACTTTGCC |            |            | 720  |
|    |            |            |            | GGGGGAGCCC |            |            | 780  |
| 50 |            |            |            | GTACAAGCGG |            |            | 840  |
|    |            |            |            | GCAAGGGAGT |            |            | 900  |
|    |            |            |            | CAGCCTGCTG |            |            | 960  |
|    |            |            |            | GATGGGCGTG |            |            | 1020 |
|    |            |            |            | CAGTGGGACC |            |            | 1080 |
| 55 |            |            |            | GCAGTTCCAG |            |            | 1140 |
|    |            |            |            | AGAGGTGGAC |            |            | 1200 |
|    |            |            |            | GGAAAACCAG |            |            | 1260 |
|    |            |            |            | CCGACACAGC |            |            | 1320 |
|    |            |            |            | GTTTAACTAC |            |            | 1380 |
| 60 |            |            |            | GCTGTGTGCC |            |            | 1440 |
|    |            |            |            | GGCTCCGAGG |            |            | 1500 |
|    |            |            |            | CCCCCTCAGC |            |            | 1560 |
|    |            |            |            | CATCTACGGC |            |            | 1620 |
|    |            |            |            | GGACGCCAAG |            |            | 1680 |
| 65 |            |            |            | GGAGTGTGAC |            |            | 1740 |
|    |            |            |            | GCTGGAGACC |            |            | 1800 |
|    |            |            |            | GGGCCCCCTG |            |            | 1860 |
|    |            |            |            | CCGCAGGGCC |            |            | 1920 |
|    |            |            |            | CCGAGAGGAG |            |            | 1980 |
| 70 |            |            |            | AGGCACTGGC |            |            | 2040 |
|    |            |            |            | GGTGGCTGTC |            |            | 2100 |
|    |            |            |            | CCTGACTGTG |            |            | 2160 |
|    |            |            |            | GCAGCTGCTA |            |            | 2220 |
| -  |            |            |            | CAGCGAGACC |            |            | 2280 |
| 75 | CCTGCGGGAG | ATCATCATCT | GCACCTACCG | CCAGGCGAAG | GCAGCGAAAG | AGGCGCAGGA | 2340 |
|    | AATGCGGAGG | CTGCAGCTGC | GGAGCCTGCA | GTACTTGGAG | CGCTATGTCT | GCCTGATTCT | 2400 |

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 2700
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 3120
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 ACCCAGTTTT CTGGACTCTC ATGCCCCCAT CTCCGACCTG GGAGACTTCA GGAATGACAA
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 GCATTAAAAA CAGCTAAATG TG
35
 Seq ID No: 171 Protein sequence:
 Protein Accession #: BAA86588.1
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 41
 6.7
40
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 ITYNCKEEFO IHDELLKAHY TLGRLSDNTP EHYLVOGAGA LPOGRYFLVR DVTEKMDVLG
 TVGSCGAPNF RQVQGGLTVF GMGQPSLLGF RRVLQKLQKD GHRECVIFCV REEVLFLRAD
 180
 EDFVSYTPRD KONLHENLOG LGPGVRVESL ELAIRKEIHD FAQLSENTYH VYHNTEDLWG
 240
 EPHAVAIHGE DDLHVTEEVY KRPLFLQPTY RYHRLPLPEQ GSPLEAQLDA FVSVLRETPS
 300
45
 LLOLRDAHGP PPALVFSCOM GVGRTNLGMV LGTLILLHRS GTTSOPEAAP TOAKPLPMEO
 360
 FOVIOSFLEM VPOGREMVEE VDRAITACAE LHDLKEVVLE NOKKLEGIRP ESPAGGSGSR
 420
 HSVWQRALWS LERYFYLILF NYYLHEQYPL AFALSFSRWL CAHPELYRLP VTLSSAGPVA
 480
 PRDLIARGSL REDDLVSPDA LSTVREMDVA NFRRVPRMPI YGTAQPSAKA LGSILAYLTD
 540
 AKRRLRKVVW VSLREBAVLE CDGHTYSLRW PGPPVAPDQL ETLEAQLKAH LSEPPPGKEG
 600
50
 PLITYRFOTCL THOEVFSOHR RACPGLITHR IPMPDFCAPR EEDFDQLLEA LRAALSKDPG
 660
 TGFVFSCLSG QGRTTTAMVV AVLAFWHIQG PPEVGEEELV SVPDAKFTKG EFQVVMKVVQ
 720
 LLPDGHRVKK EVDAALDTVS ETMTPMHYHL REIIICTYRO AKAAKEAOEM RRLOLRSLOY
 780
 LERYVCLILF NAYLHLEKAD SWORPFSTWM OEVASKAGIY EILNELGFPE LESGEDQPFS
 840
 RIRYRWORDS CSLEPSAPED LL
55
 Seq ID NO: 172 DNA sequence
 Nucleic Acid Accession #: AK021806.1
 Coding sequence: 1-645 (underlined sequences correspond to start and stop codons)
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 41
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 AACCTTCATG AGAACCTCCA GGGCCTTGGA CCCGGGGTCC GGGTGGAGAG CCTGGAGCTG
 120
65
 GCCATCCGGA AAGAGATCCA CGACTTTGCC CAGCTGAGCG AGAACACATA CCATGTGTAC
 180
 CATAACACCG AGGACCTGTG GGGGGAGCCC CATGCTGTGG CCATCCATGG TGAGGACGAC
 240
 TTSCATGTGA CGGAGGAGGT GTACAAGCGG CCCCTCTTCC TGCAGCCCAC CTACAGGTAC
 300
 CACCGCCTGC CCCTGCCCGA GCAAGGGAGT CCCCTGGAGG CCCAGTTGGA CGCCTTTGTC
 360
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 420
70
 GCCCTCGTCT TCAGCTGCCA GATGGGCGTG GGCAGGACCA ACCTGGGCAT GGTCCTGGGC
 480
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 GCCAAGCCCC TGCCTATGGA GCAGTTCCAG GTGATCCAGA GCTTTCTCCG CATGGTGCCC
 600
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 660
 AGTITICIGG ACTOTOATGO COCCATOTOC GACOTGGGAG ACTICAGGAA TGACAACCIA
 720
75
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 780
 AGCCCCTCTC ATGGGGAGGA AAGAGCTTCC AGGGGGCGAA CGCAGCACAG AGGAAGAGGC
```

|    | CTGCTCCACT | TGTCTGGGAA | CCTGGGCAGG | AGGCACAGAG | GAAGCCAAGG | CCTGGAGCTG | 900  |
|----|------------|------------|------------|------------|------------|------------|------|
|    | CAGGTCCCCC | GGCATCTCTC | TCTGTCCCGG | CAGCCCAGGA | TGGCCTGGTG | CCCCCACCTG | 960  |
|    | CTGCAGCAGG | AGCCCCAAGG | AGTGCTAGCT | GAGGGTGGTT | GCTGGGGTGG | TCCTCATGGA | 1020 |
|    | CAGTGAGGTG | TGCAAGGGTG | CACTGAGGGT | GGTGGGAGGG | GATCACCTGG | GTTCCAGGCC | 1080 |
| 5  | ATCCTTGCTG | AGCATCTTTG | AGCCTGCCTT | CCGGTGGGAG | CAGAAAAGGC | CAGACCCTGC | 1140 |
|    | TGAGTTAGAG | GCTGCTGGGA | TCCACTGTTT | CCACACAGCG | GGAAGGCTGC | TGGGAACAGG | 1200 |
|    | TGGCAGAGAA | GTGCCATGTT | TGCGTTGAGC | CTTGCAGCTC | TTCCAGCTGG | GGACTGGTGC | 1260 |
|    | TTGCTGAAAC | CCAGGAGCTG | AACAGTGAGG | AGGCTGTCCA | CCTTGCTTGG | CTCACTGGGA | 1320 |
|    | CCAGGAAAGC | CTGTCTTTGG | TTAGGCTCGT | GTACTTCTGC | AGGAAAAAA  | AAAAAGGATG | 1380 |
| 10 | TGTCATTGGT | CATGATATTT | GAAAAGGGGA | GGAGGCCGAA | GTTGTTCCCA | TTTATCCAGT | 1440 |
|    | ATTGGAAAAT | ATTTGACCCC | CTTGGCTGAA | TTCTTTTGCA | GAACTACTGT | GTGTCTGTTC | 1500 |
|    | ACTACCTTTT | CAGGTTTATT | GTTTTTTTT  | TTGCATGAAT | TAAGACGTTT | TAATTTCTTT | 1560 |
|    | GCAGACAAGG | TCTAGATGCG | GAGTCAGAGA | TGGGACTGAA | TGGGGAGGGA | TCCTTTGTGT | 1620 |
|    | TCTCATGGTT | GGCTCTGACT | TTCAGCTGTG | TTGGGACCAC | TGGCTGATCA | CATCACCTCT | 1680 |
| 15 | CTGCCTCAGT | TTCCCCATCT | GTAAAATGGG | AGAATAATAC | TTGCCTACCT | ACCTCACGGG | 1740 |
|    | GGTGTTGTGA | GGATTCATTT | GTGATTTTTT | TTTTTTTTT  | TGTACAGAGC | TTTTAAGCAT | 1800 |
|    | TAAAAACAGC | TAAATGTG   |            |            |            |            |      |
|    |            |            |            |            |            |            |      |

Seq ID No: 173 Protein sequence: Protein Accession #: AX021806.1

TULFLEADED FVSYTPRDKQ MIEBHLQGIG FOVRVESILEL AIRKEIHDFR QLSENTYHYV 60
HHYDDINGEP HAVAIHGED LHVYERVYER PERIOPTYEY HELFERGOS PLEADLDAFV 120
SVJETPSLI QLERANGPP ALVESQUAV GRYLLGHVLG TLILLHRSGT TSQPRAAPTQ 180
ARPLINGEQF VIQSELMNP QGRRIVERVD BSIM 

Seq ID NO: 174 DNA sequence Nucleic Acid Accession #: NM\_016580.2

Coding sequence: 1212-4766 (underlined sequences correspond to start and stop codons)

|    | 1          | 11         | 21 ,       | 31         | 41         | 51         |      |
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| 40 | l          | }          |            | }          | l          | 1          |      |
| 40 |            | AGGAGAGCCA |            |            |            |            | 60   |
|    |            | CACCCTCATA |            |            |            |            | 120  |
|    |            | GCCATAGGGT |            |            |            |            | 180  |
|    |            | CCTGTGACTC |            |            |            |            | 240  |
|    |            | ACAGTTTCCT |            |            |            |            | 300  |
| 45 | AGATGAGGTA | ATGGAGGCCC | AGGAAAGTTA | AGTGACTTGT | CCCAGATGAC | ACCGCTGGTA | 360  |
|    | AGTTGCAAAG | TCAGAATTTG | AACTCAGGCA | GTTTACCTCT | GATGGCTGCT | CTGTTAATCA | 420  |
|    |            | CCAGTGAGAC |            |            |            |            | 480  |
|    |            | GAAAAAGACA |            |            |            |            | 540  |
|    | GAGAGTTGGG | GAAGGGGAGA | GAAACAGGAA | ACATGACTTG | CCCGGGAGGG | GCATCAGTCC | 600  |
| 50 |            | AGGTGGAGGC |            |            |            |            | 660  |
|    |            | CCGCCTTGCT |            |            |            |            | 720  |
|    | CCGGCCTCAT | CCTCCTCAGC | GGCAGGCCAC | TTAGCTTCAC | AGGAAATGCT | CTTTCTCTAA | 780  |
|    | TTGGCATTGA | AACTCACAGC | CCTCCCTTTT | CCTGTAGGTG | GGGTTTCCAT | AGGAAAAAGC | 840  |
|    |            | TTTCCCCAGC |            |            |            |            | 900  |
| 55 | ACTGGGTCAG | GTCCCTCTTA | GACCAGCTCT | TGTCCATCAT | TTGCTGAAGT | GGACCAACTA | 960  |
|    | GTTCCCCAGT | AGGGGGTCTC | CCCTGGCAAT | TCTTGATCGG | CGTTTGGACA | TCTCAGATCG | 1020 |
|    | CTTCCAATGA | AGATGGCCTT | GCCTTGGGGT | CCTGCTTGTT | TCATAATCAT | CTAACTATGG | 1080 |
|    | GACAAGGTTG | TGCCGGCAGC | TCTGGGGGAA | GGAGCACGGG | GCTGATCAAG | CCATCCAGGA | 1140 |
|    | AACACTGGAG | GACTTGTCCA | GCCTTGAAAG | AACTCTAGTG | GTTTCTGAAT | CTAGCCCACT | 1200 |
| 60 |            | CATGATGCAA |            |            |            |            | 1260 |
|    | ACTTATTTCT | TTTAGGGGAT | TGTCAGGAGG | TGACCACTCT | CACGGTGAAA | TACCAAGTGT | 1320 |
|    | CAGAGGAAGT | GCCATCTGGT | ACAGTGATCG | GGAAGCTGTC | CCAGGAACTG | GGCCGGGAGG | 1380 |
|    | AGAGGCGGAG | GCAAGCTGGG | GCTGCCTTCC | AGGTGTTGCA | GCTGCCTCAG | GCGCTCCCCA | 1440 |
|    |            | CTCTGAGGAA |            |            |            |            | 1500 |
| 65 |            | GTGGGATCCC |            |            |            |            | 1560 |
|    | CTCTGATCCA | TGTGGAGATC | CAAGTGCTGG | ACATCAATGA | CCACCAGCCA | CGGTTTCCCA | 1620 |
|    |            | GGAGCTGGAA |            |            |            |            | 1680 |
|    |            | TGACCCAGAC |            |            |            |            | 1740 |
|    | GTGAGCACTT | TGCCTTGGAT | GTCATTGTGG | GCCCTGATGA | GACCAAACAT | GCAGAACTCA | 1800 |
| 70 |            | GGAGCTGGAC |            |            |            |            | 1860 |
|    |            | GAACCCCCCC |            |            |            |            | 1920 |
|    | CCAATGACAA | TAGCCCTGCG | TTTGCTGAGA | GTTCACTGGC | ACTGGAAATC | CAAGAAGATG | 1980 |
|    |            | TACGCTTCTC |            |            |            |            | 2040 |
|    | GGGAGGTGGA | GTTCTTCCTC | AGTAAGCACA | TGCCTCCAGA | GGTGCTGGAC | ACCTTCAGTA | 2100 |
| 75 |            | GACAGGCCAG |            |            |            |            | 2160 |
|    | CCTACGAGGT | GGATGTTCAG | GCAAGGGACC | TGGGTCCCAA | TCCTATCCCA | GCCCATTGCA | 2220 |
|    |            |            |            |            |            |            |      |

|    | A A COMMONORM | CT & COTTOCTC | CATCTCAATC | ACAACATCCC               | ANGENTOCAC   | CTCACATGGG | 2280 |
|----|---------------|---------------|------------|--------------------------|--------------|------------|------|
|    |               |               |            | TTCCCAAGGA               |              |            | 2340 |
|    |               |               |            | GTTTGGTCCA               |              |            | 2400 |
|    |               |               |            | GCAACACATA               |              |            | 2460 |
| 5  |               |               |            | CCCTCACTCT               |              |            | 2520 |
| ,  | TOCAGGGGGG    | AGAGCAGIGG    | CCCMMINIA  | GCATTCAGAT               | CACTGACATC   | AACCACAATC | 2580 |
|    | OT COMOCCCIT  | MICHOLCANG    | AAACAGCICA | TCTCCACGCG               | CCSSSSCSSC   | TTACCCTCTC | 2640 |
|    | THE COURSE    | TURGHALAGO    | GOTGATGATG | CAGACTTGGG               | CAMMAATCCA   | BARCECTCAC | 2700 |
|    |               |               |            | TAGTAGCTAT               |              |            | 2760 |
| 10 |               |               |            | AGATGGCCGG               |              |            | 2820 |
| 10 | TCACTGCTCA    | GAGGTCACTG    | AACTATGAAG | CCAGTGTCTC               | mamamaaama   | MAGGIGATEG | 2880 |
|    | CAGAGGACAG    | CGGGCAACCC    | ATGCTTGCAT | AGCCTGTGCT               | OR COCK TOCK | ABACCOCTCO | 2940 |
|    |               |               |            |                          |              |            | 3000 |
|    |               |               |            | ACCTGCTGGT<br>CACTGGCCAC |              |            | 3060 |
| 15 |               |               |            |                          |              |            | 3120 |
| 13 | TTTTGACAAC    | CATTGTGGCA    | AGAGATGCAG | ACTCGGGGGC               | AAATGGAGAG   | CCCCTCTACA | 3180 |
|    | GCATCCGCAG    | TGGAAATGAA    | GCCCACCTCI | TCATCCTCAA               | CCCTCATACG   | GGGCAGCTGT |      |
|    |               |               |            | TTGGGAGTGA               |              |            | 3240 |
|    |               |               |            | CCCGAGCCCT               |              |            |      |
| 20 |               |               |            | GCAAGCCTGG               |              |            | 3360 |
| 20 |               |               |            | GCATCTTCGG               |              |            | 3420 |
|    |               |               |            | ACAGGGCCTA               |              |            | 3480 |
|    |               |               |            | AGAAACACAT               |              |            | 3540 |
|    |               |               |            | AGCCTTGTGA               |              |            | 3600 |
|    | ATGTGGACAA    | GGAGGCGATG    | ATGGAAGCAG | GCTGGGACCC               | CTGCCTGCAG   | GCCCCCTTCC | 3660 |
| 25 | ACCTCACCCC    | GACCCTGTAC    | AGGACGCTGC | GTAATCAAGG               | CAACCAGGGA   | GCACCGGCGG | 3720 |
|    | AGAGCCGAGA    | GGTGCTGCAA    | GACACGGTCA | ACCTCCTTTT               | CAACCATCCC   | AGGCAGAGGA | 3780 |
|    |               |               |            | AGCCCCAGCC               |              |            | 3840 |
|    |               |               |            | CAGGGAGGCT               |              |            | 3900 |
|    |               |               |            | CTGCAACCCT               |              |            | 3960 |
| 30 |               |               |            | GGCCCCGTCA               |              |            | 4020 |
|    |               |               |            | ACCCCGTGGA               |              |            | 4080 |
|    | CTCCTGTTCA    | GCAAATCTCC    | CAGCTGCTGT | CCTTGCTGCA               | TCAGGGCCAA   | TTCCAGCCCA | 4140 |
|    | AACCAAACCA    | CCGAGGAAAT    | AAGTACTTGG | CCAAGCCAGG               | AGGCAGCAGG   | AGTGCAATCC | 4200 |
|    | CAGACACAGA    | TGGCCCAAGT    | GCAAGGGCTG | GAGGCCAGAC               | AGACCCAGAA   | CAGGAGGAAG | 4260 |
| 35 | GGCCTTTGGA    | TCCTGAAGAG    | GACCTCTCTG | TGAAGCAACT               | GCTAGAAGAA   | GAGCTGTCAA | 4320 |
|    | GTCTGCTGGA    | CCCCAGCACA    | GGTCTGGCCC | TGGACCGGCT               | GAGCGCCCCT   | GACCCGGCCT | 4380 |
|    | GGATGGCGAG    | ACTUTUTTTG    | CCCCTCACCA | CCAACTACCG               | TGACAATGTG   | ATCTCCCCGG | 4440 |
|    | ATGCTGCAGC    | CACGGAGGAG    | CCAAGGACCT | TCCAGACGTT               | CGGCAAGGCA   | GAGGCACCAG | 4500 |
|    | AGCTGAGCCC    | AACAGGCACG    | AGGCTGGCCA | GCACCTTTGT               | CTCGGAGATG   | AGCTCACTGC | 4560 |
| 40 | TGGAGATGCT    | GCTGGAACAG    | CGCTCCAGCA | TGCCCGTGGA               | GGCCGCCTCC   | GAGGCGCTGC | 4620 |
|    |               |               |            | GTTTAGACTT               |              |            | 4680 |
|    | GCATGAAAGT    | GCAAGGGGAC    | CCAGGTGGAA | AGACGGGGAC               | TGAGGGCAAG   | AGCAGAGGCA | 4740 |
|    | GCAGCAGCAG    | CAGCAGGTGC    | CTGTGAACAT | ACCTCAGACG               | CCTCTGGATC   | CAAGAACCAG | 4800 |
|    | GGGCCTGAGG    | ATCTGTGGAC    | AAGAGCTGGT | TTCTAAAATC               | TTGTAACTCA   | CTAGCTAGCG | 4860 |
| 45 | GCGGCCTGAG    | AACTTTAGGG    | TGACTGATGC | TACCCCCACA               | GAGGAGGCAA   | CAGCCCCAGG | 4920 |
|    | ACTAACAGCT    | GACTGACCAA    | AGCAGCCCCT | TGTAAGCAGC               | TCTGAGTCTT   | TTGGAGGACA | 4980 |
|    | GGGACGGTTT    | GTGGCTGAGA    | TAAGTGTTTC | CTGGCAAAAC               | ATATGTGGAG   | CACAAAGGGT | 5040 |
|    | CAGTCCTCTG    | GCAGAACAGA    | TGCCACGGAG | TATCACAGGC               | AGGARAGGGT   | GGCCTTCTTG | 5100 |
|    | GGTAGCAGGA    | GTCAGGGGGC    | TGTACCCTGG | GGGTGCCAGG               | AAATGCTCTC   | TGACCTATCA | 5160 |
| 50 | ATAAAGGAAA    | AGCAGTGATT    | САЛАЛАЛАЛА | AAAAAAAAA                | AAAAAAAAA    |            |      |
|    |               |               |            |                          |              |            |      |

# Seq ID No: 175 Protein sequence: Protein Accession #: NP\_057664.1

| 55 |            |             |            |            |            |            |      |
|----|------------|-------------|------------|------------|------------|------------|------|
|    | 1          | 11          | 21         | 31         | 41         | 51         |      |
|    | 1          |             | 1          | 1          | 1          | 1          |      |
|    |            |             |            | TVKYQVSEEV |            |            | 60   |
|    |            |             |            | RLDREQLCRQ |            |            | 120  |
| 60 |            |             |            | RTRIPLDRAL |            |            | 180  |
|    |            |             |            | DLVLTAYDNG |            |            | 240  |
|    |            |             |            | PDQGPNGEVE |            |            | 300  |
|    |            |             |            | PIPAHCKVLI |            |            | 360  |
|    |            |             |            | CWLSQELGHF |            |            | 420  |
| 65 | EQWPKYTLTL | LAQUQGLQPL  | SAKKQLSIQI | SDINDNAPVF | EKSRYEVSTR | ENNLPSLHLI | 480  |
|    |            |             |            | DSNTGEVTAQ |            |            | 540  |
|    |            |             |            | SDGKASLSVL |            |            | 600  |
|    |            |             |            | NGEPLYSIRS |            |            | 660  |
|    |            |             |            | LRVMFVTSVD |            |            | 720  |
| 70 |            |             |            | NCREAESTYR |            |            | 780  |
|    | LRGQAGEPCE | VGQSHKDVDK  | EAMMEAGWDP | CLOAPFHLTP | TLYRTLRNQG | NQGAPAESRE | 840  |
|    | VLQDTVNLLF | NHPRORNASR  | ENLNLPEPQP | ATGOPRSRPL | KVAGSPTGRL | AGDQGSBEAP | 900  |
|    | ORPPASSATL | RRORHLINGKV | SPEKESGPRQ | ILRSLVRLSV | AAFAERNPVE | ELTVDSPPVQ | 960  |
|    | QISQLLSLLH | QGQFQPKPNH  | RGNKYLAKPG | GSRSAIPDTD | GPSARAGGQT | DPEQEEGPLD | 1020 |
| 75 |            |             |            | SAPDPAWMAR |            |            | 1080 |
|    | TEEPRTFOTF | GKAEAPELSP  | TGTRLASTFV | SEMSSLLEML | LEGRSSMPVE | AASEALRRLS | 1140 |

VCGRTLSLDL ATSAASGMKV QGDPGGKTGT BGKSRGSSSS SRCL

Sec ID NO: 176 DNA secuence

Nucleic Acid Accession #: AL109712.1

5 Coding sequence: 2-128 (underlined sequences correspond to start and stop codons)

51 11 22 41 10 GAGTOTOTTT GGGCCAGCCG GGCTGCTGCA GACAGACAGG AAGCACGCCT GACGCTCCTC 60 TACCCTCGGG CAGCACAGCG GGGCTGGGAC TCACTCTAGC TTGCCCAGCA ACTTGCTTTC 120 CTGTGTGAAC TCTGGCAGGC TGCCCTCTCT GTGCAAAGCT GCCACTGGGG CCTGCTCAGG 180 GTGGCCTGGA ACTTGGAGGT GGGCAGTCAG GGCCTAGGAT GGGCCTGTGT CACCAGGGCA 240 TGTGCCCTTG GGCCAGTTAC TTCCTCTCAG AGCCTTGGGC TCCTCCTCTG AGGATGGGGC 300 TTGTTGGTGT GAAATGAGGT GAGCATGTTG AGTTGGGGAG CAGCAGGACA CGCACCTGCA 360 GGCAGCCGCC CTGGCCACGC TCCCTCCCTA CCTTCCGAGT CCTGGGACAG ACACAGTAGA 420 GCACAGCGGG CCAGCCTGCT CTCTTCTCTG TCTACTTTTT GCAGAAGAGT CAACAGATAC 480 AACAGGCCCA GGGAGGTGCC CCTGGGGGCC CCAGTCCCCA TCACTCCAAG GGGCAGTCCT 540 GCAAGTGACA AGGTGGGCCC AATCCCTGTG GAACAGGTCT CTGAGGACCA CAGAGTGGGG 600 CCCCAGGGAA AGCTGGGAGC CGAGCTAGAG GCAGGCAGCA AGTAAGGGCA AAGCTGTGCC 660 CCTGCCCGGA AGACCTTCCT GCCCCCAGAA CCCGACCCTC CGCAGATAGC CCTCCCTGGG 720 CAGCAGCCCC CCAGCTTCCA AGGCCCGTGC CTCACCAGAC GCCATGCTCT CACGGACTTG 780 TTTGCTGCTC TGTACCCTGC AGATCTGCCC CAGAGGAGCA GGTGAAAAGC CGCGCCTGCC 840 GAGGTGCTGT GGCGGTGGAG TTTTGGGCAG AGGAGTGGGG GGAAGAGTTT CTCACTTTTA 900 25 AGATTCTCCA AATCCAAGAT GAAGTCATGC TGTGCTTTGG AATGGTAGAT GCTCATTTAT 960 GTARAATCAT AATAAATGTT ACACAAACTG TTAAAAAAAA AAAAAAAAA AAAAAA

Seq ID No: 177 Protein sequence: Protein Accession #: AL109712.1

35 Seq ID NO: 178 <u>DNA sequence</u> Nucleic Acid Accession #: none found

Coding sequence: 3-107 (underlined sequences correspond to start and stop codons)

40 11 21 51 AATGGAGCAC TCCAAAGAAC GATTTGACCA ATAGCATTTC TTCTCTGGGG GTTGTATTTC 60 AAAGCATGCA ACTCTCCAGG GAACCAGAAC TAAATTGCTT AAAATGAAGT CATTCCTCAG 120 ATTAACTICC TCAGATAAAG TGTCAGCGGT CTGCAGAAAC GAAGAAGACA AAACTGAGAT 180 TATCACTCAT AATTCTCTTA CTTACTATGT CAGTGAAACA ATGAGTTTGC ATTTTTGCAA 240 TCCTAGAACA TTCTTCATTA GCCCTGGGTC ATGACCTCTT CCAGTTAATT CTCTTTCACA 300 CCTTTAGGAA AGATTTAAGA TGAACCTTCA ATAGGATATT AACATAACTC ATAGCCAATA 360 CCACAGCTGC CTTTCAAATT AATGAGGTTA ATTGTTCTCC AGCAAACATG AGTTTGTCTT TGGCATTTTA AATGCTTCCC ATTGATCTGA CATTTTGCTG TTTCAAGTTT TAAAGGGCTC 480 50 AAATCAAAGA CTATTGATAA CTGAGCAAAG AGCGAAGATC CAGAAATACG AAAACATTGT 540 CTTTTTTTT CCATGRAAA CAATCATAGC CTTTTGRATT CAATCGRAGT TTCTACATTA GCCATCTAGG ACTTATTTAT TTATTTTGTT TTCTAGTCAR GCTAATCTAT TTTAAAATC TTTTTTAAATC TTTTTTAAATC TTTTTTTATTAT TAAGTTTGTA 600 660 720 GARAGCTCT GGGGCCATGA CCACTTACGT ARATGTTTCA GTTTARARAC ARAGATTCA 780 GGCCTCTAAT TTGAGCCAAA TCCAGGTGAT CTTGTTTGAA ATTTTTGATG AATTTGAAAA 840 GATGAAAGTG GAACTTTTAA CATTCATGTT CCCCAAATTT TTCACTGGGA AGGGATGCTA 900 ATTGCCTACT TAAGATATAA GTTCAAGAAT AACATTTTCA TAGAAAATTC AGAAAACTGC 960 TTGACACAGC AGTGACATAG TTAGATGTGG CTCAGATGCC TTCCAAACCT GAGGGTCCCC 1020 AARGATTICT TTACCAGTTG TTTTTAACTA TGAATCTTAA TCTTGTTCAT TCCCCTGCCA 1080 60

Seq ID No: 179 Protein sequence: Protein Accession #: none found

70 Seq ID NO: 180 <u>DNA secuence</u> Nucleic Acid Accession #: none found Coding sequence: 2-176 (underlined sequences correspond to start and stop codons)

75 1 11 21 31 41 51

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COGGTGGGG CCTCGGGATG CAGGCGCCGG TGCCCGGGCC CCTGGGCCTG CTGGACCCCG
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 CAGAAGGGCT TTCGAGGAGG AAGAAGACGT CGCTCTGGTT TGTGGGGTCT CTGCTGCTGG
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 TGTCCTTCCT CATAGTCACC GTCGGGCTGG CTGCATCAGC AGGACGGAGA ATGTGACCGT
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 TGGGGGCTAC TACCCAGGGA TCATTCTCGG CTTTGGATCT TTCTTAGGAA TTATTGGCAT
 240
 5
 CAACTTGGTG GAGAATAGAA GGCAAATGCT GGTGGCAGCG ATCGTGTTTA TCAGTTTTGG
 300
 COTGSTGGCC GCCTTCTGCT GCGCCATCGT GGACGCGTA TTTGCAGCAC AGCACATTGA
 360
 ACCGAGGCCC CTCACCACGG GAAGATGCCA GTTTTACTCC AGTGGGGTGG GGTACTTGTA
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 CGATGTCTAC CAGACAGAGG TGAGCAGGAG CACTGAGATT CATGTGGGTT TTGCTCAGCT
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 AACCCCGCCG ACCCCACGCG GTTTTCCCTG CACATAGGCG TGGTCTGAAT ATTTGGATTC
 540
 TAATAGTTCC TGGGGGTCAC CCCTGCAGCT GGTGAACCGT TGATGCCCCC TGTGTAAGGG
 600
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 720
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15
 Seq ID No: 181 Protein sequence:
 Protein Accession #: none found
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 Seq ID NO: 182 DNA sequence
 Nucleic Acid Accession #: AK001579.1
 Coding sequence: 1150-2637 (underlined sequences correspond to start and stop codons)
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 CCCATACAGC CCCGGCCCCT GGTCTCTGGC TGTCAGGGTT TGGCCTCCTT CGTGGTGACC
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 TGCGGCGGCT ACAGGAGATC AGTGTGGTTT CTGCAGCTGA CACCCCAGAT AAGAAAGAGC
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 480
 AGCAGCAGAT GAGCCGGGGT GACATCCCCA TCATCGTGGA TGCCTGCATC AGTTTTGTTA
CCCAGCATGG GCTCCGGCTG GAAGGTGTAT ACCGGAAAGG GGGCGCTCGT GCCCGCAGCC
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 TGAGACTCCT GGCTGAGTTC CGTCGGGATG CCCGGTCGGT GAAGCTCCGA CCAGGGGAGC
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 720
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 780
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 840
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 GGAAGGGGGC AGAGACACAT CCATCCTGCA TTTGTGCCTA AAAATCCCTC CCTCTGTACC
 960
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 TGCACTGACG AGGATGAAAT GTGGGATTGG ACCACCAGCA TCCTTAAAGC CCAGCACGAT
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 2400
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 2460
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 TTOOTON ARCCCCCATG CACTTCCAGT CCACCCTCCA GCCAGCCCCT CACATGACCC
 TAGGACCAGC AGTCTGAGAG GGTAGGTACC AGAAGACCCA GAAACTCTTA TCGTGGCACT
 2700
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 2760
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2820

2880

GAGCACTGGA CTAAAGGCTT CAGTGGCTGC GTGTCCCAGG ACAGGTCATG GCCCCTCTCT

GOGCCCAGCC CATTTATCTA TACCATGAGG TAACTGAAGT AAGGAGAGCA GTGAATGTCA

75

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 ACTGCATTAA AGAAAAAAA TGCTTTGGAA ACCAGAGGCC TGGGTGATGT TAAAGTCTAT
 3060
 CCTGTCCCAC TTCCTACATT CTGGGACTAC CGTGAAGCCT GGAGTAGGGA GAGCGAGTTT
 3120
 GGGRGCTGGG ACTCGGGGAG TCAAAAATAG ATGAGTAATT GTCAATAAAC CTGGGAACC
 Seq ID No: 183 Protein sequence:
 Protein Accession #: AK001579.1
10
 11
 21
 31
 41
 51
 MSLTHSNASF VSSMTLPLHG CCLAGGRLLV FLRSLRAKAQ PGSLPSPTRI HGLAALRPIT
 SHPGGSSRDL ACGEVGRGOR HIHPAFVPKN PSLCTSCHSF FPGPPOPSSI PSPELPOKNO
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 RLEKYKDVIG CLPRVNRRTL ATLIGHLYRV OKCAALNOMC TRNLALLFAP SVFOTDGRGE
 HEVRYLORLI DOYISVEDID SDOVACIDLE VSLITTWKDV OLSCAGDLIM EVYIROOLPD
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 WCOLPEPCSA SLLLKKVPLA QAGCLFTGIR RESPRVGLLR CREEPPRLLG SRFQERFFLL
 360
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 Nucleic Acid Accession #: none found
 Coding sequence: 1-81 (underlined sequences correspond to start and stop codons)
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 41
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 GTATTAAGCT TARAAAGT<u>TA A</u>TTCAGTTTA AGGAATATAA ACCARATTAT TTTATATTTG
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 Protein Accession #: none found
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 VELVENCIEY TEFINIFSKE VLSLES
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70
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 Coding sequence: 43-3588 (underlined sequences correspond to start and stop codons)
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 GGGGCCGCGC CGCTGCCGCT GCTGCTGGTG TTAGCGCTCA GTCAAGGCAT TTTAAATTGT
```

|     | TGTTTGGCCT                              | ACAATGTTGG | TCTCCCAGAA | GCAAAAATAT  | TTTCCGGTCC   | TTCAAGTGAA                             | 180          |
|-----|-----------------------------------------|------------|------------|-------------|--------------|----------------------------------------|--------------|
|     | CAGTTTGGGT                              | ATGCAGTGCA | GCAGTTTATA | AATCCAAAAG  | GCAACTGGTT   | ACTGGTTGGT                             | 240          |
|     | TCACCCTGGA                              | GTGGCTTTCC | TGAGAACCGA | ATGGGAGATG  | TGTATAAATG   | TCCTGTTGAC                             | 300          |
| 5   | CTATCCACTG                              | CCACATGTGA | AAAACTAAAT | TTGCAAACTT  | CAACAAGCAT   | TCCAAATGTT                             | 360          |
| 3   | ACTGAGATGA                              | AAACCAACAT | GAGCCTCGGC | TTGATCCTCA  | CCAGGAACAT   | GGGAACTGGA                             | 420<br>480   |
|     | GGTTTTCTCA                              | CATGIGGICC | TC1G1GGGCA | CAGCAATGIG  | CONCOMMONO   | TTACACAACG<br>ACCTGCAACT               | 540          |
|     | CAGCCCTGCC                              | CTGACATCAG | AGATGTTCTG | CAGCICICAG  | ATGAATCAAA   | TAGTATTTAT                             | 600          |
|     | CCTTGGGATG                              | CACTABAGAA | TTTTTTGAA  | ANATTTGTAC  | AAGGCCTTGA   | TATAGGCCCC                             | 660          |
| 10  | ACAAAGACAC                              | AGGTGGGGTT | AATTCAGTAT | GCCAATAATC  | CAAGAGTTGT   | GTTTAACTTG                             |              |
|     | AACACATATA                              | AAACCAAAGA | AGAAATGATT | GTAGCAACAT  | CCCAGACATC   | CCAATATGGT                             | 780          |
|     | GGGGACCTCA                              | CAAACACATT | CGGAGCAATT | CAATATGCAA  | GAAAATATGC   | CTATTCAGCA                             | 840          |
|     | GCTTCTGGTG                              | GGCGACGAAG | TGCTACGAAA | GTAATGGTAG  | TTGTAACTGA   | CGGTGAATCA                             | 900          |
| 15  | CATGATGGTT                              | CAATGTTGAA | AGCTGTGATT | GATCAATGCA  | ACCATGACAA   | TATACTGAGG                             | 960          |
| 15  | TTTGGCATAG                              | CAGITCTTGG | GTACTTAAAC | AGAAACGCCC  | TTGATACTAA   | AAATTTAATA                             | 1020<br>1080 |
|     | AAAGAAATAA                              | AAGCGATCGC | TAGTATICCA | ACAGAAAGAT  | ACTITICAA    | TGTGTCTGAT                             | 1140         |
|     | ACTOTTCARC                              | CACCACACAA | CTTTCAGATG | CARATGTCAC  | AAGTGGGATT   | CAGTGCAGAT                             | 1200         |
|     | TACTOTTOTO                              | AAAATGATAT | TOTGATGOTG | GGTGCAGTGG  | CACCTTTTCC   | CTGGAGTGGG                             | 1260         |
| 20  | ACCATTGTCC                              | AGAAGACATC | TCATGGCCAT | TTGATCTTTC  | CTAAACAAGC   | CTTTGACCAA                             | 1320         |
|     | ATTCTGCAGG                              | ACAGAAATCA | CAGTTCATAT | TTAGGTTACT  | CTGTGGCTGC   | AATTTCTACT                             | 1380         |
|     | GGAGAAAGCA                              | CTCACTTTGT | TGCTGGTGCT | CCTCGGGCAA  | ATTATACCGG   | CCAGATAGTG                             | 1440         |
|     | CTATATAGTG                              | TGAATGAGAA | TGGCAATATC | ACGGTTATTC  | AGGCTCACCG   | AGGTGACCAG                             | 1500         |
| 0.5 | ATTGGCTCCT                              | ATTTTGGTAG | TGTGCTGTGT | TCAGTTGATG  | TGGATAAAGA   | CACCATTACA                             |              |
| 25  | GACGTGCTCT                              | TGGTAGGTGC | ACCAATGTAC | ATGAGTGACC  | TAAAGAAAGA   | GGAAGGAAGA                             | 1620         |
|     | GTCTACCTGT                              | TTACTATCAA | AAAGGGCATT | TTGGGTCAGC  | ACCAATTTCT   | TGAAGGCCCC                             | 1680         |
|     | GAGGGCATTG                              | AAAACACICG | ATTTGGTTCA | GCAATTGCAG  | ATTORONATION | CATCAACATG<br>TGGAGCTGTA<br>AATCTTGGGA | 1900         |
|     | CATGGCTTTA<br>CATGGCTTTA                | ATGATGIGAT | CCCCACTATC | CCCCCACAAAA | ATTOCCAGAA   | AATOTTGGGA                             | 1060         |
| 30  | TCCGATGGAG                              | CCTTTAGGAG | CCATCTCCAG | TACTTTGGGA  | GGTCCTTGGA   | TGGCTATGGA                             | 1920         |
|     | CTTTTAAATC                              | GGGATTCCAT | CACCGATGTG | TCTATTGGTG  | CCTTTGGACA   | AGTGGTTCAA                             | 1980         |
|     |                                         |            |            |             |              | AGAAAAAATC                             |              |
|     | ACTTTGGTCA                              | ACAAGAATGC | TCAGATAATT | CTCAAACTCT  | GCTTCAGTGC   | AAAGTTCAGA                             | 2100         |
|     | CCTACTAAGC                              | AAAACAATCA | AGTGGCCATT | GTATATAACA  | TCACACTTGA   |                                        | 2160         |
| 35  | TTTTCATCCA                              | GAGTAACCTC | CAGGGGGTTA | TTTAAAGAAA  | ACAATGAAAG   |                                        | 2220         |
|     | AAGAATATGG                              | TAGTAAATCA | AGCACAGAGT | TGCCCCGAGC  | ACATCATTTA   | TATACAGGAG                             | 2280         |
|     | CCCTCTGATG                              | TTGTCAACTC | TTTGGATTTG | CGTGTGGACA  | TCAGTCTGGA   | AAACCCTGGC<br>TCCTTTCCAC               | 2340<br>2400 |
|     | ACTAGCCCTG                              | CCCTTGAAGC | CTATTCTGAG | ACTGCCAAGG  | TOTTOMGTAT   | CCGACAAATA                             | 2460         |
| 40  | CCAGCTGCTC                              | BAGBACABCC | CTTTATIGTC | AGCAACCAAA  | ACAAAAGGTT   | AACATTTCA                              | 2520         |
|     | GTAACACTGA                              | AAAATAAAAG | GGAAAGTGCA | TACAACACTG  | GAATTGTTGT   | TGATTTTTCA                             | 2580         |
|     | GAAAACTTGT                              | TTTTTGCATC | ATTCTCCCTA | CCGGTTGATG  | GGACAGAAGT   | AACATGCCAG                             | 2640         |
|     | GTGGCTGCAT                              | CTCAGAAGTC | TGTTGCCTGC | GATGTAGGCT  | ACCCTGCTTT   |                                        | 2700         |
|     | CAACAGGTGA                              | CTTTTACTAT | TAACTTTGAC | TTCAATCTTC  | AAAACCTTCA   |                                        | 2760         |
| 45  | TCTCTCAGTT                              | TCCAAGCCTT | AAGTGAAAGC | CAAGAAGAAA  | ACAAGGCTGA   | TAATTTGGTC                             | 2820         |
|     | AACCTCAAAA                              | TTCCTCTCCT | GTATGATGCT | GAAATTCACT  | TAACAAGATC   | TACCAACATA                             | 2880         |
|     | AATTTTTATG                              | AAATCTCTTC | GGATGGGAAT | GTTCCTTCAA  | TCGTGCACAG   | TTTTGAAGAT<br>AGTAAGCATG               | 2940         |
|     | CONTROCTO                               | TOTTO COT  | CCCTCACTAT | BCCSSSCSS   | AGAACCCACT   | GATGTACCTA                             | 3060         |
| 50  | ACTGGGGGTGC                             | BBBCBGBCBB | CCCTCAGTAI | ATCACTTGTA  | ATGCAGATAT   | CARTCCACTG                             | 3120         |
| • • | AAAATAGGAC                              | AAACATCITC | TTCTGTATCT | TTCAAAAGTG  | AAAATTTCAG   | GCACACCAAA                             | 3180         |
|     | GAATTGAACT                              | GCAGAACTGC | TTCCTGTAGT | AATGTTACCT  | GCTGGTTGAA   | AGACGTTCAC                             | 3240         |
|     | ATGAAAGGAG                              | AATACTTTGT | TAATGTGACT | ACCAGAATTT  | GGAACGGGAC   | TTTCGCATCA                             | 3300         |
|     | TCAACGTTCC                              | AGACAGTACA | GCTAACGGCA | GCTGCAGAAA  | TCAACACCTA   | TAACCCTGAG                             | 3360         |
| 55  | ATATATGTGA                              | TTGAAGATAA | CACTGTTACG | ATTCCCCTGA  | TGATAATGAA   | ACCTGATGAG                             | 3420         |
|     | AAAGCCGAAG                              | TACCAACAGG | AGTTATAATA | GGAAGTATAA  | TTGCTGGAAT   | CCTTTTGCTG                             | 3480<br>3540 |
|     | TTAGCTCTGG                              | TTGCAATTTT | ATGGAAGCTC | GGCTTCTTCA  | AAAGAAAATA   | TGAAAAGATG                             | 3600         |
|     | ACCIDIODATE                             | GGNACCGGCA | CATCCCACC  | CAGGGTTTGC  | TOTTTGCCTG   | CAGCAGACCT<br>CATGGATTTC               | 3660         |
| 60  | TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT | CCATATTTTT | TTTATCATGT | CGTAGGTAAA  | CTAACCTGGT   | ATTTTAAGAG                             |              |
| 00  | AAAACTGCAG                              | GTCAGTTTGG | ATGAAGAAAT | TGTGGGGGGT  | GGGGGAGGTG   | CGGGGGGCAG                             | 3780         |
|     | GTAGGGAAAT                              | AATAGGGAAA | ATACCTATTT | TATATGATGG  | GGGAAAAAA    | GTAATCTTTA                             | 3840         |
|     | AACTGGCTGG                              | CCCAGAGTTT | ACATTCTAAT | TTGCATTGTG  | TCAGAAACAT   | GAAATGCTTC                             | 3900         |
|     | CAAGCATGAC                              | AACTTTTAAA | GAAAAATATG | ATACTCTCAG  | ATTTTAAGGG   | GGAAAACTGT                             | 3960         |
| 65  | TCTCTTTAAA                              | ATATTTGTCT | TTAAACAGCA | ACTACAGAAG  | TGGAAGTGCT   | TGATATGTAA                             | 4020         |
|     | GTACTTCCAC                              | TTGTGTATAT | TTTAATGAAT | ATTGATGTTA  | ACAAGAGGGG   | AAAACAAAAC                             | 4080         |
|     | ACAGGTTTTT                              | TCAATTTATG | CTGCTCATCC | AAAGTTGCCA  | CAGATGATAC   | TTCCAAGTGA<br>ACGGCTGCCC               | 4140<br>4200 |
|     | TAATTTTATT                              | TATAAACTAG | GTAAAATTIG | ANACATOOTT  | CTITIATACC   | GCTTAGAGTA                             | 4260         |
| 70  | TACCTCCTAT                              | ATGTCCATTT | AAGTTAGGAG | AGGGGGGCGAT | ATAGAGACTA   | AGGCACAAAA                             | 4320         |
| . • | TTTTGTTTAA                              | AACTCAGAAT | ATAACATTTA | TGTAAAATCC  | CATCTGCTAG   | AAGCCCATCC                             | 4380         |
|     | TGTGCCAGAG                              | GAAGGAAAAG | GAGGAAATIT | CCTTTCTCTT  | TTAGGAGGCA   | CAACAGTTCT                             | 4440         |
|     | CTTCTAGGAT                              | TTGTTTGGCT | GACTGGCAGT | AACCTAGTGA  | ATTTTTGAAA   | GATGAGTAAT                             | 4500         |
| ~~  | TTCTTTGGCA                              | ACCTTCCTCC | TCCCTTACTG | AACCACTCTC  | CCACCTCCTG   | GTGGTACCAT                             | 4560         |
| 75  | TATTATAGAA                              | GCCCTCTACA | GCCTGACTTT | CTCTCCAGCG  | GTCCAAAGTT   | ATCCCCTCCT                             | 4620         |
|     | TTACCCCTCA                              | TCCAAAGTTC | CCACTCCTTC | AGGACAGCTG  | CIGIGCATTA   | GATATTAGGG                             | 4680         |
|     |                                         |            |            |             |              |                                        |              |

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 TTCAGGGAGC TATTTTCATT TAGTGCTAAA CAAGTAAGAA AAATAAGCTA GAGTGAATTT
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 5160
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 CAAGAATTIG ACTIGGAAAA G
 Seq ID NO: 187 Protein sequence:
15
 Protein Accession #: NP 002194.1
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 RNMGTGGFLT CGPLWAGOCG NOYYTTGVCS DISPDFOLSA SFSPATOPCP SLIDVVVVCD
 180
 ESNSIYPWDA VKNFLEKFVQ GLDIGPTKTQ VGLIQYANNP RVVFNLNTYK TKEEMIVATS
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 QTSQYGGDLT WTFGAIQYAR KYAYSAASGG RRSATKVMVV VTDGESHDGS MLKAVIDQCN
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 HDNILRFGIA VLGYLNRNAL DTKNLIKBIK AIASIPTERY FFNVSDEAAL LEKAGTLGEO
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25
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 AHRGDQIGSY FGSVLCSVDV DKDTITDVLL VGAPMYMSDL KKEBGRVYLF TIKKGILGQH
 540
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 600
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 660
30
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 1020
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 1380
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70
 1500
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75
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 TTTTTATGGA ATATCOGTTG GATTATAGAA CAGCTGCTGA TACAACAGGC TTGCAACCCA 1860
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|    |                  |                 |                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | man ar mmamn                            | common concent | 1920 |
|----|------------------|-----------------|-----------------|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------|----------------|------|
|    | TTCTTAACCA       | GTTCACGCCT      | GCTAACATTA      | GTCGACAGGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TCACATTCIA                              | CITGACIGIG     |      |
|    | GTGAAGACAA       | TGTCTGTAAA      | CCCAAGCTGG      | AAGTTTCTGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AGATAGTGAT                              | CAAAAGAAGA     | 1980 |
|    | TCTATATTGG       | CONTENTANT      | CCTCTGACAT      | TGATTGTTAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GGCTCAGAAT                              | CAAGGAGAAG     | 2040 |
|    | GTGCCTACGA       |                 | * maaaammaaa    | mmaca araca                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | CCCTCATTTC                              | ATCGGGGGTTG    | 2100 |
| -  | GIGCCTACGA       | AGCTGAGCTC      | ATCGITTCCA      | TICCACIGCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GGCIGHIIIC                              |                |      |
| 5  | TCCGAAACAA       | TGAAGCCTTA      | GCAAGACTTT      | CCTGTGCATT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TAAGACAGAA                              | AACCAAACTC     | 2160 |
|    | CCCACCTCCT       | ATGTGACCTT      | GGAAACCCAA      | TGAAGGCTGG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AACTCAACTC                              | TTAGCTGGTC     | 2220 |
|    | DECCHOOLCOL      | TGTGCACCAG      | GP CAMOR CP CP  | TOGATACTTC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TOTOLABATTT                             | CACTTACAAA     | 2280 |
|    | TTCGTTTCAG       | TOTGUACCAG      | CAGICAGAGA      | IGGNINCIIC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 1010001111                              | 01101111011111 | 2340 |
|    | TCCAAAGCTC       | AAATCTATTT      | GACAAAGTAA      | GCCCAGTTGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATCTCACAAA                              | GITGMICITG     |      |
|    | CTGTTTTAGC       | TGCAGTTGAG      | ATAAGAGGAG      | TCTCGAGTCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TGATCATATC                              | TTTCTTCCGA     | 2400 |
| 10 | TITO CO O O OTO  | GGAGCACAAG      | CACAACCCTG      | ACACTCAAGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | DOCUMENTAL                              | CCACTTGTTC     | 2460 |
| 10 | TICCHARCIG       | GOMGCACARIG     | GNGRINGCCCTG    | ACTION OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 010011011000                            | 300000000000   | 2520 |
|    | AGCACATCTA       | TGAGCTGAGA      | AACAATGGTC      | CAAGTTCATT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CAGCAAGGCA                              | MIGCICCATC     |      |
|    | TTCAGTGGCC       | TTACAAATAT      | AATAATAACA      | CTCTGTTGTA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TATCCTTCAT                              | TATGATATTG     | 2580 |
|    | ATCCACCAAT       | GAACTGCACT      | TOTAGETATION    | AGATCAACCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TTTGAGAATT                              | AAGATCTCAT     | 2640 |
|    | ATGGACCAAT       | AACTGAAAAG      | I CAGAIA COO    | Managagagaga                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 3000030000                              | CACCATOTO      | 2700 |
|    | CTTTGCAAAC       | AACTGAAAAG      | AATGACACGG      | TTGCCGGGCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | MGGTGMGCGG                              | GACCATCICA     |      |
| 15 | TCACTAAGCG       | GGATCTTGCC      | CTCAGTGAAG      | GAGATATTCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CACTTTGGGT                              | TGTGGAGTTG     | 2760 |
|    | CTCACTCCTT       | GAAGATTGTC      | TROCEDARTER     | GGAGATTAGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CAGAGGAAAG                              | AGTGCAATCT     | 2820 |
|    | CICAGIGCII       | GTCATTACTG      | maga cmaaca     | CONTROL DICE &                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | TO BE SCHOOL SAN                        | CACAATCATT     | 2880 |
|    | TGTACGTAAA       | GTCATTACTG      | TGGMCTGMGM      | CITITATORA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | IMMOMMANI                               | DAGRATORE .    | 2940 |
|    | CCTATTCTCT       | GAAGTCGTCT      | GCTTCATTTA      | ATGTCATAGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GTTTCCTTAT                              | AAGAATCTTC     |      |
|    | Charrondon       | TATCACCAAC      | TCCACATTGG      | TTACCACTAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TGTCACCTGG                              | GGCATTCAGC     | 3000 |
| 20 | CARTINGON        | GCCTGTGCCT      | amamaaaaaa      | TOATTTACC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | AGTTCTAGCA                              | GCATTCTTGC     | 3060 |
| 20 | CAUCGCCCAT       | GCCIGIGCCI      | GIGIGGGION      | ICALITINGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | MOTICINGON                              | amagaacaa.     | 3120 |
|    | TACTGGCTGT       | TTTGGTATTT      | GTAATGTACA      | GGATGGGCTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TTTTARACGG                              | GICCOGCCAC     |      |
|    | CTCAAGAAGA       | ACAAGAAAGG      | GAGCAGCTTC      | AACCTCATGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AAATGGTGAA                              | GGAAACTCAG     | 3180 |
|    | AAACTEAACT       | GCAGTTTTTA      | ACTTATICTA      | CATCTTGACC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CACTAGAATT                              | AGCAACTTTA     | 3240 |
|    | JUDICI INCI      | ARACTTTCTT      | ASTERNOOM.      | A A B B B B COCKA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | CCCTTTACTC                              | CTCATACTCC     | 3300 |
|    | TTATAGATTT       | ARACTITCIT      | CATGAGGAGT      | MANAMICCOM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GGCITIACIG                              | CIGNINGIGC     | 3360 |
| 25 | TAATTGGCAT       | TAACCACAAA      | ATGAGAATTA      | TATTTGTCAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCTTCTCCTT                              | ATAAATAAGT     |      |
|    | TORGROWTHO       | ATTTAATAAC      | ATAGGGTGAC      | TTGTGTTTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AGGTATTTAA                              | TAAAAAAT       | 3420 |
|    | TCMUNCATAC       | AGTTTTTATT      | CHATCHATAT      | ANCACAGGTA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CTCCCTCATT                              | TACTACTTTA     | 3480 |
|    | TTCAAGGGAT       | AGIIIIIAII      | CAMIGINIAL      | AAGACAGGAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | mont occurry                            | mmm a mmm cmm  | 3540 |
|    | TATAAAATAG       | TACCTCCTTC      | AGITACIGIT      | TCTGATTTAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TGTACGGMAC                              | TTIMITIGIT     |      |
|    | GTTGTTGTTG       | TTGTTGTTGT      | TGTTGTTTTA      | AAGCAGTCCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AATTTGGACC                              | TTAGCAATCA     | 3600 |
| 30 | TOTOTTTCT        | ATAGGTACTT      | ATATTTAATA      | CATATTACAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TACAGTTTAC                              | TTTTCAGAAT     | 3660 |
| 50 |                  | TTATAACTGC      | A MOR & CHETCO  | ACCOMPANDA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TCACTCATAT                              | CCTACAATTT     | 3720 |
|    | ACTAAAGACT       | TTATAACTGC      | MIGHACIIGG      | MILITIAN                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | TORCEONERS                              | ma craama mmm  | 3780 |
|    | TATAAACACA       | TACATGATAC      | CATCCAAATT      | CTTGCTTTTA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATAACAAAGG                              | TACAATATTT     |      |
|    | TGTTTTAGTA       | TGAAAATCTG      | GTAGATCCTA      | TTACACTTCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GTTTATATTA                              | AATCCACAAT     | 3840 |
|    | a mmmmamma C     | ATTTTTAACT      | TOTAL A A TITLE | TENGGEGAAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TOOTTOWAGO                              | CAACCTATAC     | 3900 |
| 20 | MITTIALIAC       | MILLIAMOL       |                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 200000000000000000000000000000000000000 | TTCACCTGAA     | 3960 |
| 35 | TAAAAATTAG       | TTCCATAATC      | ACAAATGGCT      | CITITGIGIA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATTGTTTAAT                              | TICACCIGAA     |      |
|    | TATCATAATG       | CTTAAAGCCA      | TATGGAGTTG      | GAAATTATTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCAAAGCATA                              | TTTATTCCAT     | 4020 |
|    | TOTTTTACTO       | TGGCTATTTA      | CAGTATAAAA      | AAAGCATTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATTAAAATAC                              | TGTGTAGTTC     | 4080 |
|    | IGITITAGEC       | TTGCTTATGC      | ********        | mamma da mmo                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | mma cacmaca                             | CCACACTTTT     | 4140 |
|    | TTTGAGATAG       | TIGCTIMIGC      | MINIMGIAMG      | IMITACATIC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | IIAGAGIAGA                              | annes a amam   | 4200 |
|    | TAGTTAGTAT       | TAATTTATTT      | TCCTCCATTC      | ATGTACTTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CCTTATATTT                              | CCAAAACTGT     |      |
| 40 | TACTORGAST       | CCCTCAAGAT      | CAGTGAGAAA      | TCTTTACAGT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TGACAGGAAC                              | CTGGACCCCT     | 4260 |
|    | TA GCCCCA A CT   | TOTATION OF THE | TOCTOTOTATO     | ABABABCTCT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TAAGGCAACT                              | CACTGATTTA     | 4320 |
|    | IMCCCCMMCI       | IIMIGMGIAM      | 1001100111      | >mm>.com.com                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | mmma accra ac                           | GTAATGTGTA     | 4380 |
|    | CTTCTAGCAA       | TAGCATGATG      | TTACAGGAAT      | ATTACCTCTG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | IIIAAGCAAG                              | GIMMIGIGIA     |      |
|    | AAATCAGTCT       | CGGCTGTCAG      | AATAACTTCT      | AAAAGGTATT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TTTATAAGCA                              | GTTCAAGTTA     | 4440 |
|    | CTGAAAACCT       | TTTAAACCTT      | TCTGAAGTTC      | GTTAGTATAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATTACTTTC                               | TAGGATTATT     | 4500 |
| 45 | 220000000        | ACATAGGTGG      | CARCTTOTAC      | TTTTATATATA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | CTCTGTAGAG                              | TGGTGAACCT     | 4560 |
| 70 | AATAAAAGCC       | ACMINGGIGG      | CANGITOTAG      | 0000000000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | magaaamam                               | CAMCACTTAT     | 4620 |
|    | TCTAGAGGAA       | TATATGATTT      | ATTCACAGTT      | CCTCAAGGCC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TGGGGATGAT                              | GMICAGIIMI     |      |
|    | ACCTATTTT        | GTGCAATTAC      | ATCATGTTGT      | ACATTAGAAA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TGGAGAGTTT                              | AATAGCTCTT     | 4680 |
|    | ma a concentrati | CCTCATTAGG      | TARTCATARA      | TATTTCCCTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AAATAATTGA                              | CTATTTTGCT     | 4740 |
|    | IAMCIGCIGI       | CCICATIAGG      | - man-mommo     | COMMANDER                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | MA AMERICANO                            | CACAAGTIGA     | 4800 |
|    | GTGTTTTAAA       | AATGATTGAA      | ATTTATCTTG      | CCATATCTCA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | IMMITICALG                              | CHCHHOTTON     |      |
| 50 | CTGAGCTAAT       | CTTGAGAATA      | TATTCGTAAA      | ATAGGAGCAC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATTTAGTTGA                              | GGTATACAAG     | 4860 |
|    | CONCORCO         | ACACAAAACC      | TTCTATTTA       | CCTTTAGTGA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATTTCAAAAG                              | TAATGGGTCT     | 4920 |
|    |                  | * WWW. WW.      | CONTROL OF      | ACACCTTA AT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | CATATGCAGT                              | AAGTATTTT      | 4980 |
|    | TGGAGTATAG       | ATTITITATIA     | GINGCIIGHA      | AGNOCITARA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |                                         | an a amanmaa   | 5040 |
|    | ATTACCAATA       | AATTTAAAAT      | TTTTTAAGAA      | AAATATTTTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ATCCTAGGGC                              | CAAGTGTTGC     |      |
|    | CTGCCACCAA       | TCAGTAAGTT      | AGTCTATAAC      | AAATTTTACC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CTAACAGTTT                              | TACCACCTAG     | 5100 |
| 55 | CARCACTCAT       | THETCHERARAT    | ATGTTCGATA      | GAAAGTCACT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CTTTGGCAAA                              | AGTGTTAGAA     | 5160 |
| 55 | CANCAGICAL       | macca marra     | mccmmmm mc      | CONTOTATO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | TOARACTART                              | CTTGTATTGG     | 5220 |
|    | TTTGCTTTTG       | TGCCATCTAT      | TCCTTTIATG      | GCMICIAICS                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TORANG TARE                             | mmm-max x x m  |      |
|    | AGATTGAAAG       | ATGCTGTAAT      | TTAGAAATTA      | ACATGATATO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TTARATTACC                              | TTTATGAAAT     | 5280 |
|    | ATAGTTTTGT       | ATAATAGCAT      | AGATTTTCCT      | TCAAAAAATG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AACATTTATA                              | TATCTACAAA     | 5340 |
|    | namaTOCAGA       | MANAGERATTT     | GANAGCCTAC      | TTTCTGAAGE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | AAATGGTGGG                              | ATTTTTTTT      | 5400 |
| 60 | MMINIGGROM       | MONOCHALLI      | moode           | man 2.2.2.00000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | A A A TOTO TOTO                         | ANCAPPTCAN     |      |
| 60 | ATCATGATTA       | . AATATCAAAA    | AATTGCCCTA      | TUMMANCTT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | AMMICICIAN                              | AACATTTGAA     | 2400 |
|    | ATACTACCAT       | ATTTGTGATT      | TATTGAGAAT      | AAAAATCCAT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | TTTGAAATGI                              | AAAATTTTTA     | 5520 |
|    | TCATCTGATT       | CAGTTTTAAG      | AAAACATGAA      | TGAACTAGAZ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | GATATTAAAA                              | ACATTTGACA     | 5580 |
|    | - GRACIONII      | 2.0011110000    | meramammora.    | THE PROPERTY AND ADDRESS OF THE PARTY AND ADDR | OT ATTTATTT                             | CAGAATTGAT     | 5640 |
|    | TIGGIAAGAA       | MINITIGATAC     | . IGNIMITUAL    | ***********                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                         | 220022002000   | 5700 |
|    |                  |                 | GAGTCATTT       | TICIGITICI                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | CITITUTETT                              | AACGATTATC     | 5/00 |
| 65 | ACTGTAATTC       | TGAATCT         |                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                         |                |      |
|    | -                |                 |                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |                                         |                |      |

Seq ID NO: 189 <u>Protein sequence:</u> Protein Accession #: NP\_002201.1

70 1 11 21 31 41 51

MARPPERELR LIFERCIPLIA SCILLIPICA PHILOVORDAS YSCREDISTYS DEVELOPMENTS
SCHEPLING REALTYPEN YSCREDISCH STROCHE BEDATENDY ALDDELBYS 120
SCHEPLING REALTYPEN SCHELLAGE LEHHICZENG EBERVICTL COUTRYWER KORDLIAD
100
GOGFCCOGFS LIDTHADRYL LEGISCHWO GULLDOVIAR IVERCHWY ZICHNOGLAF
REALDIDDS YLLDSVANGE PROSILLOPS VERRARLIA GWYLTZORI MSGLIADY 300
300

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OMAAYFOFSV AATDINGDDY ADVFIGAPLF MDRGSDGKLO EVGOVSVSLO RASGDFOTTK
 LNGFEVFARF GSAIAPLGDL DODGFNDIAI AAPYGGEDKK GIVYIFNGRS TGLNAVPSOI
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 LEGOWAARSM PPSFGYSMKG ATDIDKNGYP DLIVGAFGVD RAILYRARPV ITVNAGLEVY
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 ALFLYSRSPS HSKNMTISRG GLMCCEELIA YLRDESEFRD KLTPITIFME YRLDYRTAAD
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 ACNOGEGAYE AELIVSIPLO ADFIGVVRNN BALARLSCAF KTENOTROVV CDLGNPMKAG
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 TOLLAGERES VHOOSEMDIS VKEDLOIOSS NEEDKVSEVV SHKVDLAVLA AVEIRGVSSP
 780
 DHIFLPIPNW BHKENPETER DVGPVVOHIY BLRNNGPSSF SKANLHLOWP YKYNNNTLLY
 840
10
 TLHYDTOGPM NOTSOMETHE LETKISSICT TEKNOTVAGO GERDHLITKE DLALSEGDIH
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 TLGCGVAQCL KIVCQVGRLD RGKSAILYVK SLLWTETFMN KENQNHSYSL KSSASFNVIE
 950
 PPYKNLPIED ITNSTLVTTN VTWGIQPAPM PVPVWVIILA VLAGLLLLAV LVFVMYRMGF 1020
 FKRVRPPOSE OEREOLOPHE NGEGNSET
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 Seq ID NO: 190 DNA sequence
 Nucleic Acid Accession #: NM 004864
 Coding sequence: 26-952 (underlined sequences correspond to start and stop codons)
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20
 CSGAACGAGG GCAACCTGCA CAGCCATGCC CSGGCAAGAA CTCAGGACGG TGAATGGCTC
 TCAGATGCTC CTGGTGTTGC TGGTGCTCTC GTGGCTGCCG CATGGGGGGCG CCCTGTCTCT
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 240
25
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 300
 AGTGCGGCTG GGATCCGGCG GCCACCTGCA CCTGCGTATC TCTCGGGCCG CCCTTCCCGA
 360
 GGGGCTCCCC GAGGCCTCCC GCCTTCACCG GGCTCTGTTC CGGCTGTCCC CGACGGCGTC
 420
 AAGGTOSTGG GACGTGACAC GACCGCTGCG GCGTCAGCTC AGCCTTGCAA GACCCCAAGC
 480
 GCCCGCGCTG CACCTGCGAC TGTCGCCGCC GCCGTCGCAG TCGGACCAAC TGCTGGCAGA
 540
30
 ATCTTOGTCC GCACGGCCCC AGCTGGAGTT GCACTTGCGG CCGCAAGCCG CCAGGGGGGCG
 600
 CCGCAGAGCG CGTGCGCGCA ACGGGGACGA CTGTCCGCTC GGGCCCGGGC GTTGCTGCCG
 TOTGCACAG GTCCGCGCCT CGCTGGAAGA CCTGGGCTGG GCCGATTGGG TGCTGTCGCC ACGGGAGGTG CAAGTGACCA TGTGCATCGG CGCGTGCCCG AGCCAGTTCC GGGCGGCAAA
 720
 780
 CATGCACGOG CAGATCAAGA CGAGCCTGCA CCGCCTGAAG CCCGACACGG AGCCAGCGCC
 R40
35
 CTGCTGCGTG CCCGCCAGCT ACAATCCCAT GGTGCTCATT CAAAAGACCG ACACCGGGGT
 900
 GTCGCTCCAG ACCTATGATG ACTTGTTAGC CAAAGACTGC CACTGCATAT GAGCAGTCCT
 960
 GGTCCTTCCA CTGTGCACCT GCGCGGGGGA GGCGACCTCA GTTGTCCTGC CCTGTGGAAT
 1020
 GGGCTCAAGG TTCCTGAGAC ACCCGATTCC TGCCCAAACA GCTGTATTTA TATAAGTCTG
 1000
 TTATTTATTA TTAATTTATT GGGGTGACCT TCTTGGGGAC TCGGGGGCTG GTCTGATGGA
 1140
40
 ACTGTGTATT TATTTAAAAC TCTGGTGATA AAAATAAAGC TGTCTGAACT GTTAAAAAAA

 Seg ID NO: 191 Protein sequence:
 Protein Accession #: NP_004855
45
 31
 41
 51
 MPGOELETVN GSOMLLVLLV LSWLPHGGAL SLABASRASF PGPSELHSED SEFRELEKRY
 FOLLTRIBAN OSWEDSNITDL VPAPAVRILI PEVRLGSGGH LHLRISRAAL PEGLPEASRL
 120
 HRALFRLSPT ASRSWDVTRP LRRQLSLARP QAPALHLRLS PPPSQSDQLL AESSSARPQL
ELHLRPQAAR GRRRARANG DDCPLGPGRC CRLHTVRASL EDLGWADWVL SPREVQVTMC
50
 180
 240
 IGACPSOFRA ANMHAQIKTS LHRLKPDTEP APCCVPASYN PMVLIQKTDT GVSLQTYDDL
 300
 LAKDCHCI
55
 Seg ID NO: 192 DNA sequence
 Nucleic Acid Accession #: XM 061731.1
 Coding sequence: 1-567 (underlined sequences correspond to start and stop codons)
 31
 41
 51
60
 ATGAGAAAAG GAAATGAGGG AGAGAACACA GAAGAGGGCA GGCTTGCTCA GCTTGCTCAA
 AGAAAGTTTC TCAAAGAAGA TGGCATTACA TTGCACATCT CTCTGTGTCT CTCTATTGCT
 120
 GTAAAAGAAC CTTTCTCTCT GATTGGACTT GACACACAGA AGGATCTCAG TAAAGATTTG
 180
 CTGTTGTTGA TGTCCACAGA CACTGGCAAG GACAGGTTTA CCAACATACT GCTGTCACAC
 240
65
 TCCCCTCCAA TGTGCACCAA ATCACGTAAA AATGGGGATA ATGACTCCCC TGCCTTCACA
 300
 TGGGGTGGCA AAGACACCAG GAGCAATACT GATCTTCCTA TCAGAGACCC TGGGGGCAAG
 360
 AGTOTITORO TORCORARCA TICCORCARG COTGTOCOTG AGCATORGIG IGACCAGAGA
 420
 CAGGITCTICC AGCCACTITC AGAGCCAGGI GIAGAAGCAG AGAIGGAAGI GIICGCIGAI
 480
 GCTGGATGGT GGATTTATCA GAGCTGTCAG GTTCCTTCCT CAACCCTTGC AAGAAAGAAG
 540
70
 ATGGTTTATT CTAAAGAAAC TGAGTGA
 Seq ID NO: 193 Protein sequence:
 protein Accession #: XP 061731.1
75
 51
 31
```

MRKGNEGENT EEGRLAQLAQ RKFLKEDGIT LHISLCLSIA VKEPFSLIGL DTQKDLSKDL LLLMSTDTGK DRFTMILLSH SPPMCTKSRK NGDNDSPAFT WGGKDTRSNT DLPIRDPGGK 120 SLSLTKHSHK PVPEHQCDQR EVFQPLSEPG VEABMEVFAD AGWWIYQSCQ VPSSTLARKK 180 MVYSKETE

Seg ID NO: 194 <u>DNA sequence</u>
Nucleic Acid Accession #: NN\_005415.2
Coding sequence: 371-2410 (underlined sequences correspond to start and stop codons)

|     |             |                          |             | -          | -           |            |              | - |
|-----|-------------|--------------------------|-------------|------------|-------------|------------|--------------|---|
| 10  | 1           | 11                       | 21          | 31         | 41          | 51         |              |   |
|     | 1           | 1                        | 1           | 1          | 1           | 1          |              |   |
|     |             | CGGTGCCGCC               |             |            |             |            | 60           |   |
|     |             |                          |             |            |             | CTTGCGTCCT | 120          |   |
| 1.5 |             |                          |             |            |             | CAAAGAAACC | 180          |   |
| 15  |             |                          |             |            |             | GTTTCTGTGC | 240          |   |
|     |             | AGTATTTAAT               |             |            |             |            | 300          |   |
|     |             |                          |             |            |             | AACAACCACT | 360          |   |
|     |             | <u>ATG</u> GCAACGC       |             |            |             |            | 420          |   |
| 20  |             |                          |             |            |             | TCTTGGCATT | 480          |   |
| 20  |             | GCCAATGATG               |             |            |             |            | 540          |   |
|     |             |                          |             |            |             | CTGTCTTACT | 600          |   |
|     |             | GTGAGCGAAA               |             |            |             |            | 660          |   |
|     |             |                          |             |            |             | CTGTGTGGCA | 720          |   |
| 25  |             | TCGTTTTTGA               |             |            |             |            | 780          |   |
| 23  |             |                          |             |            |             | AACTGATAAA |              |   |
|     |             |                          |             |            |             | GAATTTTATT | 900          |   |
|     |             |                          |             |            |             | GTTTGCGAGC | 960          |   |
|     |             |                          |             |            |             | TGTATACTGG |              |   |
| 30  |             |                          |             |            |             | TCTCGGTGGG |              |   |
| 30  |             |                          |             |            |             | TGAAGAGAAA | 1140         |   |
|     |             |                          |             |            |             | AAAAGAATAG | 1200         |   |
|     |             | GACCATGAAG<br>GTAGGGCCTG |             |            |             |            | 1260<br>1320 |   |
|     |             | CTTGGAGATT               |             |            |             |            | 1320         |   |
| 35  |             |                          |             |            |             | TGCCTAATGG | 1440         |   |
| 33  |             |                          |             |            |             | GCCACTCCCA | 1500         |   |
|     |             |                          |             |            |             | AATTACATCT |              |   |
|     |             |                          |             |            |             | GCAATAATAG |              |   |
|     |             |                          |             |            |             | GTGCCAAAGA |              |   |
| 40  |             |                          |             |            |             | ACTCCAAGAA |              |   |
| 70  |             |                          |             |            |             | TTCACTCAGC |              |   |
|     |             |                          |             |            |             | AAGGAAGTAA |              |   |
|     |             |                          |             |            |             | TCTTCCAGTT |              |   |
|     |             |                          |             |            |             | ACGTAAGCAA | 1980         |   |
| 45  |             |                          |             |            |             | TTTCTTCAAA |              |   |
|     |             |                          |             |            |             | TTGGTCTGTG |              |   |
|     |             |                          |             |            |             | TCACACCCTC |              |   |
|     |             |                          |             |            |             | CAAATATTGG | 2220         |   |
|     |             |                          |             |            |             | GCTGGCTCCG | 2280         |   |
| 50  |             | GCTGTTGACT               |             |            |             |            | 2340         |   |
|     |             | TCTGGAGTTA               |             |            |             |            | 2400         |   |
|     | CAGAATGTGA  | AGCTGTTTGA               | GATTAAAATT  | TGTGTCAATG | TTTGGGACCA  | TCTTAGGTAT | 2460         |   |
|     |             | CTGAAGAATG               |             |            |             |            | 2520         |   |
|     | TGGGAGCAGA  | GGAGGGAAGT               | GTTACTTGTG  | CTATAACTGC | TTTTGTGCTA  | AATATGAATT | 2580         |   |
| 55  | GTCTCAAAAT  | TAGCTGTGTA               | AAATAGCCCG  | GGTTCCACTG | GCTCCTGCTG  | AGGTCCCCTT | 2640         |   |
|     | TCCTTCTGGG  | CTGTGAATTC               | CTGTACATAT  | TTCTCTACTT | TTTGTATCAG  | GCTTCAATTC | 2700         |   |
|     | CATTATGTTT  | TAATGTTGTC               | TCTGAAGATG  | ACTTGTGATT | TTTTTTTTTTT | TTTTTTAAAC | 2760         |   |
|     |             | CGTTTGACAG               |             |            |             |            | 2820         |   |
|     | ACATGCACAG  | GGATTTAACA               | ACAAAAATAT  | AACTACAACT | TCCCTTGTAG  | TCTCTTATAT | 2880         |   |
| 60  |             | CTTGGTACTC               |             |            |             |            | 2940         |   |
|     |             | TAGAGGGATG               |             |            |             |            | 3000         |   |
|     |             |                          |             |            |             | AAGCCTGTTG | 3060         |   |
|     |             |                          |             |            |             | GAAGTGGAAT |              |   |
|     |             |                          |             |            | CATTTGTCTA  | CCTCTTAACT | 3180         |   |
| 65  | GAATAAAAAA  | GCCTACAGTT               | TTTAGAAAAA  | ACCCGAATTC |             |            |              |   |
|     |             |                          |             |            |             |            |              |   |
|     |             | 195 Protein              |             |            |             |            |              |   |
|     | Protein Acc | ession #: 1              | IP 005406.2 |            |             |            |              |   |

Protein Accession #: NP\_005406.2

70 11 41 51 MATLITSTTA ATRASGPLVD YLWMLILGFI IAFVLAFSVG ANDVANSFGT AVGSGVVTLK QACILASIFE TVGSVLLGAK VSETIRKGLI DVEMYNSTQG LLMAGSVSAM FGSAVWQLVA 60 120 SPLKLPISGT HCIVGATIGF SLVAKGORGV KWSELIKIVM SWFVSPLLSG IMSGILFFLV RAFILHKADP VPNGLRALPV FYACTVGINL FSIMYTGAPL LGFDKLPLWG TILISVGCAV 240 PCALIVWFFV CPRMKRKIER BIKCSPSESP LMEKKNSLKE DHEETKLSVG DIENKHPVSE 300

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VGPATVPLOA VVEERTVSFK LGDLEEAPER ERLPSVDLKE ETSIDSTVNG AVOLPNGNLV
 QFSQAVSNOI NSSGHSQYHT VHKDSGLYKE LLHKLHLAKV GDCMGDSGDK PLRRNNSYTS
 420
 YTMAICGMPL DSFRAKEGEQ KGEEMEKLTW PNADSKKRIR MDSYTSYCNA VSDLHSASEI
 480
 DMSVKAAMGL GDRKGSNGSL EEWYDODKPE VSLLFOFLOI LTACFGSFAH GGNDVSNAIG
 540
 PLVALYLVYD TGDVSSKVAT PIWLLLYGGV GICVGLWVWG RRVIQTMGKD LTPITPSSGF
 600
 SIELASALTV VIASNIGLPI STTHCKVGSV VSVGWLRSKK AVDWRLFRNI FMAWFVTVPI
 660
 SGVISAAIMA IFRYVILRM
 Seq ID NO: 196 DNA sequence
10
 Nucleic Acid Accession #: NM_000020.1
 Coding sequence: 283-1794 (underlined sequences correspond to start and stop codons)
 11
 21
 31
 41
15
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 AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC
 120
 GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT
 180
 CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA
 240
 AGGCTAGGGC CCCGCCACCC GCAGAGGGGG CCCAGAGGGA CCATGACCTT GGGCTCCCCC
 200
20
 AGGAAAGGCC TTCTGATGCT GCTGATGGCC TTGGTGACCC AGGGAGACCC TGTGAAGCCG
 360
 TCTCGGGGCC CGCTGGTGAC CTGCACGTGT GAGAGCCCAC ATTGCAAGGG GCCTACCTGC
 420
 CGGGGGGCCT GGTGCACAGT AGTGCTGGTG CGGGAGGAGG GGAGGCACCC CCAGGAACAT
 480
 COGGGCTGCG GGAACTTGCA CAGGGAGCTC TGCAGGGGGC GCCCCACCGA GTTCGTCAAC
 540
 CACTACTGCT GOGACAGCCA CCTCTGCAAC CACAACGTGT CCCTGGTGCT GGAGGCCACC
 600
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 CTGGCCTTGC TGGCCCTGGT GGCCCTGGGT GTCCTGGGCC TGTGGCATGT CCGACGGAGG
 720
 CAGGAGAAGC AGCGTGGCCT GCACAGCGAG CTGGGAGAGT CCAGTCTCAT CCTGAAAGCA
 780
 TCTGAGCAGG GCGACACGAT GTTGGGGGAC CTCCTGGACA GTGACTGCAC CACAGGGAGT
 840
 GGCTCAGGGC TCCCCTTCCT GGTGCAGAGG ACAGTGGCAC GGCAGGTTGC CTTGGTGGAG
 900
30
 TGTGTGGGAA AAGGCCGCTA TGGCGAAGTG TGGCGGGGCT TGTGGCACGG TGAGAGTGTG
 960
 GCGGTCAAGA TCTTCTCCTC GAGGGATGAA CAGTCCTGGT TCCGGGAGAC TGAGATCTAT 1020
AACACAGTAT TGCTCAGACA CGACAACATC CTAGGCTTCA TCGCCTCAGA CATGACCTCC 1080
 CGCAACTCGA GCACGCAGCT GTGGCTCATC ACGCACTACC ACGAGCACGG CTCCCTCTAC 1140
 GACTITCTGC AGAGACAGAC GCTGGAGCCC CATCTGGCTC TGAGGCTAGC TGTGTCCGCG 1200
 GCATGCGGCC TGGCGCACCT GCACGTGGAG ATCTTCGGTA CACAGGGCAA ACCAGCCATT 1260
 ACGGACTGCT TIGAGTCCTA CAAGTGGACT GACATCTGGG CCTTTGGCCT GGTGCTGTGG 1500
40
 GAGATTGCCC GCCGGACCAT CGTGAATGGC ATCGTGGAGG ACTATAGACC ACCCTTCTAT 1560
 GATGTGGTGC CCAATGACCC CAGCTTTGAG GACATGAAGA AGGTGGTGTG TGTGGATCAG 1620
 CAGACCCCCA CCATCCCTAA CCGGCTGGCT GCAGACCCGG TCCTCTCAGG CCTAGCTCAG 1680
 ATGRIGGGG AGIGCTGGTA CCCAAACCC TCTGCCCGAC TCACCGCGCT GCGGATCAAG 1740
 AAGACACTAC AAAAAATTAG CAACAGTCCA GAGAAGCCTA AAGTGATTCA ATAGCCCAGG 1800
 AGCACCTGAT TCCTTTCTGC CTGCAGGGGG CTGGGGGGGT GGGGGGCAGT GGATGGTGCC 1860
 CTATCTGGGT AGAGGTAGTG TGAGTGTGGT GTGTGCTGGG GATGGGCAGC TGCGCCTGCC 1920
 TGCTCGGCCC CCAGCCCACC CAGCCAAAAA TACAGCTGGG CTGAAACCTG
 Seq ID NO: 197 Protein sequence:
 Protein Accession #: NP 000011.1
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50

|     | 1          | 11         | 21                | 31         | 41         | 51         |     |
|-----|------------|------------|-------------------|------------|------------|------------|-----|
|     |            | 1          | 1                 |            | 1          | 1          |     |
|     | MTLGSPRKGL | LMLLMALVTQ | GDPVKPSRGP        | LVTCTCESPH | CKGPTCRGAW | CTVVLVREEG | 60  |
| 55. | RHPQEHRGCG | NLHRELCRGR | PTEFVNHYCC        | DSHLCNHNVS | LVLEATQPPS | EQPGTDGQLA | 120 |
|     | LILGPVLALL | ALVALGVLGL | WHVRRRQEKQ        | RGLHSELGES | SLILKASEQG | DTMLGDLLDS | 180 |
|     |            | PFLVQRTVAR |                   |            |            |            | 240 |
|     | RETEIYNTVL | LRHDNILGFI | ASDMTSRNSS        | TOLWLITHYH | EHGSLYDFLQ | ROTLEPHLAL | 300 |
|     | RLAVSAACGL | AHLHVEIFGT | <b>OGKPAIAHRD</b> | FKSRNVLVKS | NLQCCIADLG | LAVMHSQGSD | 360 |
| 60  | YLDIGNNPRV | GTKRYMAPEV | LDEQIRTDCF        | ESYKWTDIWA | FGLVLWEIAR | RTIVNGIVED | 420 |
|     | YRPPFYDVVP | NDPSFEDMKK | VVCVDQQTPT        | IPNRLAADPV | LSGLAQMMRE | CWYPNPSARL | 480 |
|     | TALRIKKTLQ | KISNSPEKPK | VIQ               |            |            |            |     |

Seq ID NO: 198 DNA sequence

65 Nucleic Acid Accession #: NM 003199.1 Coding sequence: 200-2203 (underlined sequences correspond to start and stop codons)

|    |            | 11         | 21         | 31         | 41         | 21         |     |
|----|------------|------------|------------|------------|------------|------------|-----|
|    | 1          | 1          | 1          | 1          | 1          | 1          |     |
| 70 |            | TTGGCTGTGT |            |            |            |            | 60  |
|    |            | GGCGCGGGAG |            |            |            |            | 120 |
|    | GACATGAACG | CCGCCTCGGC | GCCGGCGGTG | CACGGAGAGC | CCCTTCTCGC | GCGCGGGCGG | 180 |
|    |            | TTTGCTAAAA |            |            |            |            | 240 |
|    | AGAGCTGAGT | GATTTACTGG | ATTTCAGTGC | GATGTTTTCA | CCTCCTGTGA | GCAGTGGGAA | 300 |
| 75 | AAATGGACCA | ACTTCTTTGG | CAAGTGGACA | TTTTACTGGC | TCAAATGTAG | AAGACAGAAG | 360 |
|    | TAGCTCAGGG | TCCTGGGGGA | ATGGAGGACA | TCCAAGCCCG | TCCAGGAACT | ATGGAGATGG | 420 |

```
GACTCCCTAT GACCACATGA CCAGCAGGGA CCTTGGGTCA CATGACAATC TCTCTCCACC
 TITTGTCAAT TCCAGAATAC AAAGTAAAAC AGAAAGGGGC TCATACTCAT CTTATGGGAG
 AGAATCAAAC TTACAGGGTT GCCACCAGCA GAGTCTCCTT GGAGGTGACA TGGATATGGG
 600
 CARCCCAGGA ACCCTTTCGC CCACCAAACC TGGTTCCCAG TACTATCAGT ATTCTAGCAA
 660
 TARTCCCCGA AGGAGGCCTC TTCACAGTAG TGCCATGGAG GTACAGACAA AGAAAGTTCG
 AAAAGTTCCT CCAGGTTTGC CATCTTCAGT CTATGCTCCA TCAGCAAGCA CTGCCGACTA
 780
 CAATAGGGAC TCGCCAGGCT ATCCTTCCTC CAAACCAGCA ACCAGCACTT TCCCTAGCTC
 840
 CTTCTTCATG CARGATGGCC ATCACAGCAG TGACCCTTGG AGCTCCTCCA GTGGGATGAA
 900
 TCAGCCTGGC TATGCAGGAA TGTTGGGCAA CTCTTCTCAT ATTCCACAGT CCAGCAGCTA
 960
10
 CTGTAGCCTG CATCCACATG AACGTTTGAG CTATCCATCA CACTCCTCAG CAGACATCAA 1020
 TTCCAGTCTT CCTCCGATGT CCACTTTCCA TCGTAGTGGT ACAAACCATT ACAGCACCTC
 1080
 TTCCTGTACG CCTCCTGCCA ACGGGACAGA CAGTATAATG GCAAATAGAG GAAGCGGGGC
 1140
 AGCCGGCAGC TCCCAGACTG GAGATGCTCT GGGGAAAGCA CTTGCTTCGA TCTATTCTCC
 1200
 AGATCACACT AACAACAGCT TTTCATCAAA CCCTTCAACT CCTGTTGGCT CTCCTCCATC
15
 TCTCTCAGCA GGCACAGCTG TTTGGTCTAG AAATGGAGGA CAGGCCTCAT CGTCTCCTAA 1320
 TTATGAAGGA CCCTTACACT CTTTGCAAAG CCGAATTGAA GATCGTTTAG AAAGACTGGA 1380
 TGATGCTATT CATGTTCTCC GGAACCATGC AGTGGGCCCA TCCACAGCTA TGCCTGGTGG 1440
 TCATGGGGAC ATGCATGGAA TCATTGGACC TTCTCATAAT GGAGCCATGG GTGGTCTGGG 1500
 CTCAGGGTAT GGAACCGGCC TTCTTTCAGC CAACAGACAT TCACTCATGG TGGGGACCCA 1560
TCGTGAAGAT GGCGTGGCCC TGAGAGGCAG CCATTCTCTT CTGCCAAACC AGGTTCCGGT 1620
20
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 CAGAGGCATG CCACCAGGAC TACAGGGGCA GAGTGTCTCC TCTGGCAGCT CTGAGATCAA 1740
 ATCCGATGAC GAGGGTGATG AGAACCTGCA AGACACGAAA TCTTCGGAGG ACAAGAAATT 1800
 AGATGACGAC AAGAAGGATA TCANATCANT TACTAGCAAT AATGACGATG AGGACCTGAC 1860
ACCAGAGCAG AAGGCAGAGC GTGAGAAGGA GCGGAGGATG GCCAACAATG CCCGAGAGCG 1220
 TCTGCGGGTC CGTGACATCA ACGAGGCTTT CAAAGAGCTC GGCCGCATGG TGCAGCTCCA 1980
 CCTCAAGAGT GACAAGCCCC AGACCAAGCT CCTGATCCTC CACCAGGCGG TGGCCGTCAT 2040
 CCTCAGTCTG GAGCAGCAAG TCCGAGAAAG GAATCTGAAT CCGAAAGCTG CGTGTCTGAA 2100
 AAGAAGGAG GAAGAGAAGG TGTCCTCGGA GCCTCCCCCT CTCTCCTTGG CCGGCCCACA 2160
30
 CCCTGGAATG GGAGACGCAT CGAATCACAT GGGACAGATG TAAAAGGGTC CAAGTTGCCA 2220
 CATTGCTTCA TTANAACAAG AGACCACTTC CTTAACAGCT GTATTATCTT AAACCCACAT 2280
 AAACACTTCT CCTTAACCCC CATTTTTGTA ATATAAGACA AGTCTGAGTA GTTATGAATC 2340
 GCAGACGCAA GAGGTTTCAG CATTCCCAAT TATCAAAAAA CAGAAAAACA AAAAAAAGAA 2400
 AGAAAAAAGT GCAACTTGAG GGACGACTTT CTTTAACATA TCATTCAGAA TGTGCAAAGC 2460
35
 AGTATGTACA GGCTGAGACA CAGCCCAGAG ACTGAACGGC
 Seq ID NO: 199 Protein sequence
 Protein Accession #: NP 003190.1
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| 40 | 1          | 11         | 21         | 31         | 41         | 51         |     |
|----|------------|------------|------------|------------|------------|------------|-----|
|    | 1          | 1          | 1          | 1          | 1          | 1          |     |
|    | MHHQQRMAAL | GTDKELSDLL | DFSAMFSPPV | SSGKNGPTSL | ASCHFTGSNV | EDRSSSGSWG | 60  |
|    |            | YGDGTPYDHM |            |            |            |            | 120 |
|    | CHQQSLLGGD | MDMGNPGTLS | PTKPGSQYYQ | YSSNNPRRRP | LHSSAMEVQT | KKVRKVPPGL | 180 |
| 45 | PSSVYAPSAS | TADYNRDSPG | YPSSKPATST | FPSSFFMQDG | HHSSDPWSSS | SGMNQPGYAG | 240 |
|    | MLGNSSHIPQ | SSSYCSLHPH | ERLSYPSHSS | ADINSSLPPM | STFHRSGTNH | YSTSSCTPPA | 300 |
|    | NGTDSIMANR | GSGAAGSSQT | GDALGKALAS | IYSPDHTNNS | FSSNPSTPVG | SPPSLSAGTA | 360 |
|    | VWSRNGGQAS | SSPNYEGPLH | SLOSRIEDRL | ERLDDAIHVL | RNHAVGPSTA | MPGGHGDMHG | 420 |
|    | IIGPSHNGAM | GGLGSGYGTG | LLSANRHSLM | VGTHREDGVA | LRGSHSLLPN | CALABOTDAC | 480 |
| 50 |            | QDPYRGMPPG |            |            |            |            | 540 |
|    | IKSITSNNDD | EDLTPEQKAE | REKERRMANN | ARERLRVRDI | NEAFKELGRM | VQLHLKSDKP | 600 |
|    | QTKLLTLHQA | VAVILSLEQQ | VRERNLNPKA | ACLKRREEEK | VSSEPPPLSL | AGPHPGMGDA | 660 |
|    | SNHMGOM    |            |            |            |            |            |     |

55 Seq ID NO: 200 <u>DNA sequence</u> Nucleic Acid Accession #: BC005987 (1-1286), BE888744 (1287-1756)

Coding sequence: 124-525 (underlined sequences correspond to start and stop codons)

|    | 1          | 11         | 21         | 31         | 41         | 51         |     |
|----|------------|------------|------------|------------|------------|------------|-----|
| 60 | 1          | 1          | 1          | 1          | 1          | 1          |     |
|    |            | GAAGATTTCT |            |            |            |            | 60  |
|    | GAGAATTGCA | CTGCAACCAT | GAGTGAGAAC | AATAAGAATT | CCTTGGAGAG | CAGCCTACGG | 120 |
|    | CAACTAAAAT | GCCATTTCAC | CTGGAACTTG | ATGGAGGGAG | AAAACTCCTT | GGATGATTTT | 180 |
|    | GAAGACAAAG | TATTTTACCG | GACTGAGTTT | CAGAATCGTG | AATTCAAAGC | CACAATGTGC | 240 |
| 65 | AACCTACTGG | CCTATCTAAA | GCACCTCAAA | GGGCAAAACG | AGGCAGCCCT | GGAATGCTTA | 300 |
|    | CGTAAAGCTG | AAGAGTTAAT | CCAGCAAGAG | CATGCTGACC | AGGCAGAAAT | CAGAAGTCTG | 360 |
|    | GTCACCTGGG | GAAACTATGC | CTGGGTCTAC | TATCACATGG | GCCGACTCTC | AGACGTTCAG | 420 |
|    | ATTTATGTAG | ACAAGGTGAA | ACATGTCTGT | GAGAAGTTTT | CCAGTCCCTA | TAGAATTGAG | 480 |
|    |            | TTGACTGTGA |            |            |            |            | 540 |
| 70 | GAAAGAGCGA | AGGTGTGCTT | TGAGAAGGCT | CTGGAAAAGA | AGCCAAAGAA | CCCAGAATTC | 600 |
|    |            | TGGCAATAGC |            |            |            |            | 660 |
|    |            | TGAGGCAAGC |            |            |            |            | 720 |
|    |            | AGCTTCATAA |            |            |            |            | 780 |
|    | TTAGTTGAAG | AAGCCTTGGA | GAAAGCCCCA | GGTGTAACAG | ATGTACTTCG | CAGTGCAGCC | 840 |
| 75 |            | GAAGAAAAGA |            |            |            |            | 900 |
|    | GAATACATAC | CAAACAATGC | CTACCTGCAT | TGCCAAATTG | GGTGCTGCTA | TAGGGCAAAA | 960 |

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GTCTTCCAAG TAATGAATCT AAGAGAGAAT GGAATGTATG GGAAAAGAAA GTTACTGGAA 1020
 CTANTAGGAC ACGUIGTGGC TOATCTGAAG AAAGCTGATG AGGCCAATGA TAATCTCTTC
 CGTGTCTGTT CCATTCTTGC CAGCCTCCAT GCTCTAGCAG ATCAGTATGA AGAAGCAGAG
 1140
 TATTACTICC AAAAGGAATI CAGTAAAGAG CITACTCCIG TAGCGAAACA ACTGCTCCAT
 1200
 CTGCGGTATG GCAACTTTCA GCTGTACCAA ATGAAGTGTG AAGACAAGGC CATCCACCAC
 1260
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 Seq ID NO: 201 Protein sequence:
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 KHYCEKFSSP YRIESPELDC BEGWTRLKCG GNONERAKYC FEKALEKKPK NPEFTSGLAI
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 LENPYTIKKH YRLYVIYKUP OVRVIDFOKV KIKERORARK MFKGKRGAOL AKDIARRSKT
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 Protein Accession #: NP 060113.1
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 FKPCMRVEVV DKRHLCRTRV AVVESVIGGR LRLVYEESED RTDDFWCHMH SPLIHHIGWS
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 TIRKVLADGF LMIGIDGSEA ADGSDWFCYH ATSPSIFPVG FCEINMIELT PPRGYTKLPF
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 TTCGGCAATG CGAAGACCGT GTACAACAAC AACTCTAGTC GCTTTGGGAA GTTTGTTCAG
 900
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|    | CTGAACATCT    | GTCAGAAAGG  | AAATATTCAG    | GGCGGGAGAA    | TTGTAGATTA               | TITATTAGAA                             | 960   |
|----|---------------|-------------|---------------|---------------|--------------------------|----------------------------------------|-------|
|    | PARAMOURAG    | TAGTAAGGCA  | AAATCCCGGG    | GAAAGGAATT    | ATCACATATT               | TTATGCACTG                             | 1020  |
|    | CINCOCO COCO  | macana ana  | ACABACACAA    | Charmenam     | TO THE COURT             | AGAAAACTAC                             | 1080  |
|    | CIGGCAGGGC    | 1 GGMACATGA | AGAMAGAAA     | CAMITITATI    | TATCHTOCCO               | GGAATCCTTT                             | 1140  |
| 5  | CACTACTTGA    | ATCAGTCIGG  | ATGTGTAGAA    | GACAAGACAA    | 1CMG1GMCCM               | MOGGGGTT T                             | TIGO  |
| J  | AGGGAAGTTA    | TTACGGCAAT  | GGACGIGATG    | CAGTICAGCA    | AGGAGGAMGT               | TCGGGAAGTG                             | 1200  |
|    | TCGAGGCTGC    | TTGCTGGTAT  | ACTGCATCTT    | GGGAACATAG    | AATTTATCAC               | TGCTGGTGGG<br>GCTGGACCCA<br>AGAGATCCTC | 1200  |
|    | GCACAGGTTT    | CCTTCAAAAC  | AGCTTTGGGC    | AGATCTGCGG    | AGTTACTTGG               | GCTGGACCCA                             | 1320  |
|    | ACACAGCTCA    | CAGATGCTTT  | GACCCAGAGA    | TCAATGTTCC    | TCAGGGGAGA               | AGAGATCCTC                             | 1380  |
|    | ACCCCTCTCA    | ATGTTCAACA  | GGCAGTAGAC    | AGCAGGGACT    | CCCTGGCCAT               | GGCTCTGTAT                             | 1440  |
| 10 | GCGTGCTGCT    | TTGAGTGGGT  | AATCAAGAAG    | ATCAACAGCA    | GGATCAAAGG               | CAATGAGGAC                             | 1500  |
|    | TTCAAGTCTA    | TTGGCATCCT  | CGACATCTTT    | CCATTTGAAA    | ACTITICACCI              | TAATCACTTT                             | 1.560 |
|    |               |             |               |               |                          | CAAGCATATT                             | 1620  |
|    | Trimmomman o  | ATALANACIA  | A MARIA COCCC | CANCELLORG    | TOTACCITCAN              | TATTGACTGG                             | 1680  |
|    |               |             |               |               |                          | AGCCCTTATC                             | 1740  |
| 15 |               |             |               |               |                          |                                        |       |
| 13 | AATGAAGAAA    | GCCATTTTCC  | TCAAGCCACA    | GACAGCACCT    | TATTGGAGAA               | GCTACACAGT                             | 1800  |
|    | CAGCATGCGA    | ATAACCACTT  | TTATGTGAAG    | CCCAGAGTTG    | CAGTTAACAA               | TTTTGGAGTG                             | 1860  |
|    | AAGCACTATG    | CTGGAGAGGT  | GCAATATGAT    | GTCCGAGGTA    | TCTTGGAGAA               | GAACAGAGAT                             | 1920  |
|    | ACATTTCGAG    | ATGACCTTCT  | CAATTTGCTA    | AGAGAAAGCC    | GATTTGACTT               | TATCTACGAT                             | 1980  |
|    | CTTTTTGAAC    | ATGTTTCAAG  | CCGCAACAAC    | CAGGATACCT    | TGAAATGTGG               | AAGCAAACAT                             | 2040  |
| 20 | CGGCGGCCTA    | CAGTCAGCTC  | ACAGTTCAAG    | GACTCACTGC    | ATTCCTTAAT               | GGCAACGCTA                             | 2100  |
|    | AGCTCCTCTA    | ATCCTTTCTT  | TOTTCGCTGT    | ATCAAGCCAA    | ACATGCAGAA               | GATGCCAGAC                             | 2160  |
|    | CAGTTTGACC    | AGGCGGTTGT  | GCTGAACCAG    | CTGCGGTACT    | CAGGGATGCT               | GGAGACTGTG                             | 2220  |
|    | ACRAMOCOCCA   | AACCTCCCTA  | TCCCCCTCCCA   | AGACCCCTTTC   | ACCACTTTTA               | CAAAAGGTAT                             | 2280  |
|    | MOMATCCOCK    | MAGCIGGGIA  | GGGGTCCGA     | ADMCCCTTTC    | abacattana<br>abacattana | CACGAGCCTG                             | 2340  |
| 25 | AAAGTGCTGA    | TGAGGAATCT  | GGCTCTGCCT    | GAGGACGICC    | GMGGGMMGTG               | CACGAGCCIG                             |       |
| 25 | CTGCAGCTCT    | ATGATGCCTC  | CAACAGCGAG    | TUGCAGCTUG    | GGAAGACCAA               | GGTCTTTCTT                             | 2400  |
|    | CGAGAATCCT    | TGGAACAGAA  | ACTGGAGAAG    | CGGAGGGAAG    | AGGAAGTGAG               | CCACGCGGCC                             | 2460  |
|    | ATGGTGATTC    | GGGCCCATGT  | CTTGGGCTTC    | TTAGCACGAA    | AACAATACAG               | AAAGGTCCTT                             | 2520  |
|    |               |             |               |               |                          | GAGATTTTTG                             | 2580  |
|    | CACCTGAAAA    | AGGCAGCCAT  | AGTTTTCCAG    | AAGCAACTCA    | GAGGTCAGAT               | TGCTCGGAGA                             | 2640  |
| 30 | GTTTACAGAC    | AATTGCTGGC  | AGAGAAAAGG    | GAGCAAGAAG    | AAAAGAAGAA               | ACAGGAAGAG                             | 2700  |
|    | CDACADAGA     | AGANACGGGA  | GGAAGAAGAA    | AGAGAAAGAG    | AGAGAGAGCG               | AAGAGAAGCC                             | 2760  |
|    | CACCECCCCC    | CCCACCACCA  | DONNONNOG     | AGGNAGCAGC    | AAGAACTCGA               | AGCCTTGCAG                             | 2820  |
|    | DAGCICCGCG    | 2002200000  | a amaa aaaam  | AND AMOUND    | PAGNACICON               | AAATAAGCAG                             | 2880  |
|    |               |             |               |               |                          |                                        | 2940  |
| 35 | GTGGAAGAGA    | TCCTCCGTCT  | GGAGIUMGAA    | ATCGAGGACC    | TGCAGCGCAT               | GAAGGAGCAG                             |       |
| 33 |               |             |               |               |                          | GGACCAGGAG                             | 3000  |
|    | CTCCGCAGGC    | TGGAGGAGGA  | AGCGTGCAGG    | GCGGCCCAGG    | AGTTCCTCGA               | GTCCCTCAAT                             | 3060  |
|    | TTCGACGAGA    | TCGACGAGTG  | TGTCCGGAAT    | ATCGAGCGGT    | CCCTGTCGGT               | GGGAAGCGAA                             | 3120  |
|    | TTTTCCAGCG    | AGCTGGCTGA  | GAGCGCATGC    | GAGGAGAAGC    | CCAACTTCAA               | CTTCAGCCAG                             | 3180  |
|    | CCCTACCCAG    | AGGAGGAGGT  | CGATGAGGGC    | TTCGAAGCCG    | ACGACGACGC               | CTTCAAGGAC                             | 3240  |
| 40 | TOCCCCAACC    | CCAGCGAGCA  | CGGCCACTCA    | GACCAGCGAA    | CAAGTGGCAT               | CCGGACCAGC                             | 3300  |
|    | GATGACTCTT    | CAGAGGAGGA  | CCCATACATG    | AACGACACGG    | TOGTGCCCAC               | CAGCCCCAGT                             | 3360  |
|    | CCCCACACCA    | COCTOCTOCT  | CCCCCCATCA    | GTGCAGGACT    | CCCCCCCCCC               | ACACAACTCC                             | 3420  |
|    |               | AGTCCACCTA  |               |               |                          |                                        | 3480  |
|    | ageer emace   | AGICCACCIA  | CIGCAIGCCC    | CHONNEGCTO    | CCAMCATOCC               | CGGCAGCAGC                             | 3540  |
| 45 | GGCGACTACG    | ACTACGACCA  | GGATGACTAT    | GAGGACGGIG    | DOWN COCOTTO             | CTCTGTGGGG                             | 3600  |
| 43 | GIGACCTICT    | CCAACTCCTA  | CGGCAGCCAG    | TGGTCCCCCG    | ACTACCGCTG               | CICIGIGGG                              |       |
|    | ACCTACAACA    | GCTCGGGTGC  | CTACCGGTTC    | AGCTCTGAGG    | GGGCGCAGTC               | CTCGTTTGAA                             | 3660  |
|    | GATAGTGAAG    | AGGACTTTGA  | TTCCAGGTTT    | GATACAGATG    | ATGAGCTTTC               | ATACCGGCGT                             | 3720  |
|    | GACTCTGTGT    | ACAGCTGTGT  | CACTCTGCCG    | TATTTCCACA    | GCTTTCTGTA               | CATGAAAGGT                             | 3780  |
|    | GGCCTGATGA    | ACTOTTGGAA  | ACCCCCCTGG    | TGCGTCCTCA    | AGGATGAAAC               | CTTCTTGTGG                             | 3840  |
| 50 | TTCCGCTCCA    | AGCAGGAGGC  | CCTCAAGCAA    | GGCTGGCTCC    | ACAAAAAAGG               | GGGGGGCTCC                             | 3900  |
|    | TOCACGCTGT    | CCAGGAGAAA  | TTGGAAGAAG    | CGCTGGTTTG    | TCCTCCGCCA               | GTCCAAGCTG                             | 3960  |
|    | MANAGERACITA  | DADAGGACAG  | CCDCCDCDAG    | CTCARGGGCA    | CCGTAGAAGT               | GCGAACGGCA                             | 4020  |
|    | ANDROGATION   | TAGATAACAC  | CACCAAGGAG    | AATGGGATGG    | ACATCATTAT               | GGCCGATAGG                             | 4080  |
|    |               | TGATTGCAGA  |               |               |                          |                                        | 4140  |
| 55 | ACTITICALC    | IGHTIGCHGM  | GICCCCAGAA    | GAIGCCAGCC    | AGIGGIICAG               | COTOCTORGI                             | 4200  |
| JJ | CAGGTCCACG    | CGTCCACGGA  | CCAGGAGATC    | CAGGAGATGC    | MIGHIGAGCA               | GGCAAACCCA                             |       |
|    |               |             |               |               |                          | CTCTGACAGC                             | 4260  |
|    |               |             |               |               |                          | CTGCAACGCC                             | 4320  |
|    |               |             |               |               |                          | AGGGGACACC                             | 4380  |
|    | AGAGTGGAGG    | GCCAGGAATT  | CATCGTGAGA    | GGATGGTTGC    | ACAAAGAGGT               | GAAGAACAGT                             | 4440  |
| 60 | CCGAAGATGT    | CTTCACTGAA  | ACTGAAGAAA    | CCCTCCTTTC    | TACTCACCCA               | CAATTCCCTG                             | 4500  |
|    | GATTACTACA    | AGAGTTCAGA  | GAAGAACGCG    | CTCANACTGG    | GGACCCTGGT               | CCTCAACAGC                             | 4560  |
|    | CACAGCACAG    | TOTTCCCCCC  | AGATGAGAAG    | DESCRIPTION   | AGACAGGCTA               | CTGGAACGTC                             | 4620  |
|    | 20000000000   | GGCGCAAGCA  | CECCES COCC   | CECENCACCO    | ACCONCUENCAN             | CCACCCACC                              | 4680  |
|    |               |             |               |               |                          | CACCCCCACC                             | 4740  |
| 65 | COGTOGTCCA    | TTCAAGATAT  | CARCOLONCI C  | madaman r con | CCCCOMICON               | CCARCACACC                             | 4800  |
| 05 | CAGCAGCTGA    | TICAMGATAT  | MAGGAGAAC     | CAMON         | TOOM TOTOGT              | GCTCCTGCCC                             |       |
|    | TACAAGCGGA    | ACCOGATOCT  | TCGATACACC    | CATCACCCCT    | TGCACTCCCC               | GUTUUTGCCC                             | 4860  |
|    | CTTCCGTATG    | GGGACATAAA  | TCTCAACTTG    | CTCAAAGACA    | AAGGCTATAC               | CACCCTTCAG                             | 4920  |
|    | GATGAGGCCA    | TCAAGATATT  | CAATTCCCTG    | CAGCAACTGG    | AGTCCATGTC               | TGACCCAATT                             | 4980  |
|    | CCAATAATCC    | AGGGCATCCT  | ACAGACAGGG    | CATGACCTGC    | GACCTCTGCG               | GGACGAGCTG                             | 5040  |
| 70 | TACTGCCAGC    | TTATCAAACA  | GACCAACAAA    | GTGCCCCACC    | CCGGCAGTGT               | GGGCAACCTG                             | 5100  |
|    | TACAGCTGGC    | AGATCCTGAC  | ATGCCTGAGC    | TGCACCTTCC    | TGCCGAGTCG               | AGGGATTCTC                             | 5160  |
|    | AAGTATCTCA    | AGTTCCATCT  | GAAAAGGATA    | CGGGAACAGT    | TTCCAGGAAC               | CGAGATGGAA                             | 5220  |
|    | AAATACGCTC    | TOTACA CTTA | CGAATCTCTT    | ANGANANCCA    | AATGCCGAGA               | GTTTGTGCCT                             | 5280  |
|    | TCCCCI NGE TO | BARTAGARCO  | TOTAL         | MCCCACCE      | TGACATCCAC               | GGTCTATTGC                             | 5340  |
| 75 | TCCCGMANTG    | ANNI MONNOC | CAMONOCARC    | AACTCCCACA    | CONCENTRATE              | GGAGGTGGTG                             | 5400  |
| 13 | CATGGCGGCG    | GCTCCTGCAA  | COCCATC       | ChChCCCCCCCC  | COMCIGUIGG               | THTTCTTTTC                             | 5460  |
|    | GAGAAGCIGA    | TCCGAGGCCT  | GGCCATGGAG    | GACAGCAGGA    | MUNICIPITEC              | IGITTGAA                               | 2460  |
|    |               |             |               |               |                          |                                        |       |

|    | AAGTTTGAAA | AGCTGGCTGC | CACATCCGAG | GTTGGGGACC | TGCCATGGAA | ATTCTACTTC  | 5580 |
|----|------------|------------|------------|------------|------------|-------------|------|
|    | AAACTTTACT | GCTTCCTGGA | CACAGACAAC | GTGCCAAAAG | ACAGTGTGGA | GTTTGCATTT  | 5640 |
|    | ATGTTTGAAC | AGGCCCACGA | AGCGGTTATC | CATGGCCACC | ATCCAGCCCC | GGAAGAAAAC  | 5700 |
| 5  | CTCCAGGTTC | TTGCTGCCCT | GCGACTCCAG | TATCTGCAGG | GGGATTATAC | TCTGCACGCT  | 5760 |
|    | GCCATCCCAC | CTCTCGAAGA | GGTTTATTCC | CTGCAGAGAC | TCAAGGCCCG | CATCAGCCAG  | 5820 |
|    |            | CCTTCACCCC |            |            |            |             | 5880 |
|    | GGGACCCTGA | GGCGGAGCTT | CCGGACAGGA | TCCGTGGTCC | GGCAGAAGGT | CGAGGAGGAG  | 5940 |
|    |            | ACATGTGGAT |            |            |            |             | 6000 |
| 10 |            | AATTTCAGGG |            |            |            |             | 6060 |
|    | ATCAAGGAGT | GGCCTGGCTA | TGGCTCGACG | CTGTTTGATG | TGGAGTGCAA | GGAAGGTGGC  | 6120 |
|    |            | AACTCTGGTT |            |            |            |             | 6180 |
|    |            | CACTGGAAGT |            |            |            |             | 6240 |
|    |            | ATAAGATCGT |            |            |            |             | 6300 |
| 15 | GTGGATGTGG | CCAAGCTCAT | GAAAGCCTAC | ATCAGCATGA | TCGTGAAGAA | GCGCTA CAGC | 6360 |
|    |            |            |            |            |            | AGCCCACCTG  | 6420 |
|    | TCTTTGCTAC | CTGAACGCAC | CACCCTCTGG | CCTAGGCTGG | CTCCAGTGTG | CCATGCCCAG  | 6480 |
|    |            | CACAGAGCTG |            |            |            |             | 6540 |
|    |            | TTTTGCCTGC |            |            |            |             | 6600 |
| 20 |            | TTCCAAAGCT |            |            |            |             | 6660 |
|    |            | CTGCCACCAA |            |            |            |             | 6720 |
|    |            | TGTGCTACTG |            |            |            |             | 6780 |
|    |            | GGGGGCATTC |            |            |            |             | 6840 |
|    |            | AAGGTGAGGG |            |            |            |             | 6900 |
| 25 |            | TGCTGCGGGC |            |            |            |             | 6960 |
|    | GTTTCATCIT | TTAAGTGTAC | GTGCTTGCCT | GTTCGTGCAT | GTGTTCATAA | ACTCAACACT  | 7020 |
|    |            | TTTCATGAGC |            |            |            |             | 7080 |
|    |            | ATTTTAATAA |            |            |            |             | 7140 |
|    |            | ACCCAAATCC |            |            |            |             | 7200 |
| 30 |            | GTTTTACATG |            |            |            |             | 7260 |
|    | ATAAGCAGCC | TACAAGATAA | CTGTATTTAT | AAACCACTCT | TCAACAGCTG | GCTCCAGTGC  | 7320 |
|    |            | ACAAGAATGA |            |            |            |             | 7380 |
|    |            | GTTACTTGGA |            |            |            |             | 7440 |
|    |            | ACTATGGGGG |            |            |            |             | 7500 |
| 35 |            |            |            |            |            | TTTATCCCAA  | 7560 |
|    | GTTTATAATG | GTGGTCTGAA | CAAGGCACCT | GTAAATAAAT | CAGCATTTAT | GACCAGAAGA  | 7620 |
|    |            |            |            |            |            | ACTTGGGCCA  | 7680 |
|    |            |            |            |            |            | AACCATGCAA  | 7740 |
| 40 | AACTGTTTGT | TGGCTCACAG | AAGTTCTGAC | AATAAAAGAT | ACTAGCT    |             |      |
| 40 |            | 207 Protei |            |            |            |             |      |
|    |            |            |            |            |            |             |      |

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### Seq ID NO: 207 <u>Protein sequence:</u> Protein Accession #: NP\_036466

| 45 | 1          | 11         | 21<br>     | 31<br>     | 41                | 51         |      |
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|    | NEEGVDDMAS | LTELHGGSIM | YNLFQRYKRN | QIYTYIGSIL | ASVNPYQPIA        | GLYEPATMEQ | 120  |
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|    |            | SCVERAILES |            |            |                   |            | 240  |
| 50 |            | VRQNPGERNY |            |            |                   |            | 300  |
|    |            | TAMDVMQFSK |            |            |                   |            | 360  |
|    | LLGLDPTQLT | DALTQRSMFL | RGEEILTPLN | VQQAVDSRDS | LAMALYACCF        | EWVIKKINSR | 420  |
|    | IKGNEDFKSI | GILDIFGFEN | FEVNHFEQFN | INYANEKLQE | YFNKHIFSLE        | QLEYSREGLV | 480  |
|    |            | ECTDFIEKKP |            |            |                   |            | 540  |
| 55 |            | GEVQYDVRGI |            |            |                   |            | 600  |
|    |            | VSSQFKDSLH |            |            |                   |            | 660  |
|    |            | AGYAVRRPPQ |            |            |                   |            | 720  |
|    | KTKVFLRESL | EQKLEKRREE | EVSHAAMVIR | AHVLGFLARK | QYRKVLYCVV        | IIQKNYRAFL | 780  |
|    | LRRRFLHLKK | AAIVFQKQLR | GQIARRVYRQ | LLAEKREQEE | KKKQEEBEKK        | KREEEERERE | 840  |
| 60 | RERREAELRA | QQEEETRKQQ | ELEALQKSQK | EAELTRELEK | <b>OKENKQVEE1</b> | PSTEKELEDP | 900  |
|    | QRMKEQQELS | LTEASLQKLQ | ERRDQELRRL | EEEACRAAQE | PLESLNFDEI        | DECVENIERS | 960  |
|    | LSVGSEFSSE | LAESACEEKP | NFNFSQPYPE | EEVDEGFEAD | DDAFKDSPNP        | SEHGHSDORT | 1020 |
|    | SGIRTSDDSS | REDPYMNDTV | VPTSPSADST | VLLAPSVQDS | GSLHNSSSGE        | STYCMPONAG | 1080 |
|    |            | YDQDDYEDGA |            |            |                   |            | 1140 |
| 65 |            | DFDSRFDTDD |            |            |                   |            | 1200 |
|    |            | QEALKQGWLH |            |            |                   |            | 1260 |
|    | VEVRTAKEII | DNTTKENGID | IIMADRTFHL | IAESPEDASQ | WFSVLSQVHA        | STDQEIQEMH | 1320 |
|    |            | GTLDVGLIDS |            |            |                   |            | 1380 |
|    |            | QEFIVRGWLH |            |            |                   |            | 1440 |
| 70 |            | VPPDEKIFKE |            |            |                   |            | 1500 |
|    |            | QDIKENCLNS |            |            |                   |            | 1560 |
|    | GYTTLQDEAI | KIFNSLQQLE | SMSDPIPIIQ | GILQTGHDLR | PLRDELYCQL        | IKQTNKVPHP | 1620 |
|    |            | ILTCLSCTFL |            |            |                   |            | 1680 |
|    | CREFVPSRDE | IEALIHRQEM | TSTVYCHGGG | SCKITINSHT | TAGEVVEKLI        | RGLAMEDSRN | 1740 |
| 75 |            | VDKAIESRTV |            |            |                   |            | 1800 |
|    | SVEFAFMFEQ | AHEAVIHGHH | PAPEENLQVL | AALRLQYLQG | DYTLHAAIPP        | LEEVYSLQRL | 1860 |
|    |            |            |            |            |                   |            |      |

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 SVYKRGEGRP LEVFOYEHIL SPGAPLANTY KIVVDERELL FETSEVVDVA KLMKAYISMI 2040
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| -   | CTGCTTCTCA  | CAGGATCTAG | TTCAGGTTCA               | AAATTAAAAG | ATCCTGAACT | GAGTTTAAAA                                           | 360  |
| 5   |             |            |                          |            |            | GGGGGAAGCA                                           | 420  |
|     |             |            | TGAAATGGTG               |            |            |                                                      | 480  |
|     |             |            |                          |            |            | GAACACAGCT                                           | 540  |
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|     | TGCCGGGTTA  | OGTCACCTAA | CATCACTGTT               | ACTTTANAAA | AGTTTCCACT | TGACACTTTG                                           | 780  |
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|     | ACGTACAAAG  | AAATAGGGCT | TCTGACCTGT               | GAAGCAACAG | TCAATGGGCA | TTTGTATAAG                                           | 900  |
|     | ACAAACTATC  | TCACACATCG | ACAAACCAAT               | ACAATCATAG | ATGTCCAAAT | AAGCACACCA                                           | 960  |
| 15  | CGCCCAGTCA  | AATTACTTAG | AGGCCATACT               | CTTGTCCTCA | ATTGTACTGC | TACCACTCCC<br>GAGAGCTTCC                             | 1020 |
|     | TTGAACACGA  | GAGTTCAAAT | GACCTGGAGT               | TACCCTGATG | алалалатаа | GAGAGCTTCC                                           | 1080 |
|     | GTAAGGOGAC  | GAATTGACCA | AAGCAATTCC               | CATGCCAACA | TATTCTACAG | TGTTCTTACT                                           | 1140 |
|     |             |            |                          |            |            | GAGTGGACCA                                           | 1200 |
|     |             |            |                          |            |            | CACTGTGAAA                                           | 1260 |
| 20  |             |            |                          |            |            | GCTCTCTATG                                           | 1320 |
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|     |             |            |                          |            |            | CGTAACTGAA                                           | 1440 |
|     |             |            | AATCTTGCTG               |            |            |                                                      | 1500 |
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| 25  | TTTCCAGACC  | CGGCTCTCTA | CCCACTGGGC               | AGCAGACAAA | TCCTGACTTG | TACCGCATAT                                           | 1620 |
|     | GGTATCCCTC  | AACCTACAAT | CAAGTGGTTC               | TGGCACCCCT | GTAACCATAA | TACCGCATAT<br>TCATTCCGAA                             | 1680 |
|     | GCAAGGTGTG  | ACTITTGTTC | CAATAATGAA               | GAGTCCTTTA | TCCTGGATGC | TGACAGCAAC                                           | 1740 |
|     | ATGGGAAACA  | GAATTGAGAG | CATCACTCAG               | CGCATGGCAA | TAATAGAAGG | AAAGAATAAG                                           | 1800 |
| • • |             |            |                          |            |            | TTGCATAGCT                                           | 1860 |
| 30  |             |            |                          |            |            | TGTGCCAAAT                                           | 1920 |
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|     | ACAGTTAACA  | AGTTCTTATA | CAGAGACGTT               | ACTTGGATTT | TACTGCGGAC | AGTTAATAAC                                           | 2040 |
|     | AGAACAATGC  | ACTACAGTAT | TAGCAAGCAA               | AAAATGGCCA | TCACTAAGGA | GCACTCCATC                                           | 2100 |
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|     |             |            |                          |            |            | CACTATGGAA                                           | 3240 |
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| 55  | ATTTGTGATT  | TTGGCCTTGC | CCGGGATATT               | TATAAGAACC | CCGATTATGT | GAGAAAAGGA                                           | 3420 |
|     | GATACTCGAC  | TTCCTCTGAA | ATGGATGGCT               | CCCGAATCTA | TCTTTGACAA | GAGAAAAGGA<br>AATCTACAGC<br>CTTAGGTGGG               | 3480 |
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 Protein Accession #: CAB43394.1
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 NVSWRYEBOO LEIONSSRFS IYTALFNRMT SVSKLTIHNI TPGDAGEYVC KLILDIFEYE
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 NM 007268
 Coding sequence:
 46-1245 (underlined sequences correspond to start and stop codons)
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70
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10
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 Nucleic Acid Accession #:
 XM 64321
 1-2079 (underlined sequences correspond to start and stop codons)
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 60
 120
25
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 180
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 240
 ATCCGTCAGG AGGATGCCTT TGATAACAAA ATTGACATTG CTGAAGATGG TGGCCAGACA
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70
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 420
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540

600

660

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VSPTHILOSE SAPNHYFPYH VSLSKFLKRK AMSHFLHLCA VVAVRRRSNM PGTRGWGGHK

OKOPCPAKYT PACHAQWETF RKPHVMAQKR GLSGRCRGQQ PPAAPRKVAD RRQQLPGAPG

CSCSQDVYLT GVSGLKASRG FIPHPWVPFG SS

75

|     | Nucleic Acid Accession #: NM 006033 |            |            |            |           |               |            |     |      |         |
|-----|-------------------------------------|------------|------------|------------|-----------|---------------|------------|-----|------|---------|
| 5   | Coding sequ                         | lence:     | 253-1752   | underlined | sequences | correspond to | start      | and | stop | codons) |
|     |                                     |            |            |            |           |               |            |     |      |         |
|     | 1                                   | 11         | 21         | 31         | 41        | 51            |            |     |      |         |
|     |                                     | !          |            | 1          | !         |               | 60         |     |      |         |
| 10  |                                     |            |            |            |           | CTGGGGCAAG    | 120        |     |      |         |
| 10  |                                     |            |            |            |           | TCATTTTCCA    | 180        |     |      |         |
|     |                                     |            |            |            |           | GGCCGGGATT    | 240        |     |      |         |
|     |                                     |            |            |            |           | GGAGGGGGTG    | 300        |     |      |         |
|     |                                     |            |            |            |           | CTGCTATTGC    | 360        |     |      |         |
| 1.5 |                                     |            |            |            |           | TAAGCTCCAC    | 420        |     |      |         |
| 15  |                                     |            |            |            |           | COGCACCTCC    | 480        |     |      |         |
|     |                                     |            |            |            |           | CTTAGAAGAC    | 540        |     |      |         |
|     |                                     |            |            |            |           | GATGAGCGGT    | 600        |     |      |         |
|     |                                     |            |            |            |           | GAAAGACGCC    | 660        |     |      |         |
| 20  |                                     |            |            |            |           | TGCGGTCAAT    | 720        |     |      |         |
| 20  |                                     |            |            |            |           | GGAGAAGGAC    |            |     |      |         |
|     |                                     |            |            |            |           | A CGTGGCCGGG  | 780<br>840 |     |      |         |
|     |                                     |            |            |            |           | TCCTGCCGGG    |            |     |      |         |
|     |                                     |            |            |            |           | AGATTTTGTG    | 900        |     |      |         |
| 0.5 |                                     |            |            |            |           | AGATGCCTGTG   | 960        |     |      |         |
| 25  |                                     |            |            |            |           | ACTCAACGAT    | 1020       |     |      |         |
|     |                                     |            |            |            |           | A GCATGAGCGA  | 1080       |     |      |         |
|     |                                     |            |            |            |           | TGCCTTCCAG    | 1140       |     |      |         |
|     |                                     |            |            |            |           | A GAACCGTTGT  | 1200       |     |      |         |
| 20  |                                     |            |            |            |           | AATGTACCTA    | 1260       |     |      |         |
| 30  |                                     |            |            |            |           | CCATGTCTTC    | 1320       |     |      |         |
|     |                                     |            |            |            |           | A TGGCACTAAT  | 1380       |     |      |         |
|     |                                     |            |            |            |           | A TGCCACCAAC  | 1440       |     |      |         |
| 35  |                                     |            |            |            |           | A GCTCACCTGG  | 1500       |     |      |         |
|     |                                     |            |            |            |           | A CCTGTCTCAA  | 1560       |     |      |         |
|     |                                     |            |            |            |           | TGGGGAAACC    | 1620       |     |      |         |
|     |                                     |            |            |            |           | CCCAGGCCGG    | 1680       |     |      |         |
|     |                                     |            |            |            |           | CAGTCCCACT    | 1740       |     |      |         |
|     |                                     |            |            |            |           | A GACTTCCTGC  | 1800       |     |      |         |
|     |                                     |            |            |            |           | GATTCTTCTC    | 1860       |     |      |         |
| 40  | AGCCTTGACC                          | CTGGAGCACT | GGGAACAACT | GGTCTCCTGT | GATGGCTGG | ACTCCTCGCG    | 1920       |     |      |         |
|     |                                     |            |            |            |           |               |            |     |      |         |

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Seq ID NO: 228 DNA sequence

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50

55

60

Protein Accession #: NP\_006024.1

|     | 1          | 11         | 21         | 31         | 41         | 51         |     |
|-----|------------|------------|------------|------------|------------|------------|-----|
| -   | 1          | 1          | 1          | 1          | 1          | 1          |     |
| 5   | MSNSVPLLCF | WSLCYCFAAG | SPVPFGPEGR | LEDKLHKPKA | TOTEVKPSVR | FNLRTSKDPE | 60  |
|     | HECCATEAGH | SOPLEDCSFN | MTAKTFFIIH | GWTMSGIFEN | WIHKLVSALH | TREKDANVVV | 120 |
|     | VDWLPLAHQL | YTDAVNNTRV | VGHSIARMLD | WLQEKDDFSL | GNVHLIGYSL | GAHVAGYAGN | 180 |
|     | FVKGTVGRIT | GLDPAGPMFE | GADIHKRLSP | DDADFVDVLH | TYTRSFGLSI | GIOMPVCHID | 240 |
| 1.0 |            |            |            | KCEHERAVHL |            |            | 300 |
| 10  | NRFKKGICLS | CRKNRCNSIG | YNAKKMRNKR | NSKMYLKTRA | GMPFRVYHYO | MKIHVYSYKN | 360 |
|     | MGEIEPTFYV | TLYGTNADSQ | TLPLEIVERI | EQNATNTFLV | YTERDLGDLL | KIOLTWEGAS | 420 |
|     |            |            | GRELWIRRIR | VKSGETQRKL | TECTEDPENT | SISPGRELWF | 480 |
|     | RKCRDGWRMK | NETSPTVELP |            |            |            |            |     |

It is understood that the examples described above in no way serve to limit the true scope of this invention, but rather are presented for illustrative purposes. All publications, sequences of accession numbers, and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

5

# WHAT IS CLAIMED IS:

1

14.

1. 1 A method of detecting an angiogenesis-associated transcript in a cell in 2 a patient, the method comprising contacting a biological sample from the patient with a 3 polynucleotide that selectively hybridized to a sequence at least 80% identical to a sequence 4 as shown in Tables 1-8. 1 2. The method of claim 1, wherein the biological sample is a tissue 2 sample. 1 3. The method of claim 1, wherein the biological sample comprises 2 isolated nucleic acids. 1 4. The method of claim 3, wherein the nucleic acids are mRNA. 1 5. The method of claim 3, further comprising the step of amplifying 2 nucleic acids before the step of contacting the biological sample with the polynucleotide. 1 6. The method of claim 1, wherein the polynucleotide comprises a 2 sequence as shown in Tables 1-8. 1 7. The method of claim 1, wherein the polynucleotide is labeled. The method of claim 7, wherein the label is a fluorescent label. 1 8. 9. 1 The method of claim 1, wherein the polynucleotide is immobilized on 2 a solid surface. 1 10. The method of claim 1, wherein the patient is undergoing a therapeutic 2 regimen to treat a disease associated with angiongenesis. The method of claim 1, wherein the patient is suspected of having 1 11. 2 cancer. 1 12 An isolated nucleic acid molecule consisting of a polynucleotide 2 sequence as shown in Tables 1-8. 1 13. The nucleic acid molecule of claim 12, which is labeled.

The nucleic acid of claim 13, wherein the label is a fluorescent label

| 1      | 15.                                                                  | An expression vector comprising the nucleic acid of claim 12.                                                                                                                     |  |  |  |  |
|--------|----------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|--|--|--|
| 1      | 16.                                                                  | A host cell comprising the expression vector of claim 15.                                                                                                                         |  |  |  |  |
| 1 2    | 17.                                                                  | An isolated polypeptide which is encoded by a nucleic acid molecule te sequence as shown in Tables 1-8 $$                                                                         |  |  |  |  |
| 1      | 18.                                                                  | An antibody that specifically binds a polypeptide of claim 17.                                                                                                                    |  |  |  |  |
| .1     | 19.                                                                  | The antibody of claim 18, further conjugated or fused to an effector                                                                                                              |  |  |  |  |
| 1<br>2 | 20. fluorescent label.                                               | The antibody of claim 19, wherein the effector component is a                                                                                                                     |  |  |  |  |
| 1 2    | 21. radioisotope.                                                    | The antibody of claim 19, wherein the effector component is a                                                                                                                     |  |  |  |  |
| 1      | 22.                                                                  | The antibody of claim 19, which is an antibody fragment.                                                                                                                          |  |  |  |  |
| 1      | 23.                                                                  | The antibody of claim 19, which is a humanized antibody                                                                                                                           |  |  |  |  |
| 1 2    | 24.                                                                  | A method of detecting a cell undergoing angiogenesis in a biological at, the method comprising contacting the biological sample with an                                           |  |  |  |  |
| 3      | antibody of claim 18.                                                |                                                                                                                                                                                   |  |  |  |  |
| 1 2    | 25. fused to an effector of                                          | The method of claim 24, wherein the antibody is further conjugated or component.                                                                                                  |  |  |  |  |
| 1 2    | 26. fluorescent label.                                               | The method of claim 25, wherein the effector component is a                                                                                                                       |  |  |  |  |
| 1 2 3  |                                                                      | The method of detecting antibodies specific to angiogenesis in a comprising contacting a biological sample from the patient with a conceded by a well-stide segment of Tables 1.8 |  |  |  |  |
| ,      | polypeptide which is encoded by a nucleotide sequence of Tables 1-8. |                                                                                                                                                                                   |  |  |  |  |